



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96453

TO: Michael Pak
Location: cm1/10e18/10d19
Art Unit: 1646
Friday, June 20, 2003
Case Serial Number: 825147

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Pak,

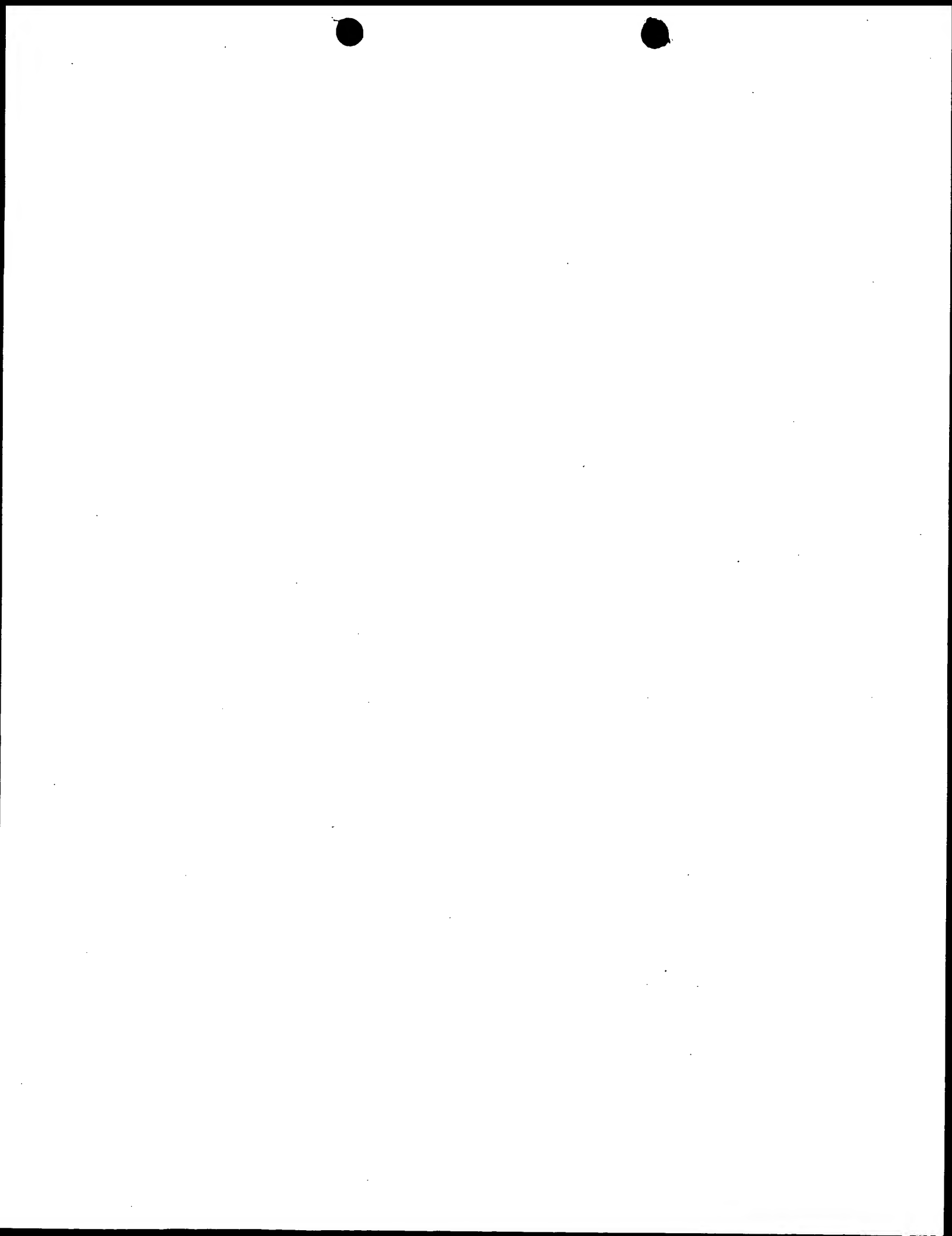
See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954





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OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:31 ; Search time 26 Seconds
(without alignments)
1044.514 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHHAGEEGSGAAGLVKVS.....SICKAGESTDALSLPHVLLK 923

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

Issued Patents -AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1792.5	37.9	722	US-09-105-058C-23	Sequence 23, Appl
2	1789.5	37.8	930	US-09-177-650-96	Sequence 96, Appl
3	1788.5	37.8	871	US-09-105-058C-20	Sequence 20, Appl
4	1784	37.7	872	US-09-177-650-2	Sequence 2, Appl
5	1761	37.2	757	US-09-177-650-89	Sequence 89, Appl
6	1620.5	34.2	872	US-09-177-650-7	Sequence 7, Appl
7	1603.5	33.9	854	US-09-105-058C-27	Sequence 27, Appl
8	1570.5	33.2	870	US-09-177-650-91	Sequence 91, Appl
9	1207.5	25.5	300	US-09-105-058C-4	Sequence 4, Appl
10	1207.5	25.5	300	US-09-105-058C-6	Sequence 6, Appl
11	1188	25.1	807	US-09-177-650-3	Sequence 3, Appl
12	1102	23.3	676	US-09-135-021-2	Sequence 2, Appl
13	1102	23.3	676	US-09-135-020-2	Sequence 2, Appl
14	1102	23.3	676	US-09-135-010A-2	Sequence 2, Appl
15	1102	23.3	676	US-09-444-871-2	Sequence 2, Appl
16	1102	23.3	676	US-09-634-920-2	Sequence 2, Appl
17	1102	23.3	676	US-09-597-735-2	Sequence 2, Appl
18	1102	23.3	676	US-09-444-295-2	Sequence 2, Appl
19	1102	23.3	676	US-09-597-732-2	Sequence 2, Appl
20	1100.5	23.3	605	US-09-105-058C-24	Sequence 24, Appl
21	1092.5	23.1	677	US-09-177-650-4	Sequence 4, Appl
22	1091.5	23.1	581	US-09-135-021-80	Sequence 80, Appl
23	1091.5	23.1	581	US-09-135-010A-116	Sequence 116, App
24	1091.5	23.1	581	US-09-597-735-116	Sequence 116, App
25	1091.5	23.1	581	US-09-597-732-116	Sequence 116, App
26	1085	22.9	310	US-09-105-058C-18	Sequence 18, Appl
27	1081.5	22.9	570	US-09-135-020-114	Sequence 114, Appl

28	1081.5	22.9	570	US-09-135-010A-114	Sequence 114, App
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34	957	20.2	298	US-09-105-058C-2	Sequence 2, Appl
35	905.5	19.1	430	US-09-105-058C-21	Sequence 21, Appl
36	898.5	19.0	376	US-09-135-020-113	Sequence 113, App
37	898.5	19.0	376	US-09-135-010A-113	Sequence 113, App
38	898.5	19.0	376	US-09-444-871-113	Sequence 113, App
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42	485.5	10.3	137	US-09-135-020-109	Sequence 109, App
43	485.5	10.3	137	US-09-135-010A-109	Sequence 109, App
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46	485.5	10.3	137	US-09-444-295-109	Sequence 109, App
47	485.5	10.3	137	US-09-597-732-109	Sequence 109, App
48	250	5.3	539	US-08-464-340A-13	Sequence 13, Appl
49	245	5.2	646	US-09-336-643A-10	Sequence 10, Appl
50	243	5.1	601	US-09-336-643A-4	Sequence 4, Appl
51	234	4.9	283	US-09-135-021-6	Sequence 6, Appl
52	232.5	4.9	655	US-09-142-791A-4	Sequence 4, Appl
53	232.5	4.9	655	US-09-178-109-2	Sequence 2, Appl
54	232	4.9	528	US-08-527-152-2	Sequence 2, Appl
55	229	4.8	636	US-09-142-791A-2	Sequence 2, Appl
56	229	4.8	636	US-09-142-791A-6	Sequence 6, Appl
57	229	4.8	636	US-09-178-109-4	Sequence 4, Appl
58	224	4.7	477	US-09-336-643A-18	Sequence 18, Appl
59	223	4.7	499	US-09-336-643A-8	Sequence 8, Appl
60	209.5	4.4	532	US-08-288-405A-10	Sequence 10, Appl
61	206.5	4.4	494	US-08-464-340A-4	Sequence 4, Appl
62	206.5	4.4	494	PCT-US94-08449A-4	Sequence 4, Appl
63	204.5	4.3	490	US-09-336-643A-6	Sequence 6, Appl
64	199.5	4.2	513	US-08-464-340A-2	Sequence 2, Appl
65	199.5	4.2	513	PCT-US94-08449A-2	Sequence 2, Appl
66	174	3.7	61	US-09-135-020-108	Sequence 108, App
67	174	3.7	61	US-09-135-010A-108	Sequence 108, App
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73	153	3.2	120	US-09-105-058C-28	Sequence 28, Appl
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75	141	3.0	2161	US-08-455-543A-49	Sequence 49, Appl
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77	141	3.0	2161	US-08-311-363-2	Sequence 2, Appl
78	141	3.0	2516	US-08-374-077C-2	Sequence 2, Appl
79	141	3.0	2516	US-08-895-590-2	Sequence 2, Appl
80	141	3.0	2516	US-09-539-879A-2	Sequence 2, Appl
81	141	3.0	2516	US-08-984-709A-50	Sequence 50, Appl
82	137.5	2.9	2353	US-08-455-543A-51	Sequence 51, Appl
83	137	2.9	2161	US-08-223-305C-51	Sequence 51, Appl
84	137	2.9	2161	US-08-384-302A-17	Sequence 17, Appl
85	135	2.9	90	US-09-243-675-5	Sequence 5, Appl
86	133	2.8	67	US-09-243-675-6	Sequence 6, Appl
87	133	2.8	67	US-09-404-650-5	Sequence 5, Appl
88	133	2.8	1835	US-09-268-163-10	Sequence 10, Appl
89	132.5	2.8	2336	US-09-135-020-112	Sequence 112, App
90	130	2.7	58	US-09-135-010A-112	Sequence 112, App
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96	129.5	2.7	75	US-09-105-058C-10	Sequence 10, Appl
97	129	2.7	2337	US-08-713-118-2	Sequence 2, Appl
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100	127	2.7	67	US-09-243-675-7	Sequence 7, Appl

101	127	2.7	67	4	US-09-243-675-8	Sequence 8, Appl 1
102	126.5	2.7	1872	6	5386025-6	Patent No. 5386025
103	126	2.7	68	4	US-09-243-675-3	Sequence 3, Appl 1
104	126	2.7	75	4	US-09-243-675-1	Sequence 1, Appl 1
105	126	2.7	510	2	US-09-021-323-1	Sequence 1, Appl 1
106	126	2.7	1873	1	US-08-336-257A-7	Sequence 7, Appl 1
107	126	2.7	2265	2	US-08-149-097D-36	Sequence 36, Appl 1
108	126	2.7	2509	2	US-08-149-097D-35	Sequence 35, Appl 1
109	125.5	2.7	897	3	US-08-975-703-6	Sequence 6, Appl 1
110	125.5	2.7	897	3	US-09-515-884-6	Sequence 6, Appl 1
111	125.5	2.7	1284	4	US-09-343-494-9	Sequence 9, Appl 1
112	125.5	2.7	2756	1	US-08-375-709-11	Sequence 11, Appl 1
113	125.5	2.7	2756	1	US-08-752-929-11	Sequence 11, Appl 1
114	125.5	2.7	2756	1	US-09-090-793-7	Sequence 7, Appl 1
115	125	2.6	67	4	US-09-243-675-4	Sequence 4, Appl 1
116	125	2.6	2339	1	US-08-455-543A-47	Sequence 47, Appl 1
117	125	2.6	2339	2	US-08-223-305C-47	Sequence 47, Appl 1
118	125	2.6	2339	4	US-09-268-163-6	Sequence 6, Appl 1
119	125	2.6	2343	4	US-09-268-163-4	Sequence 4, Appl 1
120	124	2.6	703	4	US-08-910-925-4	Sequence 4, Appl 1
121	123.5	2.6	1984	3	US-08-836-325-10	Sequence 10, Appl 1
122	122.5	2.6	2175	4	US-09-404-650-2	Sequence 2, Appl 1
123	122.5	2.6	2188	4	US-09-404-650-4	Sequence 4, Appl 1
124	122	2.6	3969	4	US-08-061-376-5	Sequence 5, Appl 1
125	121.5	2.6	2237	1	US-08-455-543A-48	Sequence 48, Appl 1
126	121.5	2.6	2237	4	US-08-223-305C-48	Sequence 48, Appl 1
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131	119.5	2.5	921	2	US-08-646-715-2	Sequence 2, Appl 1
132	119.5	2.5	1159	2	US-08-956-242-13	Sequence 13, Appl 1
133	119.5	2.5	1159	4	US-09-351-215-13	Sequence 13, Appl 1
134	119.5	2.5	1159	4	US-09-226-012-2	Sequence 2, Appl 1
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137	116	2.5	59	4	US-09-384-302A-16	Sequence 16, Appl 1
138	116	2.5	1315	3	US-08-899-595-3	Sequence 3, Appl 1
139	116	2.5	1989	3	US-08-836-325-12	Sequence 12, Appl 1
140	116	2.5	2273	4	US-09-426-998-5	Sequence 5, Appl 1
141	115	2.4	1170	4	US-09-749-588-2	Sequence 2, Appl 1
142	114.5	2.4	586	4	US-09-643-597-152	Sequence 152, Appl 1
143	114.5	2.4	1248	2	US-09-080-897-2	Sequence 2, Appl 1
144	114.5	2.4	1248	4	US-09-323-735-2	Sequence 2, Appl 1
145	113.5	2.4	823	1	US-07-745-206A-15	Sequence 15, Appl 1
146	113.5	2.4	823	2	US-08-311-363-15	Sequence 15, Appl 1
147	113.5	2.4	1754	1	US-07-745-206A-13	Sequence 13, Appl 1
148	113.5	2.4	1754	2	US-08-311-363-13	Sequence 13, Appl 1
149	112	2.4	907	3	US-08-938-830-26	Sequence 26, Appl 1
150	112	2.4	907	3	US-09-020-222-26	Sequence 26, Appl 1

ALIGNMENTS

RESULT 1

US-09-105-058C-23

Sequence 23, Application US/09105058C

Patent No. 6403360

GENERAL INFORMATION:

APPLICANT: Blannar, Michael A.

APPLICANT: Dworetzky, Steven

APPLICANT: Gribkoff, Valentin K.

APPLICANT: Levesque, Paul C.

APPLICANT: Little, Wayne A.

APPLICANT: Neubauer, Michael G.

APPLICANT: Yang, Wen-Pin

TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: 3053-4052

CURRENT APPLICATION NUMBER: US/09/105,058C

CURRENT FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

PRIOR FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 23

LENGTH: 722

TYPE: PRT

ORGANISM: mouse

US-09-105-058C-23

Query Match

Best Local Similarity 37.9%; Score 1792.5; DB 4; Length 722;

Best Similarity 53.4%; Pred. No. 8.8e-151;

Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;

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DB	9	GYPPTSGEKKLVGFVGLDPGA-----PDSTDGALLIGSEAPK---RSTVLSKPT	59
QY	81	GKQAGMRLSGKPLDYTSOSSCRNRVYRQNTLYNLEPRGNAFYHAFVLLFGC	140
DB	60	GGAGA-----GK-----PKRNATYKQNTLYNLEPRGNAFYHAFVLLFVSC	106
QY	141	LILSVSTPEHTKLASSCLLIEFWIVGFLEFIRMSAGCCCRYGMRGLRFAK	200
DB	107	LVLVSSTLKEKSESGALYILEIYIVGFVEFYFVMAAGCCCRYRGNRGLRFAK	166
QY	201	PCFVIDITVLASIAVSAKTOGNIFFATSLRSLRFLQILMVRMDRGGTKLGSVY	260
DB	167	PCFVIDITVLASIAVSAKTOGNIFFATSLRSLRFLQILMVRMDRGGTKLGSVY	226
QY	261	ANSKELITAMYIGFLVIFSSFLVLYVEKDNKESTYADALMWTITLTIGYDKTPL	320
DB	227	ANSKELITAMYIGFLVIFSSFLVLYVEKDNKESTYADALMWTITLTIGYDKTPO	286
QY	321	TWGLRLSGFALGTSFPLPAGLIGSGFALKVQEDHROHFEKRRPANALOCVRS	380
DB	287	TWGLRLSFTLIGVSEFALPAGLIGSGFALKVQEDHROHFEKRRPANALOCVRS	346
QY	381	VAAD-----EKSVSIAATWK--PHLKALHTC-----SPT	406
DB	347	YATNLSRTDLHSTWQYERTVTVPMRLPPLNGLELRLNLSKSGLFRKEPPEP	405
QY	407	NOKLSKEVRYRASPGQSIKSQASVGD--RNSPSTIDTAEGSPYKQKMSFENDRTF	464
DB	406	SKQVSLKDRV--FSSPGMAKSGSPQAGTVRSPASDOSLDDSPKPKSMSFGDRST	464
QY	465	RSRLKSSQPKVIDADTALGTDVYDEKGCODVSEDLTPPLKYTRIRLIMKEFVA	524
DB	465	RSRLKSSQPKVIDADTALGTDVYDEKGCODVSEDLTPPLKYTRIRLIMKEFVA	524
QY	525	KRFEKTLRPYDVYKIEQYSAGHLDMLCRKISLQTRVDDILGKQITSDKRSREKITA	584
DB	524	KRFEKTLRPYDVYKIEQYSAGHLDMLCRKISLQTRVDDILGKQITSDKRSREKITA	584
QY	585	HTTDDLSMLGRVAVYKQVQSTIESKLDLDLYOVLKRGASALALASFOIPPEEC	642
DB	583	TELPEDPSMGRIGKQVLSMEKRLDPLVSTYTO--RMG-----IPAEFEA	629
QY	643	-----PDTSYQSPVDSKDLGSAQNSGC-----LSRSTANISRGQITLTPNEFSQOT	692
DB	630	YFGAKEPEPAPRYHSPEDSRD---HADKHCILIKIVASTS-----TGOR	671
QY	693	FYALSPTMHSQATQVAPISQS 712	
DB	672	NYAAPPAI--PPAQCPPTS 689	

RESULT 2

US-09-177-650-96

Sequence 96, Application US/09177650

Patent No. 6413719

GENERAL INFORMATION:

APPLICANT: Iepert, Mark F.

APPLICANT: Slugh, Nanda

APPLICANT: Charlier, Carole

```

; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 96
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-177-650-96

Query Match      37.8%; Score 1789.5; DB 4; Length 930;
Best Local Similarity 43.9%; Pred. No. 2,5e-150;
Matches 433; Conservative 109; Mismatches 246; Indels 199; Gaps 26;

QY 21 GAAAAAGGRLSGMDVSGRGRVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
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QY 81 GKGARMSLLGKPLSTYSOSCRNRVRYRQNYLYNLEBRGNAFYHAFFLLVEGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFYVLEBRGNAFYHAFFLLVEGC 106
QY 141 LILSVFTIPHTKLASSCLLLEFVMTVGFLEFIIRWSAGCCCRYGWGRLEFARK 200
DB 107 LVLSVFSTIKYEKSESEALYILETVTVGVGEYFVRIMAGCCCRYGWGRLEFARK 166
QY 201 PCFYIDTVLTAIAVSAKQGNIFATSLRSLRFLQILIRMRDRGRTKLLGSVY 260
DB 167 PCFYIDTVLTAIAVSAKQGNIFATSLRSLRFLQILIRMRDRGRTKLLGSVY 226
QY 261 AHSKELTAWYIGLVLFSSFLVYLVKEDANKKESTYADALMWGTLITTTGYGDKTPL 320
DB 227 AHSKELTAWYIGLVLFSSFLVYLVKEDANKKESTYADALMWGTLITTTGYGDKTPL 286
QY 321 TWLGRLLSAGPALLGISFFALPAGILGSGFALKVQDQHRQKFEKRRNPAANLIQCVMS 380
DB 287 TWNGRLAATPTLLIGVSEFALPAGILGSGFALKVQDQHRQKFEKRRNPAANLIQCVMS 346
QY 381 YAAD-----EKSVSIATWK-----PHKALHT----- 402
DB 347 YATNLSRDLHSTWQYERTVTPMYSOTQTYGASRLPLPNOLELLNLNLSKSLAR 406
QY 403 -----CSP-----TNOKLSFKERVRMASPRGOSIKSROASVGD--RR 437
DB 407 KDPPEPSPKSGPCRGPLCGCCPGRSSQKVSILKDRV--ESSPRGVAAGKGSPOACTVRR 465
QY 438 SPSIDITAESEPTKYQKSMSPNDTRFRPSLFLKSSQRPVIDADPALTDDVYDEKGCQ 497
DB 466 SPSADQSLSEDSKPKVMSFGRSRAQAFRIKGAASQNSE--EASLGEDVIDDQSCP 524
QY 498 CDVASEDTPLPLKTVIRAIRIMKFFHAKKFEKTLRPYVKDYIDEOYSAGHDLMLRIKS 557
DB 525 CEPTEDITPLGLKSTRVAVKRVKSKRKESLRLPYVMQVYIDEOYSAGHDLMLRIKS 584
QY 558 LQTRVQDILGKQGITSDKRSREKITAHEHTTDLMSLGNVYKQVOSIESKLDCLLDI 617
DB 585 LQSRVQDILGKQGITSDKRSREKITAHEHTTDLMSLGNVYKQVOSIESKLDCLLDI 643
QY 618 YQOVLKRSASALALASFOIPEPEC-----EOTSQYQSPVDSKDLGSGNQNSCLS 668
DB 644 YMO-----RMG-----IPPETEAVFGAKEPEAPYHSPEDSRE---HYDRGCIIV 687
QY 669 RSTSANIRGLQFILTPNEFSAQTFFALSPTMHSQATQVPIQSODSASAVATNTIANQIN 728
DB 668 KIVRSSSSSG----- 700
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DB 701 FSAPPAAP-PLYQPPSTWQPOSHPRGCHTSPVGDHSLVRIIPPAHERSLSATYGGGN 759
QY 776 VASKENVOYAOASULTK--DRSMKSPFMGEFTLLSVCPMPKDKGLSLVQNLIRSEEL 833
DB 760 RASMEFLROEDTGRCPREPCNLDS-----DTSISIPVHEELERSFSFSISQSENL 814
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RESULT 3
US-09-105-058C-20
; Sequence 20, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blannet, Michael A.
; APPLICANT: Dwojletzky, Steven
; APPLICANT: Gribkoft, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-105-058C-20

Query Match      37.8%; Score 1788.5; DB 4; Length 871;
Best Local Similarity 46.8%; Pred. No. 2,8e-150;
Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAAAGGRLSGMDVSGRGRVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLVGFVGLDPA-----PDSTRGALLIAGSEAPK---RGSILSKPRA 59
QY 81 GKGARMSLLGKPLSTYSOSCRNRVRYRQNYLYNLEBRGNAFYHAFFLLVEGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFYVLEBRGNAFYHAFFLLVEGC 106
QY 141 LILSVFTIPHTKLASSCLLLEFVMTVGFLEFIIRWSAGCCCRYGWGRLEFARK 200
DB 107 LVLSVFSTIKYEKSESEALYILETVTVGVGEYFVRIMAGCCCRYGWGRLEFARK 166
QY 201 PCFYIDTVLTAIAVSAKQGNIFATSLRSLRFLQILIRMRDRGRTKLLGSVY 260
DB 167 PCFYIDTVLTAIAVSAKQGNIFATSLRSLRFLQILIRMRDRGRTKLLGSVY 226
QY 261 AHSKELTAWYIGLVLFSSFLVYLVKEDANKKESTYADALMWGTLITTTGYGDKTPL 320
DB 227 AHSKELTAWYIGLVLFSSFLVYLVKEDANKKESTYADALMWGTLITTTGYGDKTPL 286
QY 321 TWLGRLLSAGPALLGISFFALPAGILGSGFALKVQDQHRQKFEKRRNPAANLIQCVMS 380
DB 287 TWNGRLAATPTLLIGVSEFALPAGILGSGFALKVQDQHRQKFEKRRNPAANLIQCVMS 346
QY 381 YAAD-----EKSVSIATWK-----PHKALHT----- 402
DB 347 YATNLSRDLHSTWQYERTVTPMYSOTQTYGASRLPLPNOLELLNLNLSKSLAR 406

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QY 403 -----CSP--TNOKLSEKERYMASPRGOSIKSROASVGD--RR 437
Db 407 KDPPEPSPKSGPCRCPLGCGCGRRSSQKVSILKDRV-FSSPRGVAAKGKSPQAQVYR 465
QY 438 SPSDITAGSPTKQKVSFNDRTFRPSLRKSSOPKPYIDADTALGTDVYDEKGCQ 497
Db 466 SPSADQSLDSSPKVKPSWFSGDRSRARQAFRIKGAASRQ--NSEASLPGEDIYDCKSCP 523
QY 498 CDVSVEDLTPPLKTVIRAIRIKKFKETLRPYDYKDYEOYSAGHDMLCRTKS 557
Db 524 CEFTVEDLTPGLKVSIRAVCVHFLVSKKFKESLRYDMVDYEOYSAGHDMLSRTKS 583
QY 558 LQTRVDQILGQOITSDDKSREKITAHEHTDDLSMLGRVYKVKOVOSIESKLDCLDI 617
Db 584 LOSRVDQIVGRPAITD-KDRTKGAPEALPEDPSSMMGRGLGKVEKQVLSMEKKLDPLVNI 642
QY 618 YOOVLKSGASALALASFOIPPEC-----EOTSQSPVDSKDLSSAONSGCLS 668
Db 643 YMO--RMG-----IPTEYAGANEPEAPPHSPDSRE--HVDHRCIV 686
QY 669 RSTSANISRGLOFILTPNEFSQOTFYALSPTHMSQATQVPISSQ-----DGSAAVAT 720
Db 687 KIVRSSSSGTG-----QKNFSAP--AAP-----VQCPSTSMQOSHPRQCHGTSVPV 732
QY 721 NTINQINTAPKPAAPTTLOI-----PP-----PLPAI 748
Db 733 GDHGLVIRIPPPAHERSLAYGCGNRASMEFLROEDTPCGRPEGLRDSSTISIPSV 792
QY 749 KHLPRPETHHPNAGLOESISDVTTCVASKENVOVAQS 787
Db 793 DH-----EELERSFSGF--SISO-----SKENLDALNS 818

RESULT 4
US-09-177-650-2
; Sequence 2, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Lepeert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCMO2 AND KCMO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 872
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-650-2

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Query Match 37.7%; Score 1784; DB 4; Length 872;
Best Local Similarity 46.8%; Pred. No. 7e-150;
Matches 411; Conservative 92; Mismatches 196; Indels 180; Gaps 25;

QY 21 GAAAAAAGGRLSGMKGMDVESGRRVILNSAARGDGLILCTRAATLGGGGGGLRESRR 80
Db 9 GYVPGSGEKKLVGVGLDPGA-----PDSTRDGLALLIGSEAPK--RGSILSKPRA 59
QY 81 GKGARSLGKPLSTYSSOSCRNVYRRYONILYANLERGRGAFIYHAFVFLVFLPGC 140
Db 60 GGGA-----GKP-----PKNARYKRLQNLNLYNLERGRGAFIYHAFVFLVFLVSC 106
QY 141 LILSVSTPEHTKLASSCLLIEFVMIIVGLEFIIRIWSAGCCRYRGRLFAFK 200
Db 107 LVLSVSTIKEYEKSSGALYILEITVIVGVEYFVIRIMAGCCCRIRGMGRKLFARK 166

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QY 201 PCQVIDITVILASIAVSATQGNIPATSAIRSLRFLDILKRVNDRRGCTKLLGSVY 260
Db 167 PCQVIDITVILASIAVLAASQGNVFAISALRSRLFLDILRIRBDRRGCTKLLGSVY 226
QY 261 AHSKELITANYIGFLVYIFSSFLVYVEKDNKESTYADALAMWGTITLTGTYGDKPL 320
Db 227 AHSKELITANYIGFLCILASFLVYLAKEGNDHFDYADALAMGLITLTITGTYGDKTPQ 286
QY 321 TWIGRLISAGFALLGISFFALLPAGILGSGFALKVOEORHOFKERRRNPANLTOCWRS 380
Db 287 TWNGRLIAAFTLLIGVSFFALLPAGILGSGFALKVOEORHOFKERRRNPAGLIGSAWRF 346
QY 381 YAAD-----EKVSITATWK-----PLKALHT-----402
Db 347 YATNLSRTDLHSTWQYERTVYPMYSSQOTYASRLIPLNDELRLNLSKSGLAER 406
QY 403 -----CSP--TNOKLSEKERYMASPRGOSIKSROASVGD--RR 437
Db 407 KDPPEPSPKSGPCRCPLGCGCGRRSSQKVSILKDRV-FSSPRGVAAKGKSPQAQVYR 465
QY 438 SPSDITAGSPTKQKVSFNDRTFRPSLRKSSOPKPYIDADTALGTDVYDEKGCQ 497
Db 466 SPSADQSLDSSPKVKPSWFSGDRSRARQAFRIKGAASRQNSE-EASLPGEDIYDCKSCP 524
QY 498 CDVSVEDLTPPLKTVIRAIRIKKFKETLRPYDYKDYEOYSAGHDMLCRTKS 557
Db 525 CEFTVEDLTPGLKVSIRAVCVHFLVSKKFKESLRYDMVDYEOYSAGHDMLSRTKS 584
QY 558 LQTRVDQILGQOITSDDKSREKITAHEHTDDLSMLGRVYKVKOVOSIESKLDCLDI 617
Db 585 LOSRVDQIVGRPAITD-KDRTKGAPEALPEDPSSMMGRGLGKVEKQVLSMEKKLDPLVNI 643
QY 618 YOOVLKSGASALALASFOIPPEC-----EOTSQSPVDSKDLSSAONSGCLS 668
Db 644 YMO--RMG-----IPTEYAGANEPEAPPHSPDSRE--HVDHRCIV 687
QY 669 RSTSANISRGLOFILTPNEFSQOTFYALSPTHMSQATQVPISSQ-----DGSAAVAT 720
Db 688 KIVRSSSSGTG-----QKNFSAP--AAP-----VQCPSTSMQOSHPRQCHGTSVPV 733
QY 721 NTINQINTAPKPAAPTTLOI-----PP-----PLPAI 748
Db 734 GDHGLVIRIPPPAHERSLAYGCGNRASMEFLROEDTPCGRPEGLRDSSTISIPSV 793
QY 749 KHLPRPETHHPNAGLOESISDVTTCVASKENVOVAQS 787
Db 794 DH-----EELERSFSGF--SISO-----SKENLDALNS 819

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RESULT 5
US-09-177-650-89
; Sequence 89, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Lepeert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCMO2 AND KCMO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-650-89

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Query Match 37.2%; Score 1761; DB 4; Length 757;

Best Local Similarity 51.8%; Pred. No. 6.2e-148; Matches 395; Conservative 77; Mismatches 200; Indels 90; Gaps 18;

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21 GAAAAAGGRLGSGKDVESGRVLLNSAARGDILLGTGTAATLGGGGGGLRESRR 80
9 GYVPGTSGEXKLLKGVGVGLDRG-----XPSITDGLLLLAGSAPK---RGXLLSKRT 59
81 GKQAGAMSLGKPLSTSSQSCRNVKRVQNTLVNLEPRGMATYAAFPVLLVFGC 140
60 GGAGX-----GKPKX-----RMAFYRLQNLVNVLEPRGXAFYHAYVFLVYFSC 106
141 LILVSTIPEHKLASSCLLLEFVIYVGFLEFIRIMAGCCCRGMRGQRLRFARK 200
107 LVLSVSTIKEYKSSGALYILEYTVVGFVYFVIMAGCCCRGMRGKRFARK 166
201 PFCVIDIYLIASIAVAVSAKTQGNIFATSLRSLRFLQILRMVMDRGTWKLIGSVY 260
167 PFCVIDIYLIASIAVAVSAKTQGNIFATSLRSLRFLQILRMVMDRGTWKLIGSVY 226
261 ASKELITAMTIGFLVLISSFLVYVLEKANKFEFTYADALMNGTITLTITIGYDKTP 320
227 ASKELITAMTIGFLVLISSFLVYVLEKANKFEFTYADALMNGTITLTITIGYDKTP 286
321 TWIGRLISAGFALLGISFALLPAGILGSGFALKVOEGRHOKHFEKRRNPAANLIQVMS 380
287 TWIGRLISAGFALLGISFALLPAGILGSGFALKVOEGRHOKHFEKRRNPAANLIQVMS 346
381 YAADEKSVSI-ATWK-----PHLKALHTCSPTNOK--LSFK 413
347 YATNLSTRTDHSITWQYEXTVYVPMYSSQITQYASRLIPPLNOLELLRNLSKSGLETR 406
414 ENRR-----MASPPROSIKRSQASVD--RRSPSTDIAGSPSTKQKSMSPNDRTFRSL 468
407 KEPQPEPSPRGAAAGKSPQAOYVRSPSADQSLDSSPKVPSFSGRSKTRQAF 466
469 RLKSGRPVYIADTALGTDDVYDEKGCQCDVSEDLTPPLKTVIRAIRIMFHAARKRF 528
467 RINGAAROMSESLRGEDEVENKSCNCEFYEDLPLGLKXSRVACXMMFLYSKRF 526
529 KETLRPYDKVADIEQYASGHLMLCRISLQTRVDQILGKQITSDKRSREKITAHEHTT 588
527 KESLRPYDKVADIEQYASGHLMLCRISLQTRVDQILGKQITSDKRSREKITAHEHTT 585
589 DDLMLGRVAVKVEQVOSIESKLDCLDIYQOVLKKSASALALSFOIPEECQTSY 648
586 EDPBMMGRIGKVEQVLSMEKKLDFLVSITQ--RMGIQPAETEAFFGAK--EPEAPPY 641
649 QSPVDSKDLGSAQNSGC---LSRSTANISRGLOFILTPNEFSAQTFYALSPTMHSQAT 705
642 HSPEDSRD---HAKHGCITIKIVSTSS-----TGQRNLAAPRA----- 677
706 QVPISQSDGSAVAATNTIANQINTAPKPAAPTLQIPPLPA 747
678 -IPPAQCPS--TSMRQSHRHGTSPVGDHSLVRI-PLPLPA 715

```

RESULT 6
US-09-177-650-7

Sequence 7, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
APPLICANT: Singh, Nanda
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BENC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147

EARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7
LENGTH: 872
TYPE: PRT

ORGANISM: Homo sapiens
US-09-177-650-7

Query Match 34.2%; Score 1620.5; DB 4; Length 872;

Best Local Similarity 42.2%; Pred. No. 2.6e-135; Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;

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7 GGEAGAAAGLVMSGAAAAAGGRLGSGKDVESGRGR-----VLLNSAARGDILL 60
14 GGGDGGGG-----GGANANAGDAAAGDEKRYGLAPDVEQVLTALGAGADKDGILL 68
61 LGTRAAITGGGGGGLRESRGGKQAGKSLGK-PLSTSSQSCRNVKRVQNTLVN 119
69 L-----EGGRDEGQRRTPOG--IGLLAKTPLSRPVK--RNNAKYRRIQTLIYDAL 115
120 EPRGMATYAHAVFLVFCILSVSTIPEHKLASSCLLLEFVIYVGFLEFIRI 179
116 EPRGMATYAHAVFLVFCILSVSTIPEHKLASSCLLLEFVIYVGFLEFIRI 175
180 WSAGCCCRKYGMRGRLFAKRPCCVIDIYLIASIAVAVSAKTQGNIFATSLRSLRFLQI 239
176 WAGCCCRKYGMRGRLFAKRPCCVIDIYLIASIAVAVSAKTQGNIFATSLRSLRFLQI 234
240 LRNVMDRGTWKLIGSVYVAHASKELITAMTIGFLVLISSFLVYVLEKANKFEFTY 291
235 LRNVMDRGTWKLIGSVYVAHASKELITAMTIGFLVLISSFLVYVLEKANKFEFTY 294
292 --NKEFTYADALMNGTITLTITIGYDKTPLTWIGRLISAGFALLGISFALLPAGILGSG 349
295 EMEKEFTYADALMNGTITLTITIGYDKTPLTWIGRLISAGFALLGISFALLPAGILGSG 354
350 FALKVOEGRHOKHFEKRRNPAANLIQVMSYAADEKSVSI-ATWK-----PHLKAL 400
355 LALKVOEGRHOKHFEKRRNPAANLIQVMSYAADEKSVSI-ATWK-----PHLKAL 414
401 HTCSPTNOKLSFEKRVMAASRQGISIKRSQASVDNRSPSTDIAGSPSTKQKSMSPND 460
415 QLEAASQKGLLDLVRLLSNRGSNTK-----KLFPLVNVDAIEESPSPKPVGLNN 468
461 RTFRPRLRLK-----SSQPKVYIADTALGTDDVYDEKGCQCDVSEDLTPPLKTVIR 514
469 KERFRTAFKMAKAFWQSS-----DAGTG--DPMADRGVNDPFIEDMPLTKAAR 520
515 AIRIMFHAARKRFKETLRPYDKVADIEQYASGHLMLCRISLQTRVDQILGKQITSD 574
521 AVRLQRLYKXKKKTELTPYDKVADIEQYASGHLMLCRISLQTRVDQILGKQITSD 580
575 KKSRR-----EKITAHEHTT--DDLMLGRVAVKVEQVOSIESKLDCLDI 615
581 KHKKSQKSAFTFSPQSSPRNEPVVAPRSTSEIQSSMGKVEKQVODGKKLDFLV 640
616 DIYQOVLK-----KGSASALALASFOIPEECQTSYDQSPVDSKDLGSAQN 663
641 DMHQMHERLQVOYTEYIPFKGTSS-----PALAEKKEDRYK--DLKTIICNISE 689
664 SGCLSRSTANISRGLOFILTPNEFSAQTFYALSPTMHSQATQVPISQSDGSAVAATNTI 723
690 TGPEPEPSYF-----QVITDKVSPYGFADHP-----VNLPRGPGSSGKVAT-- 733
724 ANQINTAPKPAAPTLQIPPLPAIKHLPRETILHPNAGIOESISDVTTCVAAKENVQ 783
734 -----PPSSATYVERPVLPIITLLDSRVSC--SOADLQGPYD-----RIS 775
784 VAQSNLTKDRSMKSFDMGGETLLSVCMPVFKDLKSLSVONLIRSTELNLTOLSGSESS 843
776 PRQ-----RSITRDSPTPLSL-----MSVNH-----EELERSPGGFSIS 810

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QY 844 GSRGSDPFP---KWRESKLFITDEVPGETETDTF 877
 Db 811 QDRDDYVFGPNCSSMWRKRYLA---GETDIDTDF 845

RESULT 7

US-09-105-058C-27
 ; Sequence 27, Application US/09105058C
 ; Patent No. 6403360
 ; GENERAL INFORMATION:
 ; APPLICANT: Blanaer, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Grubkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Men-Pin
 ; TITLE OF INVENTION: KClO4 POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: 3053-4052
 ; CURRENT APPLICATION NUMBER: US/09/105, 058C
 ; CURRENT FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055, 599
 ; PRIOR FILING DATE: 1997-08-12
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 854
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-105-058C-27

Query Match 33.9%; Score 1603.5; DB 4; Length 854;
 Best Local Similarity 42.7%; Pred. No. 8.2e-134;
 Matches 393; Conservative 109; Mismatches 252; Indels 167; Gaps 29;

QY 20 SGAAAAAGG--GRGSGMKDYESGRGVLLNSAARGCLLGLRAATLGGGGGLRE 77
 Db 11 AGGAAAAAGDEBERKGLAPDVEQ---VTLALGAGADKGGTLL-----GGGGDEG 59
 QY 78 SRRKOGARMSILGK-PLSYTSSQSCRNVKRYRVONYLVNLEPRGMAFIYHAFVELL 136
 Db 60 QRRPQG--IGLLAKTPLSRPVK---RNNAKYRRIOTLLYDALERRGMAHLHALVELL 114
 QY 137 VEGGLISVSTIEBHTKLASSCLLLEFVMTVGELEFIIRISWAGCCCRYGMOGRRL 196
 Db 115 VLGLLILAVLTFFKYEYFVSGDWMLLLEFFAIFGAEFALRIMAGCCCRYGMRGRRL 174
 QY 197 FARRPCVIDITVLIASIAVYSAKTOGNIFATSLRLEFLOLRVVRMDRGRGTLG 256
 Db 175 FARRPCLMDLFIYLIASVYVAVNGQNLATS-LRSLRFLQILRLMDRGRGTWKLIG 233
 QY 257 SVVYAHSKELITAWYIGFLVLIFFSFLVYLVEKDA-----NKESTYDALMTWGT 306
 Db 234 SAICAHSKELITAWYIGFLVLIFFSFLVYLVEKDOPEVDAOGEEMKEEFTYDALMTWGL 293
 QY 307 ITLTITIGYKTPILWGLRLLSAGFALLGISFALPAGLISGFAKLVQDQHRQHEKR 366
 Db 294 ITLTATIGYKTPKTEWGRLLAATFSLGVSFFALPAGLISGFAKLVQDQHRQHEKR 353
 QY 367 RNPAAALIQCVWRSYADDEKSVS--IATWK-----PHLKALHCSPTNOKLSFERVR 417
 Db 354 RKPAAELIQAAKRYATNPRIIDLVAITRPFESVVSFPFRKEOLEAASSCKGLIDRVR 413
 QY 418 MASPPGOSIKSROASVQDRSPSTDTITAESEPTKQKSWSFNDRTFRPSLRK----- 471
 Db 414 LSNPRGSNTK-----GLFPLPNVDALEESPSKPKPGVGLNNKERRAFRAFRKAAFAFWQ 467
 QY 472 SSQPKPIVDALCTDQDYDEKGCQCQCVSVEDLPLPLKTVIRAIRIMKFFHAKRKFET 531
 Db 468 SSE-----DAGTG--DPMADRGYGNDFPLEDMITPLKAAIRAVRILOFRLYKKKFKET 519
 QY 532 LRPDYADVIEQYSAGHLDMLCRISLOTFRVQDILGKQITSDKKS----- 578
 |||||||

Db 520 LRPDYADVIEQYSAGHLDMLCRISLOTFRIDMTFTPGPSPPTPKKKSKSGSAFTPPSQ 579
 QY 579 -----EKTAHEHT--DLSMLGRVAVYKOVQSTIESKLDCLDITYQVLR----- 623
 Db 580 SPRNEPVYARPSSTSEIDQSMGKFKYERQVODMKRKLDFVDHMQMERLOQVTEY 639
 QY 624 ---GGSALALIASFOIPPECQTSQVDSVDSKLSGSAONSCLSRSTANISRGIO 680
 Db 640 YPKGTSS-----PAEKKEDRRYS-DLKTILCNSETPPEPPYSFH----- 682
 QY 681 FILTPNEFSQOTFYALSPTMHSQATOVPISSQDSASAVATMTIANQITAPKPAPTLQ 740
 Db 683 -QVITDKVSPYGFADHP-----VNPJRGSSSKVQAT-----PPSATIYVE 725
 QY 741 IPPPLAIKILPPEETIHPNAGIQESTIDVTTCLVASKENVQAQSLTKDRSMKSF 800
 Db 726 RPTVLEPILTLILDSRSCH--SQADQGPYSD-----RISPRQ-----RSIT 765
 QY 801 MGGETLLVCPMPVKDGLKSLSYONLIRSTPELNIQLSGSSSGSRGSDPFP---KWR 856
 Db 766 RSDTFLSL-----MSVNH-----EELERSPSGFSISQDRDDYVFGPNCSSMW 809
 QY 857 ESKLFTDEVPGETETDTF 877
 Db 810 REKRYLA---GETDIDTDF 827

RESULT 8

US-09-177-650-91
 ; Sequence 91, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177, 650
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063, 147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 91
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-177-650-91

Query Match 33.2%; Score 1570.5; DB 4; Length 870;
 Best Local Similarity 41.6%; Pred. No. 7.4e-131;
 Matches 388; Conservative 109; Mismatches 273; Indels 163; Gaps 28;

QY 7 GGEGBGAGLWVKSAAAAAGG-----RLSGMKDYESGRGRVLLNSAARGD 57
 Db 12 GGGEGGGG-----GGAANPAGDSAVAGDEERKVGILAPDVEQ---VTLALGAGADKDG 63
 QY 58 LILTLRAATLGGGGGLRESRRKOGARNSLIGK-PLSYTSSQSCRNVKRYRVONYLV 116
 Db 64 TLL-----EGGREGGQRTPOG--IGLLAKTPLSRPVK---RNNAKYRRIOTLTY 110
 QY 117 NVLEPRGMATFYHAFVFLVFGCLLSVSTIEBHTKLASSCLLLEFVMTVGELEFI 176
 Db 111 DALEPRGMATLYHAFVFLVFLVIGCLLAVLTFFKYEYVSGDWMLLLETFALIFGAEFA 170
 QY 177 IRISWAGCCCRYRGMOGRLEFARKPCVITDITVLIASIAVYSAKTOGNIFATSLRLRF 236
 Db 171 LRIMWAGCCCRYRGMOGRLEFARKPCVITDITVLIASIAVYVAVNGQNLATS-LRSLRF 229
 QY 237 LQILRVMDRGRGTWKLIGSVVYAHSKELITAWYIGFLVLIFFSFLVYLVEKDA----- 291
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Db 230 LQILRLBMDRGGTWKLGSAICASHKELITAWYIGFLILLSSFLVYLVKQVEMDA 289
QY 292 -----NKESTYADALWGTITLTITIGYDKTPTLWIGRLLSAGFALLGISFPALPAGIL 346
Db 290 QGEMKEEFTYADALWGLTITATIGYDTPKTWEGRLTAAFTSLIGVSFFALPAGIL 349
QY 347 GSGFALKVOOHOKHFEKRRNPANLIOCVRSYADEXSVS-IATK-----PHL 397
Db 350 GSGLALKVOOHOKHFEKRRNPANLIOCVRSYADEXSVS-IATK-----PHL 397
QY 398 KALHTSPYOKLSFKERVMASPRGOSIKSROASVGDRRSPSDITAEAGSPTRVOKSWS 457
Db 410 RKQGLEAASQKIGLIDRLVRLSNRGSNTK-----GKLFPLNVALDIEESPKEPKPVG 463
QY 458 FNDTRPRSLRLKS-----SQPKVIADTALGTDVYDEKGCQCVSEDLTPPLKT 511
Db 464 LNKKEFRRTAFRMKAYAFWQXSE-----DAGTG---DEMAEDRGXNXLIDMI PXKA 515
QY 512 VIRAIRIMKPVAKRKETRLRPYDKVIOEYSGHIDMLCRISLQTRVDQILGKQOI 571
Db 516 ATRAVRLQRLKKEKRETLRPYDKVIOEYSGHIDMLSRILYLOTRIDMITTPGPP 575
QY 572 TSDK-KSREKIT-----AEHTTDLMLGRVYVYKQVQSIIESKID 612
Db 576 STPKHKKSQGTATPTYSQSPRNEPYARAATSEEDQSMGKFVKYERQVHDGKKLD 635
QY 613 CLLDIYQVLRKGSASALALASFOIPECEOTSIQSPVD---SKLDSGSQNSGCLSR 669
Db 636 XLVDMHMOHMER-----LOVHYEYVPTKASSPAEKEKEDNEYSLKTLICNY 685
QY 670 STANISRGLOFLTP-NEFSAQTFYALSPMHQSOATQVPISSQSGSAVAANTIANQIN 728
Db 686 SETPPPPPPSYFHOVPIPDVRCYGFANDP-----VKLTRGSPSSKAAQANLPS--- 734
QY 729 TAPKPAATLQIPLPPPAIKHLPRPEHLHPNAGLOESIDVTCVLASKENVOYAQSN 788
Db 735 -----SSTYAEKRPVLPITFLDLSCVSYH-----SQETLQGPYSD 770
QY 789 LTKRSMKSPDMGCEITLSCPMVKPLDGLSKLSYONLIRTEELNIQLSSESSSRSS 848
Db 771 HISPR-QRRSITRSDPLSL-----MSVNH-----EELERSPSGISISODRDD 813
QY 849 QDFP-----KWRSKLFTDEEVGPEETETDTE 877
Db 814 YVFGPSGGSSMGEKRYIAE---GETDIDTDF 843

RESULT 9
US-09-105-058C-4
; Sequence 4, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 300 amino acids of human KCNQ2

```

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US-09-105-058C-4
Query Match 25.5%; Score 1207.5; DB 4; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.7e-99;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

QY 91 GKPLSTSSQSCRRNVKRYRQVNYLVNLEPRGMATYHAFVLLVFGCLISVFTIP 150
Db 5 GKP-----PKRNATFRKLONFLVNLVLEPRGMATYHAFVLLVFGCLISVFTIP 56
QY 151 EHTKLASSCLLIEFWIVVGLFEITIRISAGCCCRYGOGULRPAKPCVYDITVL 210
Db 57 EYKSSGALYIIEIVIVVGLFEITIRISAGCCCRYGOGULRPAKPCVYDITVL 116
QY 211 IASIAVAAQSQGVAFVSRSLRFLQILRLIMDRGGTWKLGSAICASHKELITAW 270
Db 117 IASIAVAAQSQGVAFVSRSLRFLQILRLIMDRGGTWKLGSAICASHKELITAW 176
QY 271 YIGFLVLIFFSFLVYLVKEDANKKESTYADALWGTITLTITIGYDKTPTLWIGRLLSAG 330
Db 177 YIGFLVLIFFSFLVYLVKEDANKKESTYADALWGTITLTITIGYDKTPTLWIGRLLSAG 236
QY 331 FALGISFPALPAGILGSGFALKVOEHOKHFEKRRNPANLIOCVRSYADEXSVSI 390
Db 237 FTLIGVSFFALPAGILGSGFALKVOEHOKHFEKRRNPANLIOCVRSYADEXSVSI 296
QY 391 -ATW 393
Db 297 HSTM 300

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RESULT 10
US-09-105-058C-6
; Sequence 6, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 300
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 300 amino acids of murine KCNQ2
US-09-105-058C-6
Query Match 25.5%; Score 1207.5; DB 4; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.7e-99;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;

QY 91 GKPLSTSSQSCRRNVKRYRQVNYLVNLEPRGMATYHAFVLLVFGCLISVFTIP 150
Db 5 GKP-----PKRNATFRKLONFLVNLVLEPRGMATYHAFVLLVFGCLISVFTIP 56
QY 151 EHTKLASSCLLIEFWIVVGLFEITIRISAGCCCRYGOGULRPAKPCVYDITVL 210
Db 57 EYKSSGALYIIEIVIVVGLFEITIRISAGCCCRYGOGULRPAKPCVYDITVL 116
QY 211 IASIAVAAQSQGVAFVSRSLRFLQILRLIMDRGGTWKLGSAICASHKELITAW 270
Db 211 IASIAVAAQSQGVAFVSRSLRFLQILRLIMDRGGTWKLGSAICASHKELITAW 270

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Db 117 IASIVLAAGSGGNFATISALNSLRFLOILRMIRMDRGSTWKLGSVVAHSELYTAW 176
 QY 271 YIGFVLVLFSSFLVLYVEKANKFESTYADALMWGTTLTIGYDGTPLTWLRLLSAG 330
 Db 177 YIGFCLILASFLVLYLAEGENDHFTYADALMWGLITLTIGYDGYPTQWNRRLAAT 236
 QY 331 FALGISEFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANLQCVARSYADEXSVSI 390
 Db 237 FTLLGVSEFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANLQCVARSYADEXSVSI 296
 QY 391 -ATW 393
 Db 297 HSTM 300

RESULT 11
 US-09-177-650-3
 ; Sequence 3, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Lepfert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; APPLICANT: Charlier, Carole
 ; TITLE OF INVENTION: KGN02 AND KGN03 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177, 650
 ; CURRENT FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 807
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-177-650-3

Query Match 25.1%; Score 1188; DB 4; Length 807;
 Best Local Similarity 37.7%; Pred. No. 8.1e-97;
 Matches 285; Conservative 118; Mismatches 186; Indels 166; Gaps 22;

QY 75 LRSRRKQKQARMMLKRPISYTSQSCRNVKRYRVQVLYNLVLERPGW-AFIYHAFV 133
 Db 77 LHDSSEGNR--KMSLVGKPLTY---KNYRTQFRFRMOKMNFLEPRGMKATYHLAV 131
 QY 134 FLVFGCLISVFEFTPEHTKLASSCLILEFVMIVVGLFIRIRMSAGCCCRYRGMG 193
 Db 132 LFWVLMGLASVFTSTPEDEFNATIVLYLLEIVYIMLATEYICRWMSAGCRSRYGISG 191
 QY 194 RLRFARKPCVIDITVILASIAVYSAKTQGNIFATSALNSLRFLOILRMIRMDRGSTW 253
 Db 192 RIRFATSAYCVIDIIVILASTIVLCIGATGVAFASAIRGLRFPQ-LRMRLRIDRRAGTW 250
 QY 254 LGSVYVAHSEKELTAMYGFLVLIFFSEFLVLYVEKANKERSTADALMWGTTLTIG 313
 Db 251 LGSVVAHSEKELTAMYGFLVLIFFSEFLVLYVEKANKERSTADALMWGTTLTIG 310
 QY 314 YGDKTPTLWMLGRLLSAGFALLGISEFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANL 373
 Db 311 YGDKTPTLWMLGRLLSAGFALLGISEFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANL 370
 QY 374 IOCVMSRYADEXSVSIATWKP--LKAALHTCSP--TNOKLSFKERYRMA SPRGOSIK 427
 Db 371 IOCLMRYSAPESTSLATWKLHARELPYVXLPLGSSNATGILNRLROSTKTRPNN 430
 QY 428 SRQASVGDERS-----PSTDT-----AEG-----SPTKQKSSMS 457
 Db 431 NQMLAVNSQATSKNLSVPRVYHDTISLVSTDSIEIOLGALGSLGWSKSKYGGSKK 490
 QY 458 FND-----RTRFRPSL-----RLKSQKRPVADADALG-- 486

Db 491 ATDDSVLQSRMLAPSNAHLDMMRRRRRSASLGRVYNTGQHLRPLQPSLTSDSDYIDY 550
 QY 487 -----TDDVYD-----EKGCQC 498
 Db 551 SLMAPIYQCEQWQVQHNSTPGEDEGVNSQLSQLQTLTCATRTREDISDGEDEAVGYQ- 609
 QY 499 DVSDEFTPLKTVYRAIRIMKFHVAKRKEETLRPYVQVYIEYXAGHLMCLRIKSL 558
 Db 610 POTEIEFTPALKVCVRAIRIQLLVARKKEEALPYDVQVIEQYSAGHDLOSRYKTV 669
 QY 559 QTRVDOILKGQITSDKSRREKITAHEHTTDDLSMLGVRVVEKOVOSIESKLDCLDIY 618
 Db 670 QAKLDFICG-----KNIEKTEPK-----IMFRIATLETYVGRMKDKLDLMAVEL 715
 QY 619 QOVLKRGASALALASQIPECEQTSIDQSPVDSKDLGSAONSGLSRTSANISRG 678
 Db 716 M-----GROASQVVFQNTSP-----RGESEPTSPARQ-----DLTRSRSRMVSD 756
 QY 679 LOFILTPNEFSQTFYALSPTHSQATQVPISQSD 713
 Db 757 MEM-----YTARSH---SPGYHGDARPT-IAQID 781

RESULT 12
 US-09-135-021-2
 ; Sequence 2, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVL0T1 WHICH CAUSES JERVELL
 ; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135,021A
 ; CURRENT FILING DATE: 1998-08-17
 ; EARLIER APPLICATION NUMBER: 08/874,655
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 676
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-135-021-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.8e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSQSCRNVKVR-RVQNYLXNLVLERPGW-AFIYHAFVFLVYGCCLISVFTPEHTKL 155
 Db 92 SIYSTRRPVLAETHQGRVYNFLRPTGKCFYHAAVFLIVVCLVSLSTIEQYAL 151
 QY 156 ASSCLLIEFWIIVVFEGLFIIRIMSAGCCCRYRGMGRFLRFAKPCVIDITVILASIA 215
 Db 152 ATGTLFWMEIYLVVEFGTYVVRIMSAGCRSKYVGLMGRIRFAKPLSTIIDLYVASMV 211
 QY 216 VSAKTQGNIFATSALNSLRFLOILRMIRMDRGSTWKLGSVVAHSEKELTAMYGFL 275
 Db 212 VLVGSKQGVATSAIRGIRFQILRLMLHVDRQGTWRLGSAVFIHQELITLTLYIGFL 271
 QY 276 VLISSFLVLYVEKA-----NKESTYADALMWGTTLTIGYDGTPLTWLGRLLSAG 330
 Db 272 GLIFSSIFVYLAEKDAVNESGVEFGSADALMWGVVYTTTIGYDGVYDPTWGTATSC 331
 QY 331 FALGISEFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANLQCVARSYADEXSVSI 390
 Db 332 FSVVAISFPALPAGILGSGFALKVOEHOHROKHEKRRNPAANLQCVARSYADEXSVSI 390
 QY 391 ATWKPHTKAL--HT-CSPYNOKLSFKERVNAPS PRGOSIKSROASVGDERSPSTDTITAE 446

Db 391 -TWKTYIRKAPRSHITLSPSPK---KSSVYVKKKKFKLDKNGVTPGKMLTVPHITCD 446
QY 447 GSPTRVOKSWS---FNDTRRPRSLRLKSQPKPYIDATGTDVDYDEKGCQCDVSVE 503
Db 447 PPRERRLDHFVSDGDSVSRKSPFL-LEVSMPH-----FMRTNSFAD---LDLEGE 494
QY 504 DLTPPL-----KVIVAIRIRMKRHHVAKRKREKTLRPYDVYDEQYSGHIDMLC 553
Db 495 TLTPRTHISQLRHHRATIKVIRMOYFVAKRKQAKPYDVYDEQYSGHIDMLV 554
QY 554 RIKSLQTRVDOILGKGQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEQVOSIESKL 611
Db 555 RIKELORRLDSDIGKPSLFISVSEKSKDR-----GSNTIGARLNREDKVTOLDQRL 606
QY 612 DCLLDIYOQVL-----RKGSA-----SALALASFOIPPE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGGPPREGGAHITOPCGSGSVDPPELFLPSNMLPYE 663

RESULT 13
US-09-135-020-2

; Sequence 2, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN IOT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-020-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
Best Local Similarity 41.9%; Pred. No. 2.8e-89;
Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
QY 98 SSOSCRANRYR-RVONYLYNVLEPRGM-AFIYHAFVFLVFGCLLSVFSIPEHTKL 155
Db 92 SIYSTRPVLARHVGGRVYVNFLEPRGMCFYHFAVFLVCLVSLSTIEQYAL 151
QY 156 ASSCLILEFVIVVGLFEIIRIWSAGCCCRYRGWGRLEFARKPCVIDITVLASIA 215
Db 152 ATGTLFMEIIVLVFGEYVRLWSAGCRSKYVGLGRLEFARKPISIIDLIVVAVSMV 211
QY 216 VVSATKOGNIFATSAIRSLRFLDILRMVRDRRGCTKLLGSSVYVYASKEKITAMYTIGFL 275
Db 212 VLVCGSGGVFAFSAIRGIRFLDILRMVHVDROGGRVRLGSSVFIHROELITLTYIGFL 271
QY 276 VLIFFSFLVYLVKDA-----NKEFSTYADALMWGTTTLTIGYGDKTPLTWLGRLISAG 330
Db 272 GLIFSSFYVYLAEKDAVNESGRVDFGSYADALMWGVYTVTTIGYGDVPPQVWVGKTIASC 331
QY 331 FALGISFFALPGILGSGALKVQEOGRKHFEKRRPANLQVCWKRSTAADEKSYSI 390
Db 332 FSVAISFFALPGILGSGALKVQOKOROKHFNROJPPAASLIQTAWRCYAENPDSS- 390

QY 391 ATWPKHLKAL---HT-CSPNTOKSEKERVWMASSRGOSIKSRQASVGRDRSPSTDTAE 446
Db 391 -TWKTYIRKAPRSHITLSPSPK---KSSVYVKKKKFKLDKNGVTPGKMLTVPHITCD 446
QY 447 GSPTRVOKSWS---FNDTRRPRSLRLKSQPKPYIDATGTDVDYDEKGCQCDVSVE 503
Db 447 PPRERRLDHFVSDGDSVSRKSPFL-LEVSMPH-----FMRTNSFAD---LDLEGE 494
QY 504 DLTPPL-----KVIVAIRIRMKRHHVAKRKREKTLRPYDVYDEQYSGHIDMLC 553
Db 495 TLTPRTHISQLRHHRATIKVIRMOYFVAKRKQAKPYDVYDEQYSGHIDMLV 554
QY 554 RIKSLQTRVDOILGKGQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEQVOSIESKL 611
Db 555 RIKELORRLDSDIGKPSLFISVSEKSKDR-----GSNTIGARLNREDKVTOLDQRL 606
QY 612 DCLLDIYOQVL-----RKGSA-----SALALASFOIPPE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGGPPREGGAHITOPCGSGSVDPPELFLPSNMLPYE 663

RESULT 14

US-09-135-010A-2
; Sequence 2, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KYLOT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-010A-2

Query Match 23.3%; Score 1102; DB 4; Length 676;
Best Local Similarity 41.9%; Pred. No. 2.8e-89;
Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
QY 98 SSOSCRANRYR-RVONYLYNVLEPRGM-AFIYHAFVFLVFGCLLSVFSIPEHTKL 155
Db 92 SIYSTRPVLARHVGGRVYVNFLEPRGMCFYHFAVFLVCLVSLSTIEQYAL 151
QY 156 ASSCLILEFVIVVGLFEIIRIWSAGCCCRYRGWGRLEFARKPCVIDITVLASIA 215
Db 152 ATGTLFMEIIVLVFGEYVRLWSAGCRSKYVGLGRLEFARKPISIIDLIVVAVSMV 211
QY 216 VVSATKOGNIFATSAIRSLRFLDILRMVRDRRGCTKLLGSSVYVYASKEKITAMYTIGFL 275
Db 212 VLVCGSGGVFAFSAIRGIRFLDILRMVHVDROGGRVRLGSSVFIHROELITLTYIGFL 271
QY 276 VLIFFSFLVYLVKDA-----NKEFSTYADALMWGTTTLTIGYGDKTPLTWLGRLISAG 330
Db 272 GLIFSSFYVYLAEKDAVNESGRVDFGSYADALMWGVYTVTTIGYGDVPPQVWVGKTIASC 331


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Db 152 ATGTLFMMELIVLVEFGETEVVRLMSAGCSKYYVGLMGRLEFARKPISITIDLIYVVASMV 211
Qy 216 VSAKTOGNIFFATRSALRSRFLQILRMVRMDRGCTKMLGSVYAAHSEKITAMYTIFPL 275
Db 212 VLVCSKSGQVFAISALRGIRFLQILRMVHVRGCTKMLGSVYFHHQELITLYIGPL 271
Qy 276 VLVCSKSGQVFAISALRGIRFLQILRMVHVRGCTKMLGSVYFHHQELITLYIGPL 271
Db 272 GLIFSSFEVYLAERDAVNESGRVEFGSYADALMMGVYVTTIGYDKNVQVWGTIAASC 331
Qy 331 FALLGISFFALPAGILGSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Db 332 FSVAISFFALPAGILGSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Qy 391 ATWKPHLAL---HT-CSPINOKLSFEKERYMASPRGOSISRSQASVGDERSPTDITAE 446
Db 391 -TWKIYIRKAPRSHLTLSPSPK---KKSYYVAKKKFKLKDNGVTPGKMLTVPHITCD 446
Qy 447 GSPTKYOKSWS---FNDRTFRPSLRKSSQPKVIDADTALGTDVYDEKCCOCDVSE 503
Db 447 PPEERLDFHSVDGYDSVRSKSPFL-LEVSMPH-----FMRNSFAED---LDLGE 494
Qy 504 DLTPPL-----KTYIRAIRIMKFAHAKKFEKTLRPYDVYDEQYSAGHLDMLC 553
Db 495 TLLPPTIHSOLREHNRATIKVIRMOYFAVAKKFOQARKPYDVYDEQYSAGHLDMLV 554
Qy 554 RIKSLQTRVDQILGKQO--ITSDKRSREKITAHEHTDLSMLGRVYKVKOVOSIESKL 611
Db 555 RIKELQRLDOSIGKPSLFSVSEKSDR-----GSNTIGARLNKRVEDKVTQLODRL 606
Qy 612 DCLLDIYQOVL-----RKGA-----SALALASFOIPFE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGPPREGAHITQPCGSGSVDEPLPNTLPTYE 663

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RESULT 19

US-09-597-732-2

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; Sequence 2, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-597-732-2

```

```

Query Match 23.3%; Score 1102; DB 4; Length 676;
Best Local Similarity 41.9%; Pred. No. 2.8e-89;
Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

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Qy 98 SSQSCRNNVYR-RVQNTLVNLERPRGW-AFIYHAFVLVFGCLLSVFTIPERTKL 155
Db 92 SITSTRPVARHNVQGVNVLFRPBGWKCFVHFAVFLVLCILSVLSTIEQYAL 151
Qy 156 ASSCLLLEFVMIVLVEFETIRISAGCCCRNMGORLFRAPRPFVIDITVLASTA 215
Db 152 ATGTLFMMELIVLVEFGETEVVRLMSAGCSKYYVGLMGRLEFARKPISITIDLIYVVASMV 211
Qy 216 VSAKTOGNIFFATRSALRSRFLQILRMVRMDRGCTKMLGSVYAAHSEKITAMYTIFPL 275
Db 212 VLVCSKSGQVFAISALRGIRFLQILRMVHVRGCTKMLGSVYFHHQELITLYIGPL 271
Qy 276 VLVCSKSGQVFAISALRGIRFLQILRMVHVRGCTKMLGSVYFHHQELITLYIGPL 271
Db 272 GLIFSSFEVYLAERDAVNESGRVEFGSYADALMMGVYVTTIGYDKNVQVWGTIAASC 331
Qy 331 FALLGISFFALPAGILGSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Db 332 FSVAISFFALPAGILGSGFALKVQOQROKHFEKRRNPANLIQCVRSYADERSVSI 390
Qy 391 ATWKPHLAL---HT-CSPINOKLSFEKERYMASPRGOSISRSQASVGDERSPTDITAE 446
Db 391 -TWKIYIRKAPRSHLTLSPSPK---KKSYYVAKKKFKLKDNGVTPGKMLTVPHITCD 446
Qy 447 GSPTKYOKSWS---FNDRTFRPSLRKSSQPKVIDADTALGTDVYDEKCCOCDVSE 503
Db 447 PPEERLDFHSVDGYDSVRSKSPFL-LEVSMPH-----FMRNSFAED---LDLGE 494
Qy 504 DLTPPL-----KTYIRAIRIMKFAHAKKFEKTLRPYDVYDEQYSAGHLDMLC 553
Db 495 TLLPPTIHSOLREHNRATIKVIRMOYFAVAKKFOQARKPYDVYDEQYSAGHLDMLV 554
Qy 554 RIKSLQTRVDQILGKQO--ITSDKRSREKITAHEHTDLSMLGRVYKVKOVOSIESKL 611
Db 555 RIKELQRLDOSIGKPSLFSVSEKSDR-----GSNTIGARLNKRVEDKVTQLODRL 606
Qy 612 DCLLDIYQOVL-----RKGA-----SALALASFOIPFE 641
Db 607 ALITDMLHQLLSLHGSGTPGSGPPREGAHITQPCGSGSVDEPLPNTLPTYE 663

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RESULT 20

US-09-105-058C-24

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; Sequence 24, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gridkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 605
; TYPE: PRT
; ORGANISM: mouse
US-09-105-058C-24

```

```

Query Match 23.3%; Score 1100.5; DB 4; Length 605;
Best Local Similarity 43.6%; Pred. No. 3.1e-89;
Matches 244; Conservative 99; Mismatches 148; Indels 69; Gaps 15;
Qy 98 SSQSCRNNVYR-RVQNTLVNLERPRGW-AFIYHAFVLVFGCLLSVFTIPERTKL 155

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;; SEQ ID NO 114
;; LENGTH: 570
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-597-735-114

Query Match 22.9%; Score 1081.5; DB 4; Length 570;
Best Local Similarity 41.6%; Pred. No. 1.4e-87;
Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

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QY 112 ONLVNLEPRGW-AFIYHAFVLLVFGCLISVSTIEPHTKLASSCLILEFVMIYV 170
D 1 QGRVYNLEPRGWCFVHFAVFLVLCIFSVLSTIEQYALATGTLFMEIVLVF 60
QY 171 FGLEFIIRWSAGCCCRKRGMOGRLEFARKPCFVITIVLAVASAKOQNIPTSA 230
D 61 FGLEFVRLMSAGCRSKYVGLMGRLEFARKPCISITIDLIYVASMVLCVSGQVFATSA 120
QY 231 LNSLRFLOILRMVMDRGGTWKLLGSVYVYASHELITAWYIGFLVLISSFLVLYEKD 290
D 121 IGRIFLOILRMVMDRGGTWKLLGSVYVYHROELITLTYIGFLGIFSSFYVLAEKD 180
QY 291 A-----NKEFTYADALMWGTTITLTIGYGDKPTLWGLSLAGFALLGISFALPAGI 345
D 181 AVNESGRVEGSDADALMWGVVTVTTIGYDKVPQTVGKTIASCFSVFALISFALPAGI 240
QY 346 LSGSFALKVQEOHQHKEFRKRNPAANLIQCVMRSYADEKSVSIATWPKHLKAL--HT 402
D 241 LSGSFALKVQOKORQHNFNQIPAAASLIOTAMRCYAAENPDS--TWKTIYIKRAPSHT 298
QY 403 -CSPTNOKLSKERVYMASPRGOSIKRQASVGDRRSPSTDTITAEGPSPTKVOKSWS--F 458
D 299 LLSPSKPK--KKSYYVKKKKFKLDKNGVTPGKMLTPHITCDPEERLHDHFSVDGY 355
QY 459 NDRTFRRLRLKSSQPKPYDADTLGTDVYDEKCCQDVSEDLTPPL----- 509
D 356 DSSVRKSPTL-LEVSMPH-----FMRTNSPSED--LDLEGETLTPITHTISQLEH 403
QY 510 -KTVIRAIRIMKFNHAKRREKFTLRPYDVADVEYQASGHLDMLCRIKSLQTRVDQILGK 568
D 404 HRATIKVIRMQYFAVAKKFKQARKPYDARDVIEQYSGHNLNMRVYIKELQRLDQSIGK 463
QY 569 GQ--ITSDKSKREKITAHEHTDDLSMLGRVYVKEKOVOSIESKLDCLDIYQVLT---- 622
D 464 PSLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDORLALITDMLHQLLSLHG 515
QY 623 -----RKGS-----SALALASFOIPPE 641
D 516 GSTPGSGGPRREGAHTTQPCGSGSVDPDLFLPSNTLPTYE 557

```

RESULT 31
US-09-444-295-114
; Sequence 114, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN IOT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444, 295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135, 020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921, 068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739, 383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019, 014
; PRIOR FILING DATE: 1995-12-22

;; PRIOR APPLICATION NUMBER: 60/094,477
;; PRIOR FILING DATE: 1998-07-29
;; NUMBER OF SEQ ID NOS: 114
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 114
;; LENGTH: 570
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-444-295-114

Query Match 22.9%; Score 1081.5; DB 4; Length 570;
Best Local Similarity 41.6%; Pred. No. 1.4e-87;
Matches 242; Conservative 105; Mismatches 158; Indels 77; Gaps 15;

```

QY 112 ONLVNLEPRGW-AFIYHAFVLLVFGCLISVSTIEPHTKLASSCLILEFVMIYV 170
D 1 QGRVYNLEPRGWCFVHFAVFLVLCIFSVLSTIEQYALATGTLFMEIVLVF 60
QY 171 FGLEFIIRWSAGCCCRKRGMOGRLEFARKPCFVITIVLAVASAKOQNIPTSA 230
D 61 FGLEFVRLMSAGCRSKYVGLMGRLEFARKPCISITIDLIYVASMVLCVSGQVFATSA 120
QY 231 LNSLRFLOILRMVMDRGGTWKLLGSVYVYASHELITAWYIGFLVLISSFLVLYEKD 290
D 121 IGRIFLOILRMVMDRGGTWKLLGSVYVYHROELITLTYIGFLGIFSSFYVLAEKD 180
QY 291 A-----NKEFTYADALMWGTTITLTIGYGDKPTLWGLSLAGFALLGISFALPAGI 345
D 181 AVNESGRVEGSDADALMWGVVTVTTIGYDKVPQTVGKTIASCFSVFALISFALPAGI 240
QY 346 LSGSFALKVQEOHQHKEFRKRNPAANLIQCVMRSYADEKSVSIATWPKHLKAL--HT 402
D 241 LSGSFALKVQOKORQHNFNQIPAAASLIOTAMRCYAAENPDS--TWKTIYIKRAPSHT 298
QY 403 -CSPTNOKLSKERVYMASPRGOSIKRQASVGDRRSPSTDTITAEGPSPTKVOKSWS--F 458
D 299 LLSPSKPK--KKSYYVKKKKFKLDKNGVTPGKMLTPHITCDPEERLHDHFSVDGY 355
QY 459 NDRTFRRLRLKSSQPKPYDADTLGTDVYDEKCCQDVSEDLTPPL----- 509
D 356 DSSVRKSPTL-LEVSMPH-----FMRTNSPSED--LDLEGETLTPITHTISQLEH 403
QY 510 -KTVIRAIRIMKFNHAKRREKFTLRPYDVADVEYQASGHLDMLCRIKSLQTRVDQILGK 568
D 404 HRATIKVIRMQYFAVAKKFKQARKPYDARDVIEQYSGHNLNMRVYIKELQRLDQSIGK 463
QY 569 GQ--ITSDKSKREKITAHEHTDDLSMLGRVYVKEKOVOSIESKLDCLDIYQVLT---- 622
D 464 PSLFTSVSEKSKDR-----GSNTIGARLNREDEKVTQDORLALITDMLHQLLSLHG 515
QY 623 -----RKGS-----SALALASFOIPPE 641
D 516 GSTPGSGGPRREGAHTTQPCGSGSVDPDLFLPSNTLPTYE 557

```

RESULT 32
US-09-597-732-114
; Sequence 114, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KYLOT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597, 732
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135, 010
; PRIOR FILING DATE: 1998-08-17

RESULT 33
 US-09-105-058C-8
 ; Sequence 8, Application US/09105058C
 ; Patent No. 6403360
 ;
 GENERAL INFORMATION:
 ; APPLICANT: Blanner, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin

Query Match	20.2%	Score 957;	DB 4;	Length 298;
Best Local Similarity	67.0%	Pred. No. 5.7e-77;		
Matches 189; Conservative	12;	Mismatches 79;	Indels 2;	Gaps 2;


```
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVL0T1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-113
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-135-010A-113
```

```
Query Match          19.0%; Score 898.5; DB 4; Length 376;
Best Local Similarity 55.3%; Pred. No. 1.4e-71;
Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5;
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```
QY 98 SSOSCRNNVKKYR-RVQNTLVNLEPRGM-AFIYHAFVLLVFGCLLSVSTIPEHTKL 155
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 SIYGRRLPFRNTINQGVYVFLERPTGKCFVYHFVLLVLLICLIFSLSSTIOQYNNL 117
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 156 ASSCLLLEFVMIYVGELEFIIRIWSAGCCCRKRYGQGRRLPFRARPCFVIDIYIATIA 215
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 118 ATEFLFMEIYLVVFFGAEYVVRMSAGCRSKYGVWGRLPFRARPCFVIDIYIATIA 177
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 216 VVSAKTQGNIFATSLRFLQILRMVMDRGGTWMKLSGVYVHAKSELITAWYIGFL 275
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 VLVGSGNGVYFATSAIRGIRFLQILRMVMDRGGTWMKLSGVYVHAKSELITAWYIGFL 237
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 276 VLIFFSEFLVYLVKDA-----NKEFSTYADALMMGTTITLTIGYGDPTPLTWLGRLLSAG 330
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 GLIFSSYFVYLAERKALDSSGEYQGSYADALMMGVYVITLTIGYGDPTPLTWLGRLLSAG 297
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 331 FALGISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 390
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 298 FSVAISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 355
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 391 ATWKPHLAL-----HTCSPT 406
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 ATWKIYIRKQSRNHIMSPS 375
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 38
US-09-444-871-113
; Sequence 113, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: KNE1 AS AN LOT GENE
; TITLE OF INVENTION: MUTATIONS IN THE KNE1 GENE ENCODING HUMAN MINK WHICH
; CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
```

```
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-444-871-113
```

```
Query Match          19.0%; Score 898.5; DB 4; Length 376;
Best Local Similarity 55.3%; Pred. No. 1.4e-71;
Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5;
```

```
QY 98 SSOSCRNNVKKYR-RVQNTLVNLEPRGM-AFIYHAFVLLVFGCLLSVSTIPEHTKL 155
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 SIYGRRLPFRNTINQGVYVFLERPTGKCFVYHFVLLVLLICLIFSLSSTIOQYNNL 117
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 156 ASSCLLLEFVMIYVGELEFIIRIWSAGCCCRKRYGQGRRLPFRARPCFVIDIYIATIA 215
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 118 ATEFLFMEIYLVVFFGAEYVVRMSAGCRSKYGVWGRLPFRARPCFVIDIYIATIA 177
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 216 VVSAKTQGNIFATSLRFLQILRMVMDRGGTWMKLSGVYVHAKSELITAWYIGFL 275
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 VLVGSGNGVYFATSAIRGIRFLQILRMVMDRGGTWMKLSGVYVHAKSELITAWYIGFL 237
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 276 VLIFFSEFLVYLVKDA-----NKEFSTYADALMMGTTITLTIGYGDPTPLTWLGRLLSAG 330
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 GLIFSSYFVYLAERKALDSSGEYQGSYADALMMGVYVITLTIGYGDPTPLTWLGRLLSAG 297
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 331 FALGISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 390
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 298 FSVAISFPALPAGILSGFALKVOEQRHOKHFEKRNPANLLOCVWSYAADEKSVSI 355
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 391 ATWKPHLAL-----HTCSPT 406
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 ATWKIYIRKQSRNHIMSPS 375
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 39
US-09-597-735-113
; Sequence 113, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVL0T1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-09-597-735-113

Query Match          19.0%; Score 898.5; DB 4; Length 376;
```



```
QY      391 ATWKPHLKAL---HTCSPT 406
      ||| :: | ||:
Db      356 ATWKIYIRKQSRNHHIMSPS 375
```

RESULT 42
MS-09-135

US-09-135-020-109
; Sequence 109, Application US/09135020
; Patent No. 6274133

Query Match	10.3%	Score 485.5;	DB 4;	Length 137;
Best Local Similarity	65.7%	Pred. No. 1.6e-35;		
Matches 90;	Conservative 22;	Mismatches 20;	Indels 5;	Gaps 1

RESULT 43
US-09-135-010A-109
; Sequence 109, Application US/09135010A
; Patent No. 6277978
; Patent No. 6277978

```

1  PRIOR APPLICATION NUMBER: 08/7739,383
2
3  PRIOR FILING DATE: 1996-10-29
4
5  PRIOR APPLICATION NUMBER: 60/019,014
6
7  PRIOR FILING DATE: 1995-12-22
8
9  NUMBER OF SEQ ID NOS: 116
10
11  SOFTWARE: PatentIn Ver. 2.0
12
13  SEQ ID NO: 100

```

Query Match	10.3%	Score 485.5	DB 4	Length 137
Best Local Similarity	65.7%	Pred. No. 1.6e-35		
Matches 90; Conservative	22;	Mismatches 20;	Indels 5;	Gaps 1.

RESULT 44
US-09-444-871-109
; Sequence 109, Application US/09444871

Query Match	10.3%;	Score 485.5;	DB 4;	Length 137;
Best Local Similarity	65.7%;	Pred. No. 1.6e-35;		
Matches 90; Conservative	22;	Mismatches 20;	Indels 5;	Gaps 1

```

1  TITLE OF INVENTION:  KVLQ1 - A LONG QT SYNDROME GENE
2
3  FILE REFERENCE:  2323-133
4
5  CURRENT APPLICATION NUMBER:  US/09/135,010A
6
7  CURRENT FILING DATE:  1998-08-17
8
9  PRIOR APPLICATION NUMBER:  60/004,477
10
11 PRIOR FILING DATE:  1998-07-29
12
13 PRIOR APPLICATION NUMBER:  08/921,068
14
15 PRIOR FILING DATE:  1997-08-29

```


OY 336 ISFPALPAGILSGSFL 352
Db 121 ISFPALPAGILSGSFL 137

RESULT 45

US-09-597-735-109
Sequence 109, Application US/09597735
Patent No. 6420124
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,735
CURRENT FILING DATE: 2000-06-19
EARLIER APPLICATION NUMBER: 09/135,010
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-597-735-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1,6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

OY 221 TCGNIFATSAIRLQILRMVMDRGGTWKLGSVVAHSEKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGGTWKLGSVVFHROELITTYIGFLGIFS 60
OY 281 SFLVYLVKDA-----NKESTYADALMWGTTITTTIGYDKPTPLTWIGRLSAGFALLG 335
Db 61 SYFYVLAEKDVAVNESGVEFGSYADALMWGVYVTTITIGDKVPQTWVGKTIASCFSVFA 120
OY 336 ISFPALPAGILSGSFL 352
Db 121 ISFPALPAGILSGSFL 137

RESULT 46

US-09-444-295-109
Sequence 109, Application US/09444295
Patent No. 6432644
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/444,295
CURRENT FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 09/135,020
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/921,068

PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-444-295-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1,6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

OY 221 TCGNIFATSAIRLQILRMVMDRGGTWKLGSVVAHSEKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGGTWKLGSVVFHROELITTYIGFLGIFS 60
OY 281 SFLVYLVKDA-----NKESTYADALMWGTTITTTIGYDKPTPLTWIGRLSAGFALLG 335
Db 61 SYFYVLAEKDVAVNESGVEFGSYADALMWGVYVTTITIGDKVPQTWVGKTIASCFSVFA 120
OY 336 ISFPALPAGILSGSFL 352
Db 121 ISFPALPAGILSGSFL 137

RESULT 47

US-09-597-732-109
Sequence 109, Application US/09597732
Patent No. 6451534
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KVLQ1 - A LONG QT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/597,732
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/094,477
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 109
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-597-732-109

Query Match 10.3%; Score 485.5; DB 4; Length 137;
Best Local Similarity 65.7%; Pred. No. 1,6e-35;
Matches 90; Conservative 22; Mismatches 20; Indels 5; Gaps 1;

OY 221 TCGNIFATSAIRLQILRMVMDRGGTWKLGSVVAHSEKELITWYIGFLVIFS 280
Db 1 SKGQVFATSAIRGIRFLQILRMHLVDRGGTWKLGSVVFHROELITTYIGFLGIFS 60

OY 281 SFLVLEKDA-----NKESTYADALMGTITLTIGYDGTPLTWLGRILSAGFALG 335
 Db 61 SYEVLAEKDAVNESGVEFSGYADALMGTITLTIGYDGTPLTWLGRILSAGFALG 120
 OY 336 ISFFALPAGILGSGFAL 352
 Db 121 ISFFALPAGILGSGFAL 137

RESULT 48

US-08-464-340A-13
 ; Sequence 13, Application US/08464340A
 ; Patent No. 5710019

GENERAL INFORMATION:
 APPLICANT: LI, ET AL.
 TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,340A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/08449
 FILING DATE: 28 JUL 1994
 ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-415
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 539 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:

TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 US-08-464-340A-13

Query Match 5.3%; Score 250; DB 1; Length 539;
 Best Local Similarity 23.3%; Pred. No. 1,6e-13;
 Matches 91; Conservative 77; Mismatches 151; Indels 72; Gaps 13;

OY 115 LYNVLEPRGMA---FIYHAFVFLVGGCLISVFSTIPHTKL-----ASGCLLILE 164
 Db 173 LMDLLEKRRSSVAANKILAIISTIFVLTALSL-NTLPLOSLDERGOSTDNQOLAHVE 231
 OY 165 FVMIVVFGLEFIRIRWSAGCCCRGRGMOGRLEFRARPCVIVITVLASIAVVAKTQGN 224
 Db 232 AVCIAMFTWEYLRLFLSP-----KKW---KFKGPLNADIDLALIPYV-----T 274
 OY 225 IFATSLSL-----RFLQILIRAMRMDRGCTWKLIGSVYVAHSEL-ITAW 270
 Db 275 IFLESNNSVLOFQNVRRVQIFRIMRILRIKLARHSTGLSLGFTLRSYNELGLIL 334
 OY 271 YIGFLVLFISFLVLEKDA-NKESTYADALMGTITLTIGYDGTPLTWLGRILS 329
 Db 335 FLAMGIMIFSS-LVFEAKEDDDTKFKSLPASFWMATITMTVGYDGLYPTKILGKIVGG 393

OY 330 GFALLISFPALPAGILGSGFALKVOBOHOKHFEKRRNPAANLIQCWMSYAADEKSVS 389
 Db 394 LCCIALGVLYALPIPIIVNNSEFYKQKQKRAIKR-----EALERAKRNGS 442
 OY 390 IATWKPALKALHTCSPTNCKLSFEKERYM-----ASPRGOSIKSNQASVGDPRSSTDLTA 445
 Db 443 IYS-----MNMKDAFARSTIEMMDIYERKGENGKKDKYODNHLSPKWKWT 489
 OY 446 EGSPTVKQKSWSPNDRTFRPSLRKSSQPK 476
 Db 490 KRLSETSSSKSFETREKQSGPEKARSSSPQ 520

RESULT 49

US-09-336-643A-10
 ; Sequence 10, Application US/09336643A
 ; Patent No. 6399761

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.
 APPLICANT: Curran, Mark Edward
 APPLICANT: Hu, Ping
 APPLICANT: Rutler, Marc
 APPLICANT: Wang, Jian-Wang
 TITLE OF INVENTION: No. 6399761el Human Potassium Channels
 FILE REFERENCE: SEQ-15P
 CURRENT APPLICATION NUMBER: US/09/336,643A
 CURRENT FILING DATE: 1999-06-18
 PRIOR APPLICATION NUMBER: 60/076,687
 PRIOR FILING DATE: 1998-08-07
 PRIOR APPLICATION NUMBER: 60/116,448
 PRIOR FILING DATE: 1999-01-19
 PRIOR APPLICATION NUMBER: PCT/US99/03826
 PRIOR FILING DATE: 1999-02-22
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10
 LENGTH: 646
 TYPE: PR
 ORGANISM: H. sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)...(646)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-336-643A-10

Query Match 5.2%; Score 245; DB 4; Length 646;
 Best Local Similarity 22.5%; Pred. No. 6,2e-13;
 Matches 107; Conservative 81; Mismatches 170; Indels 118; Gaps 22;

OY 115 LYNVLEPR-----GNAFIYHAFVFLVPGCLISVFSTIP-----ERTKL 155
 Db 172 LRAFEHPHTSTAALVFYVTFVFIAV---SVIANVETIPCRGSARRSSREOPCGEFPQ 229
 OY 156 ASSCLLIEFVMIIVFGLFIRIRWSAGCCCRGRGMOGRLEFRARPCVIVITVLIA-SI 214
 Db 230 AFECC---MDTACVLLFTGXYLLRLRAA-----PSKCRPLRSWMSLIDVAIILPYIT 277
 OY 215 AVSAKTQGNIPATSLRSLRFLQILIRVMDRGGCTWKLIGSVYVAHSELITAVYIGP 274
 Db 278 GLIVPK---NDVVSAGFVTLRFVFRIRPKFSRHSGGLRILGYTLKSCASEL-----GF 328
 OY 275 L-----VLFFSSFLVLEKDAWK-ESTYADALMGTITLTIGYDGTPLTWLGRIL 326
 Db 329 LIFSILMAIIPAIWMEY-AEKGTKNTNPTSIPAFWYITVMTLIGYDWMVSTIAGKI 387
 OY 327 LSAGFALGISFPALPAGILGSGFALKVOEOROKHFEKRRNPAANLIQC----- 376
 Db 388 FGSICSLGSLVLYALPVPVYVNSF---RIYHONQRAKRR---AOKVLAIRLAKSGT 442
 OY 377 -----VMSYAADEKSVI-----ATWKPALKALH-----TCSPTNCKLSFKR 415
 Db 443 TNAFLQYKQNGLEDGSGGEQALCVNRSAPEOQHHLHLEKTYCHEFTDELTFPSA 502

[illegible]

RESULT 50

```

US-09-336-643A-4
; Sequence 4A, Application US/09336643A
; Patent No. 6399761
;
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
;
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;
; FILE REFERENCE: SEQ-15P
;
; CURRENT APPLICATION NUMBER: US/09/336, 643A
;
; CURRENT FILING DATE: 1999-06-18
;
; PRIOR APPLICATION NUMBER: 60/076, 687
;
; PRIOR FILING DATE: 1998-08-07
;
; PRIOR APPLICATION NUMBER: 60/116, 448
;
; PRIOR FILING DATE: 1999-01-19
;
; PRIOR APPLICATION NUMBER: PCT/US99/03826
;
; PRIOR FILING DATE: 1999-02-22
;
; NUMBER OF SEQ ID NOS: 87
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 4
;
; LENGTH: 601
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; TYPE: .prt
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; ORGANISM: H. sapiens
;
; US-09-336-643A-4

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5.18;	243;	DB 4;	601;

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QY	65	AATLGGGGGLRESRRKQAGAMSLGKPLSTSSQSCRNKKYRRVQNYLYNVLERP---	122			
				::: ::		
Db	159	AAGLGGP-----GKSG-	188	---RWRLRQPRMMALEFDPYS		
QY	123	RGMAFIYHAPFYELVFG--CL-----	162	ILSVESNIPBHTKLASSCLLI		
				::: ::		
Db	189	SRARERLFASEFLFLVSTTFTECLETHEAFNIVKNTKEPVINGSTSVLQYEIETDPALTY	248			
QY	163	LEFVIVVGFGEFIIRIMWAGCCCRVGRQGRLEFRARPCVYDITVLI-----	217	ASIAVY		
				::: ::		
Db	249	VEGCVVWFTEFELYRIVS-----	299	PNKLEFIKNLNIIDFALLPYLEVGLSGI		
				::: ::		
QY	218	SAKTQGNIFATSAALSRLFQLILRWMDRRGGTWKLLGSVYVAHSKE-LITAWYIGFLV	276			
				::: ::		
Db	300	SSKAKDVDL--GELRVRRFVRLIRFELKLRHFGVGLHTLRASANEELLLIIFALCV	357			
				::: ::		
QY	277	LIFSEFLVLYLAK-----	326	DANKESTYADALMWGITLITLTGYGDKPLTYLGR		
				::: ::		
Db	358	LIFAF-MIYYARVGAQPNPDPSASEHTQKNPIGFWMAVVMITTLGYGDMYFQYWSGML	416			
				::: ::		
QY	327	LSAGFALLGISFFALPAGIL-----	362	HSROKH		
				::: ::		
Db	417	VGALCALGCVLTITAMPVPVIVNNFGYVSLAMAKQQLPDKRKKH	460			
				::: ::		

Search completed: June 14, 2003, 17:45:42
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:27 ; Search time 74 Seconds

(without alignments)
1662.031 Million cell updates/sec

Title: US-09-825-147-2

Perfect score: 4733
Sequence: 1 MPRHAGEGGAAGLWVKS.....SICKAGESTDLSPVKLK 923Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database :

A_Geneseq_101002:*

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2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	4733	100.0	923	22	Human ion-channel
2	4699.5	99.3	932	22	Human KCNQ5 protel
3	4547	96.1	888	22	Human voltage gate
4	4527.5	95.7	897	22	Human voltage gate
5	4527.5	95.7	897	22	Human KCNQ5 potass
6	4524.5	95.6	897	22	Human KCNQ5 potass
7	4524.5	95.6	897	22	Human voltage gate
8	4524.5	95.6	897	22	Human voltage gate
9	4523.5	95.6	897	22	Human voltage gate
10	4521.5	95.5	897	22	Human voltage gate

11	4269.5	90.2	846	21	Human KCNQ5 (KCN6q
12	1991	42.1	695	23	Human KCNQ4 potassium ch
13	1991	42.1	695	23	Human KCNQ4 potassium ch
14	1793	37.9	844	23	Human KCNQ5 potassium ch
15	1792.5	37.9	722	20	Human KCNQ5 potassium ch
16	1790.5	37.8	912	22	Human KCNQ5 potassium ch
17	1789.5	37.8	930	20	Human KCNQ5 potassium ch
18	1788.5	37.8	914	22	Human KCNQ5 potassium ch
19	1788.5	37.8	914	22	Human KCNQ5 potassium ch
20	1786	37.7	854	20	Human KCNQ5 potassium ch
21	1784	37.7	872	20	Human KCNQ5 potassium ch
22	1761	37.2	757	20	Human KCNQ5 potassium ch
23	1711.5	36.2	942	22	Human KCNQ5 potassium ch
24	1620.5	34.2	872	23	Human KCNQ5 potassium ch
25	1620.5	34.2	872	23	Human KCNQ5 potassium ch
26	1603.5	33.9	854	20	Human KCNQ5 potassium ch
27	1570.5	33.2	870	20	Human KCNQ5 potassium ch
28	1544	32.6	877	22	Human KCNQ5 potassium ch
29	1544	32.6	1375	22	Human KCNQ5 potassium ch
30	1540	32.5	875	22	Human KCNQ5 potassium ch
31	1227.5	25.9	393	18	Human KCNQ5 potassium ch
32	1188	25.1	807	20	Human KCNQ5 potassium ch
33	1104	23.3	676	22	Human KCNQ5 potassium ch
34	1103	23.3	676	22	Human KCNQ5 potassium ch
35	1102	23.3	676	22	Human KCNQ5 potassium ch
36	1102	23.3	676	22	Human KCNQ5 potassium ch
37	1102	23.3	676	22	Human KCNQ5 potassium ch
38	1102	23.3	676	22	Human KCNQ5 potassium ch
39	1102	23.3	676	22	Human KCNQ5 potassium ch
40	1102	23.3	676	22	Human KCNQ5 potassium ch
41	1101	23.3	676	22	Human KCNQ5 potassium ch
42	1101	23.3	676	22	Human KCNQ5 potassium ch
43	1101	23.3	676	22	Human KCNQ5 potassium ch
44	1101	23.3	676	22	Human KCNQ5 potassium ch
45	1099	23.2	676	22	Human KCNQ5 potassium ch
46	1098	23.2	676	22	Human KCNQ5 potassium ch
47	1097	23.2	676	22	Human KCNQ5 potassium ch
48	1097	23.2	676	22	Human KCNQ5 potassium ch
49	1096	23.2	676	22	Human KCNQ5 potassium ch
50	1095	23.1	676	22	Human KCNQ5 potassium ch
51	1094	23.1	676	22	Human KCNQ5 potassium ch
52	1093	23.1	676	22	Human KCNQ5 potassium ch
53	1092.5	23.1	676	22	Human KCNQ5 potassium ch
54	1091.5	23.1	581	18	Human KCNQ5 potassium ch
55	1091.5	23.1	581	18	Human KCNQ5 potassium ch
56	1091.5	23.1	581	18	Human KCNQ5 potassium ch
57	1088	23.0	676	22	Human KCNQ5 potassium ch
58	1081.5	22.9	570	21	Human KCNQ5 potassium ch
59	993.5	21.0	245	20	Human KCNQ5 potassium ch
60	976	20.6	439	22	Human KCNQ5 potassium ch
61	976	20.6	439	22	Human KCNQ5 potassium ch
62	938.5	19.8	529	22	Human KCNQ5 potassium ch
63	898.5	19.0	376	18	Human KCNQ5 potassium ch
64	898.5	19.0	376	18	Human KCNQ5 potassium ch
65	898.5	19.0	376	18	Human KCNQ5 potassium ch
66	829.5	17.5	500	22	Human KCNQ5 potassium ch
67	829.5	17.5	500	22	Human KCNQ5 potassium ch
68	803.5	17.0	355	22	Human KCNQ5 potassium ch
69	726.5	15.3	356	22	Human KCNQ5 potassium ch
70	710	15.0	138	22	Human KCNQ5 potassium ch
71	697	14.7	343	22	Human KCNQ5 potassium ch
72	528	11.2	108	22	Human KCNQ5 potassium ch
73	528	11.2	108	22	Human KCNQ5 potassium ch
74	485.5	10.3	137	21	Human KCNQ5 potassium ch
75	386.5	8.2	88	22	Human KCNQ5 potassium ch
76	348.5	7.4	234	22	Human KCNQ5 potassium ch
77	348.5	7.4	234	22	Human KCNQ5 potassium ch
78	311	6.6	469	22	Human KCNQ5 potassium ch
79	291.5	6.2	858	20	Human KCNQ5 potassium ch
80	291.5	6.2	858	20	Human KCNQ5 potassium ch
81	255	5.4	446	22	Human KCNQ5 potassium ch
82	255	5.4	446	22	Human KCNQ5 potassium ch
83	255	5.4	446	22	Human KCNQ5 potassium ch

84	255	5.4	446	22	AAM57124	Human brain expres
85	255	5.4	446	22	AAM69516	Human bone marrow
86	255	5.4	446	22	AAM17348	Peptide #3782 enco
87	255	5.4	446	22	AAM29855	Peptide #3892 enco
88	255	5.4	446	22	AAM05037	Peptide #3719 enco
89	255	5.4	446	22	ABG39141	Human peptide enco
90	250	5.3	1057	22	ABG00601	Novel human diago
91	248	5.2	647	22	AAM25597	Human protein sequ
92	247	5.2	481	20	AAY50342	Murine Kv6.2 prote
93	245	5.2	646	22	AAY34123	Human potassium ch
94	245	5.2	646	22	ABB63128	Human Kv4.1 protei
95	243	5.1	601	20	AAV34120	Human potassium ch
96	243	5.1	638	23	AA014201	Human transporter
97	242	5.1	1019	22	ABB67198	Drosophila melanog
98	239.5	5.1	616	20	AAY32013	Drosophila melanog
99	239	5.0	985	22	ABBS7774	Drosophila melanog
100	235.5	5.0	630	22	AAY13523	Amino acid sequenc
101	234	4.9	283	22	ABBA9495	Mutant human KVLQT
102	232.5	4.9	655	19	AAW79590	Human Kv potassium
103	232.5	4.9	655	19	ABW79584	Human Kv4.3 potass
104	229.5	4.8	495	20	AAY32014	Human Kv4.3 potass
105	229	4.8	636	19	AAW79589	Human cation chann
106	229	4.8	636	19	AAW79591	Human Kv potassium
107	229	4.8	636	23	ABW79585	Human Kv4.3 potass
108	227.5	4.8	629	22	ABW86319	Human Kv4.2 protei
109	226	4.8	495	23	ABW7250	Mouse ischaemic co
110	226	4.8	556	20	AAY32016	Caenorhabditis ele
111	224	4.7	477	20	AAY34127	Human potassium ch
112	224	4.7	466	22	ABG14127	Human Kv6.2 protei
113	223	4.7	466	22	ABG14144	Novel human diago
114	223	4.7	499	22	ABG14122	Human potassium ch
115	222.5	4.7	571	22	ABW71722	Drosophila melanog
116	222	4.7	526	22	ABG14353	Novel human diago
117	220.5	4.7	506	21	AAV44564	Mouse Voltage-gate
118	220.5	4.7	506	21	AAV44566	Mouse Voltage-gate
119	220.5	4.7	506	21	AAV44567	Mouse Voltage-gate
120	220.5	4.7	506	21	AAV44568	Mouse Voltage-gate
121	217.5	4.6	655	22	ABW86321	Human Kv4.3 protei
122	214.5	4.5	495	20	AAY33766	hKv5.1 human brain
123	214	4.5	41	23	AAE1611	Human KCNQ5 immuno
124	213	4.5	869	22	ABG06674	Novel human diago
125	212	4.5	498	22	ABW59446	Drosophila melanog
126	212	4.5	519	21	AAV44565	Human Voltage-gate
127	212	4.5	519	21	AAV44566	Human Voltage-gate
128	212	4.5	519	21	AAV44567	Human Voltage-gate
129	212	4.5	519	21	AAV44570	Human Voltage-gate
130	212	4.5	519	21	AAV44571	Human Voltage-gate
131	212	4.5	519	21	AAV44572	Human Voltage-gate
132	209.5	4.4	532	16	AAW82937	Mouse Kv1.7 voltag
133	209	4.4	552	22	ABW11807	Human K channel ho
134	208.5	4.4	559	22	AAU08660	Human NOV4 protei
135	208.5	4.4	249	22	AAU087098	Novel central nerv
136	206.5	4.4	250	22	AAU18283	Human endocytosis
137	206.5	4.4	494	17	AAU90765	Human K+ channel 2
138	206.5	4.4	494	19	AAW42966	Putative mature po
139	204.5	4.3	431	22	AAW93519	Human hSK2 protei
140	204.5	4.3	456	23	AAE23655	Prostate cancer-as
141	204.5	4.3	490	20	AAV34121	Human potassium ch
142	204.5	4.3	491	21	AAV70454	Human potassium ch
143	204	4.3	491	21	AAV53780	Human membrane cha
144	203.5	4.3	446	23	ABG11445	Novel human diago
145	203.5	4.3	446	23	ABW76166	Human potassium ch
146	199.5	4.2	518	22	ABW60654	Drosophila melanog
147	199.5	4.2	513	17	AAW90764	Human K+ channel 1
148	198.5	4.2	513	19	AAW42995	Putative mature po
149	198.5	4.2	579	23	ABW63707	Human hSK2 protei
150	198.5	4.2	847	23	ABG61870	Prostate cancer-as
					ABW6164	Human potassium ch

ALIGNMENTS

AAW67678	ID	AAW67678 standard; Protein; 923 AA.
AAW67678	AC	AAW67678;
21-JAN-2002 (first entry)	DT	
Human ion-channel forming protein.	DE	
Human ion-channel forming protein.	XX	
Ion-channel forming protein; voltage-gated potassium channel; fetal; Brain; thymus; prostate; heart; skeletal muscle; probe.	KW	
Homo sapiens.	OS	
MO200175108-A1.	PN	
11-OCT-2001.	PD	
03-APR-2001; 2001MO-US10875.	XX	
03-APR-2001; 2000US-194255P.	XX	
(LEXI-) LEXICON GENETICS INC.	PA	
Hu Y, Kiehe JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B; Sands AT;	PI	
MP1: 2001-656987/75.	DR	
N-PSDB; AAH43633, AAH43634.	XX	
New human ion channel protein and polynucleotides encoding the protein, useful in diagnosing or treating diseases, in drug screening, and in clinical trial monitoring	PT	
Claim 2: Page 35-37; 41pp: English.	PS	
This sequence represent a novel ion-channel forming protein. This protein shares structural similarity with mammalian ion channel proteins, particularly voltage-gated potassium channel proteins. The protein is expressed in many human cell lines including fetal brain, brain, thymus, prostate, heart and skeletal muscle. The novel protein can be used in the diagnosis or treatment of diseases, in drug screening, and in clinical trial monitoring. The oligonucleotides may be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high throughput chip format). The nucleic acids and novel protein can also be used in the identification, selection and validation of novel molecular targets for drug discovery, to screen collections of genetic material from patients who have a particular medical condition, to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, and to screen for drugs which can be used to treat symptomatic or phenotypic manifestations of perturbing the normal function of novel human protein. The polypeptides are further used in generating antibodies.	CC	
Sequence 923 AA:	XX	
Query Match 100.0%; Score 4733; DB 22; Length 923;	XX	
Best Local Similarity 100.0%; Pred. No. 0;	XX	
Matches 923; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
1 MPRHAGGEGGAGAGIWMVSGAAGGRLSGMKDVGSGRVLLNSAARGDILL 60	QY	
1 MPRHAGGEGGAGAGIWMVSGAAGGRLSGMKDVGSGRVLLNSAARGDILL 60	DB	
61 LGTRATATGGGGGGRGRRGKOGAMSLGKPLSTYSQSGRRNVKRYRQNYLYNLE 120	QY	
61 LGTRATATGGGGGGRGRRGKOGAMSLGKPLSTYSQSGRRNVKRYRQNYLYNLE 120	DB	
121 RPRGNAFYHAFFVFLVFGCLLTSVSTIPERHKLSSCLLLEFWIVYEGLEFTRIRW 180	QY	
121 RPRGNAFYHAFFVFLVFGCLLTSVSTIPERHKLSSCLLLEFWIVYEGLEFTRIRW 180	DB	

Same people

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OY 181 SAGCCRYRGMQGLRFARPKPCVDTIVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
DB 181 SAGCCRYRGMQGLRFARPKPCVDTIVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
OY 241 RMYRMDRRGGTWKLLGSVYVAHAKSKELLTAWYIGFLVLIFSSFLVYLVEKDANKKEFTYAD 300
DB 241 RMYRMDRRGGTWKLLGSVYVAHAKSKELLTAWYIGFLVLIFSSFLVYLVEKDANKKEFTYAD 300
OY 301 ALMMGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFALKVQDQHQ 360
DB 301 ALMMGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFALKVQDQHQ 360
OY 361 KHFEKRRNPANLITOCVWRSYAADKSVSIATWPKHLALHTCSPTNOKLSFKERERMA 420
DB 361 KHFEKRRNPANLITOCVWRSYAADKSVSIATWPKHLALHTCSPTNOKLSFKERERMA 420
OY 421 PRGOSIKSRQASVGDRRSPSTDTIAEGSPITVQKSWSFNDRTFRPSRLKSSQPKPV 480
DB 421 PRGOSIKSRQASVGDRRSPSTDTIAEGSPITVQKSWSFNDRTFRPSRLKSSQPKPV 480
OY 481 ADTALGTDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEETLRPYDVKY 540
DB 481 ADTALGTDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEETLRPYDVKY 540
OY 541 IEQYSAGHLDMLCRISLQTRVQDILGKQITSDKRSREKITAHEHTTDLMLGHRVYK 600
DB 541 IEQYSAGHLDMLCRISLQTRVQDILGKQITSDKRSREKITAHEHTTDLMLGHRVYK 600
OY 601 EKQVOSIESKLDCLDITVQVLRKGSASALASQIIPPEECQTSYDQSPVDSKDLSS 660
DB 601 EKQVOSIESKLDCLDITVQVLRKGSASALASQIIPPEECQTSYDQSPVDSKDLSS 660
OY 661 AONGCISRSNTSANISRLQFLTPNESAOFVYALSPMHSAOTVPISSQSGSAVAAT 720
DB 661 AONGCISRSNTSANISRLQFLTPNESAOFVYALSPMHSAOTVPISSQSGSAVAAT 720
OY 721 NTIANQINTAPKPAATLQIPPLPAIKHLPRPETLHPNPAQLOESISDVTTCLVAASKE 780
DB 721 NTIANQINTAPKPAATLQIPPLPAIKHLPRPETLHPNPAQLOESISDVTTCLVAASKE 780
OY 781 NVQVQASMLTKDRSKRSKFDMDGGETLLSYCPMPYKDLGKSLSYQNIIRSTEELNIO 840
DB 781 NVQVQASMLTKDRSKRSKFDMDGGETLLSYCPMPYKDLGKSLSYQNIIRSTEELNIO 840
OY 841 ESSSGRSQDFFPKWRESKLFITDEVEGPEETDTFDAAPOPARAAFAASDLSLRTGRSR 900
DB 841 ESSSGRSQDFFPKWRESKLFITDEVEGPEETDTFDAAPOPARAAFAASDLSLRTGRSR 900
OY 901 SSOSICKAGESTDALSLPHVKIK 923
DB 901 SSOSICKAGESTDALSLPHVKIK 923

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RESULT 2
AAB86979 standard: Protein: 932 AA.

AAB86979:
11-DEC-2001 (first entry)
Human KCNQ5 protein.
KCNQ5: potassium channel protein; human; neurological; cardiovascular;
anticonvulsant; excitability modulator; membrane potential; neuron;
voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
screening; central nervous system disease; cardiovascular disease.
Homo sapiens.
DE10013732-A1.
27-SEP-2001.
PD

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XX 21-MAR-2000; 2000DE-1013732.
XX 21-MAR-2000; 2000DE-1013732.
XX 21-MAR-2000; 2000DE-1013732.
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
XX Steilmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
XX WPI; 2001-571700/65.
XX N-PSDB; AAH49499.
XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX for specific modulators, potential agents for treating central nervous
XX system and cardiovascular diseases
XX Claim 1b; Page 10-14; 20pp; German.
XX This invention describes a novel DNA sequence (I) encoding: (i) a
XX polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
XX polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
XX the invention have neurological, cardiovascular and anticonvulsant
XX activity and act as modulators of the voltage-dependent KCNQ5 potassium
XX channel, a key regulator of membrane potential and modulator of
XX excitability of electrically activated cells such as neurons and
XX cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (ii)
XX are used to screen for compounds that modulate the activity of KCNQ5,
XX potentially useful for treating central nervous system (e.g. epilepsy)
XX and cardiovascular diseases. This sequence represents the human
XX potassium channel KCNQ5 protein described in the invention.
XX Sequence 932 AA:
XX
XX Query Match 99.3%; Score 4699.5; DB 22; Length 932;
XX Best Local Similarity 96.7%; Pred. No. 0;
XX Matches 920; Conservative 1; Mismatches 2; Indels .9; Gaps 1;
OY 1 MPRHAGSEEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVYLLNSAARGDGLL 60
DB 1 MPRHAGSEEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVYLLNSAARGDGLL 60
OY 61 LGTRAATLGGGGGGLRESRROKQARMSLQKPLSYTSQSCRNVKRYRQNYLYNLE 120
DB 61 LGTRAATLGGGGGGLRESRROKQARMSLQKPLSYTSQSCRNVKRYRQNYLYNLE 120
OY 121 RPRGMAFTYHAFVFLVGCILLVSFTIPERTKLASSCLLLEFMYVFGLEFIRIM 180
DB 121 RPRGMAFTYHAFVFLVGCILLVSFTIPERTKLASSCLLLEFMYVFGLEFIRIM 180
OY 121 RPRGMAFTYHAFVFLVGCILLVSFTIPERTKLASSCLLLEFMYVFGLEFIRIM 180
DB 121 RPRGMAFTYHAFVFLVGCILLVSFTIPERTKLASSCLLLEFMYVFGLEFIRIM 180
OY 181 SAGCCRYRGMQGLRFARPKPCVDTIVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
DB 181 SAGCCRYRGMQGLRFARPKPCVDTIVLASIAVSAKTOGNIFATLSALSLRFLQTL 240
OY 241 RMYRMDRRGGTWKLLGSVYVAHAKSKELLTAWYIGFLVLIFSSFLVYLVEKDANKKEFTYAD 300
DB 241 RMYRMDRRGGTWKLLGSVYVAHAKSKELLTAWYIGFLVLIFSSFLVYLVEKDANKKEFTYAD 300
OY 301 ALMMGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFALKVQDQHQ 360
DB 301 ALMMGTITLTITIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFALKVQDQHQ 360
OY 361 KHFEKRRNPANLITOCVWRSYAADKSVSIATWPKHLALHTCSPTNOKLSFKERERMA 420
DB 361 KHFEKRRNPANLITOCVWRSYAADKSVSIATWPKHLALHTCSPTNOKLSFKERERMA 420
OY 412 FKERERMAASPRGOSIKSRQASVGDRRSPSTDTIAGSPITVQKSWSFNDRTFRPSRLK 471
DB 412 FKERERMAASPRGOSIKSRQASVGDRRSPSTDTIAGSPITVQKSWSFNDRTFRPSRLK 471
OY 421 FKERERMAASPRGOSIKSRQASVGDRRSPSTDTIAGSPITVQKSWSFNDRTFRPSRLK 480
DB 421 FKERERMAASPRGOSIKSRQASVGDRRSPSTDTIAGSPITVQKSWSFNDRTFRPSRLK 480
OY 472 SSQPKPVADATLGTDDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEET 531
DB 472 SSQPKPVADATLGTDDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEET 531
OY 481 SSQPKPVADATLGTDDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEET 540
DB 481 SSQPKPVADATLGTDDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKPHVARKKKEET 540

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QY 532 LRPDYKQVIEQYSGAGHLDMLCRKISQTRVDQILGQITSDKKSREKITAHEHTTDL 591
 DB 541 LRPDYKQVIEQYSGAGHLDMLCRKISQTRVDQILGQITSDKKSREKITAHEHTTDL 600
 QY 592 SMLGRVYKVEKQVQSTESKLDCLLDIYOQVLRKGSASALALASFOIPPEECOTSDYOSP 651
 DB 601 SMLGRVYKVEKQVQSTESKLDCLLDIYOQVLRKGSASALALASFOIPPEECOTSDYOSP 660
 QY 652 VDSKDISSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYALSPYMHQAOTQVPISQ 711
 DB 661 VDSKDISSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYALSPYMHQAOTQVPISQ 720
 QY 712 SSGSAVAANTANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPETLHPNPAQLGSESISDV 771
 DB 721 SSGSAVAANTANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPETLHPNPAQLGSESISDV 780
 QY 772 TTVCLVASKENVOYAQSNLITKDRSMRKSFDKGGFELLSCYPVWPDKLSLVONLIRSTE 831
 DB 781 TTVCLVASKENVOYAQSNLITKDRSMRKSFDKGGFELLSCYPVWPDKLSLVONLIRSTE 840
 QY 832 ELNIDLSGSESSGSGSODFYPKWRRESKLETTDEEVGPEETETDTPDAAPQAPAREAPAS 891
 DB 841 ELNIDLSGSESSGSGSODFYPKWRRESKLETTDEEVGPEETETDTPDAAPQAPAREAPAS 900
 QY 892 DSLRTGRSRSSOSICKAGESTDALSLPHVRLK 923
 DB 901 DSLRTGRSRSSOSICKAGESTDALSLPHVRLK 932

RESULT 3

AAU09021
 ID AAU09021 standard: Protein; 888 AA.

AAU09021;

18-DEC-2001 (first entry)

Human voltage gated potassium channel hKCNQ5-2.

KW Human: voltage-gated potassium channel; hKCNQ5-2; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; splice variant.

OS Homo sapiens.

XX WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US09328.

XX 21-MAR-2000; 2000US-190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2001-611467/70.

XX N-PSDB; AAS14653.

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for

XX identifying a compound modulating ion flux in eukaryotic cell or cell

XX subunits

XX Claim 17; Page 64; 78pp; English.

CC The invention relates to an isolated polypeptide comprising an
 CC alpha subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC encoded by a splice variant of hKCNQ5 and is hKCNQ5-2.

XX Sequence 888 AA;

Query Match 96.1%; Score 4547; DB 22; Length 888;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 MKDVESEGRVILNSAARGDGLLITRAATLGGGGGLRSGRGKQAGRMSLGKPLS 95
 DB 1 MKDVESEGRVILNSAARGDGLLITRAATLGGGGGLRSGRGKQAGRMSLGKPLS 60
 QY 96 YTSQSCRRNVKYYRVONYLVLEPRGMAFIYAFVLLVFGCLLSVFSSTIPEHTKL 155
 DB 61 YTSQSCRRNVKYYRVONYLVLEPRGMAFIYAFVLLVFGCLLSVFSSTIPEHTKL 120
 QY 156 ASSCLLLEFVMIVFGLFETIRIWSAGCCCRYRMQGRRLRARRPCYDITVILASTA 215
 DB 121 ASSCLLLEFVMIVFGLFETIRIWSAGCCCRYRMQGRRLRARRPCYDITVILASTA 180
 QY 216 VVSATQGNIFATLSALSLRFLQILRMVRRMGRGTWKLGSVVAHSELTAWYIGTL 275
 DB 181 VVSATQGNIFATLSALSLRFLQILRMVRRMGRGTWKLGSVVAHSELTAWYIGTL 240
 QY 276 VLFSSFLVYLVKEDANKFESTYDALMWGITTTTIGYGKTPPLTWLGRLLSAGFALLG 335
 DB 241 VLFSSFLVYLVKEDANKFESTYDALMWGITTTTIGYGKTPPLTWLGRLLSAGFALLG 300
 QY 336 ISFFALPAGILGSGFALKVOEHOHKHEKRRNPAANLIOCWRSYADEKSVSIATWKP 395
 DB 301 ISFFALPAGILGSGFALKVOEHOHKHEKRRNPAANLIOCWRSYADEKSVSIATWKP 360
 QY 396 HUKALHTCSPTNOKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAECSPTKVOKS 455
 DB 361 HUKALHTCSPTNOKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDITAECSPTKVOKS 420
 QY 456 WSPNDRTRRPSSLRLKSSQPKPVADADTALGTDVYDEKGGQCDVSEDLPLPLTVIRA 515
 DB 421 WSPNDRTRRPSSLRLKSSQPKPVADADTALGTDVYDEKGGQCDVSEDLPLPLTVIRA 480
 QY 516 IRIIMKHFVAKRKKEFLRPYDVKDVIQYSGHGLDMCRKISQTRVDQILGQITSDK 575
 DB 481 IRIIMKHFVAKRKKEFLRPYDVKDVIQYSGHGLDMCRKISQTRVDQILGQITSDK 540
 QY 576 KSRKREKITAHEHTTDLISMLGRVYKVEKQVQSTESKLDCLLDIYOQVLRKGSASALALASF 635
 DB 541 KSRKREKITAHEHTTDLISMLGRVYKVEKQVQSTESKLDCLLDIYOQVLRKGSASALALASF 600
 QY 636 QIPPECEQOTSDYQSPVDSKLSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYA 695
 DB 601 QIPPECEQOTSDYQSPVDSKLSGSAQNSGCLSRSTSANISRGLOFLTPNEFSQAOTFYA 660
 QY 696 ISPTMHQAOTQVPISSODGSAVAANTANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPE 755
 DB 661 ISPTMHQAOTQVPISSODGSAVAANTANTANQINTAPKPAAPPTLQIIPPEPAIKHLPRPE 720

QY 756 TLHPNPAGIIESIDVTCTLVASKENVOYAOSNLTKDRSMRKSEFDMGGETLLSYCPVVPK 815
 DB 721 TLHPNPAGIIESIDVTCTLVASKENVOYAOSNLTKDRSMRKSEFDMGGETLLSYCPVVPK 780
 QY 816 DLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLETTDEVEGETETD 875
 DB 781 DLGKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLETTDEVEGETETD 840
 QY 876 TFDAPQAPAREAAFPASDSLRTGSRSSQSTCKRAGESTDALSLPHVKLK 923
 DB 841 TFDAPQAPAREAAFPASDSLRTGSRSSQSTCKRAGESTDALSLPHVKLK 888

RESULT 4
 AAU09020 standard; Protein; 897 AA.
 ID AAU09020
 AC AAU09020;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human voltage gated potassium channel hKvN05-1.
 KM Human: voltage-gated potassium channel; hKCN05-1; nontropic;
 KM cerebrioprotective; neurotropic; analgesic; vision disorder;
 KM central nervous system disorder; epilepsy; migraine; hearing disorder;
 KM psychologic disorder; seizure; learning disorder; memory disorder;
 KM stroke; pain; gene therapy; splice variant.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 343..640
 FT /label="Conserved region
 FT /note="This sequence is specifically claimed in
 FT claim 13."
 PN MO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR MPI: 2001-611467/70.
 DR N-PSDB: AAS14652.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCN05 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCN0 alpha
 PT subunits
 XX
 Claim 17; Page 64; 78pp; English.

CC KCN0 nucleic acid when used in gene therapy)is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCN05 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCN05 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCN05. The present sequence is
 CC encoded by a splice variant of hKCN05 and is hKCN05-1.
 XX
 SQ Sequence 897 AA;
 Query Match 95.7%; Score 4527.5; DB 22; Length 897;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
 QY 36 MKDVEGGRVLLNSAARGDGLLLGTRAAVLGGGGGLRESRKGKOGARMSLKGKPLS 95
 DB 1 MKDVEGGRVLLNSAARGDGLLLGTRAAVLGGGGGLRESRKGKOGARMSLKGKPLS 60
 QY 96 YTSOSCRNRYRKYONLTVLWLEPRGMATFYHAFVFLVNGCLLSVFTIPERTKL 155
 DB 61 YTSOSCRNRYRKYONLTVLWLEPRGMATFYHAFVFLVNGCLLSVFTIPERTKL 120
 QY 156 ASSCLLIEFVMIYVEGLEFIRIMAGCCCRYRGOGLRFAKPCVDTIVLASIA 215
 DB 121 ASSCLLIEFVMIYVEGLEFIRIMAGCCCRYRGOGLRFAKPCVDTIVLASIA 180
 QY 216 VVSATOGNIFATSLRSLRFLQILRMVMDRGRGTWKLKLGSVYVASHKELITAWYIGFL 275
 DB 181 VVSATOGNIFATSLRSLRFLQILRMVMDRGRGTWKLKLGSVYVASHKELITAWYIGFL 240
 QY 276 VLISSFLVYLVKQANKEFSTYADALMGTITLTITIGYDKRPLTWLGLSAGFLLG 335
 DB 241 VLISSFLVYLVKQANKEFSTYADALMGTITLTITIGYDKRPLTWLGLSAGFLLG 300
 QY 336 ISFPALPAGIILSGFALQVOEORHOKHFEKRRNPANLQCVRSYAADEKSVSIATWKP 395
 DB 301 ISFPALPAGIILSGFALQVOEORHOKHFEKRRNPANLQCVRSYAADEKSVSIATWKP 360
 QY 361 HLKALHTCSPTKKEQGEASSQKLSFEKERYRMASSPGQSIKRSQASVGDHRRSPSTDTAE 446
 DB 361 HLKALHTCSPTKKEQGEASSQKLSFEKERYRMASSPGQSIKRSQASVGDHRRSPSTDTAE 420
 QY 447 GSPTVQKWSFNDRIRFRPSJLKLSSQPPVADATAGTDVYDEKGCQCDVSVEDLT 506
 DB 421 GSPTVQKWSFNDRIRFRPSJLKLSSQPPVADATAGTDVYDEKGCQCDVSVEDLT 480
 QY 507 PELKTYIRAIRIMKFFVAKRKFEKTLRPYDVKDIQYSAHMDMLCRISLQTRVQIL 566
 DB 481 PELKTYIRAIRIMKFFVAKRKFEKTLRPYDVKDIQYSAHMDMLCRISLQTRVQIL 540
 QY 567 GKQIITSDKRSREKITAHEHTTDLMLGRVYVERKOVOSIESKLDCLDIYOQVLRKS 626
 DB 541 GKQIITSDKRSREKITAHEHTTDLMLGRVYVERKOVOSIESKLDCLDIYOQVLRKS 600
 QY 627 ASALALASFOIPPEEEOGTSIDVOSPYDSKDLSSAONSGCLSTSTANISRGLOFIFPN 686
 DB 601 ASALALASFOIPPEEEOGTSIDVOSPYDSKDLSSAONSGCLSTSTANISRGLOFIFPN 660
 QY 687 EFSAGTFYALSPFMHQAOVPIOSDGSVAANTNTIANQINAPKRAAFTTIOIPPLP 746
 DB 661 EFSAGTFYALSPFMHQAOVPIOSDGSVAANTNTIANQINAPKRAAFTTIOIPPLP 720
 QY 747 AIKHLRPREPTLHPNPAGIIESIDVTCTLVASKENVOYAOSNLTKDRSMRKSEFDMGGETL 806
 DB 721 AIKHLRPREPTLHPNPAGIIESIDVTCTLVASKENVOYAOSNLTKDRSMRKSEFDMGGETL 780
 QY 807 LSVCPVAPDGLKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLETTDEE 866
 DB 781 LSVCPVAPDGLKSLSYONLIRSTEELNIOLSGSESSSGSGSDDFYPKWRESKLETTDEE 840

QY 867 VGEETETDTPDAAPAPAREAFASDSLRTGRSSSOSICKAGESTDALSLPHVKLK 923
 DB 841 VGEETETDTPDAAPAPAREAFASDSLRTGRSSSOSICKAGESTDALSLPHVKLK 897

RESULT 5
 ID AAB47046 standard; Protein: 897 AA.
 AC AAB47046;
 DT 20-APR-2001 (first entry)
 DE Human KCNQ5 potassium channel subunit.

Human KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease; central nervous system; CNS; Alzheimer's disease; anxiety; ataxia; CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia; compulsive behaviour; dementia; depression; Huntington's disease; mania; memory impairment; memory dysfunction; spinal cord damage; phobia; Pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy.

Homo sapiens.

Key Location/Qualifiers
 FT Binding-site 93..0 /Label= Site 1
 FT Binding-site 120..138 /Label= Site 2
 FT Binding-site 166..185 /Label= Site 3
 FT Binding-site 188..213 /Label= Site 4
 FT Binding-site 230..252 /Label= Site 5
 FT Binding-site 265..284 /Label= Site 6
 FT Binding-site 291..314 /Label= Site 6
 FT Binding-site 495..544 /Label= Site 6
 FT Domain /Label= A-domain

MO200077035-A2.
 21-DEC-2000.
 29-MAY-2000; 2000MO-DK00289.
 11-JUN-1999; 99DK-0000828.
 (NEUR-) NEUROSEARCH AS.
 Jentsch TJ;
 WPI: 2001-080678/09.
 N-PSDB: AAC85414.

Novel genes encoding KCNQ5 potassium channel subunits, useful for treating Alzheimer's disease, anxiety, ataxia, stroke, dementia, depression, Huntington's disease, schizophrenia and Parkinson's disease

Claim 8: Page 48-50; 50pp; English.

This sequence shows the human KCNQ5 protein. The KCNQ5 protein forms heteromeric channels with other KCNQ channel subunits, in particular KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5 are useful for diagnosis, treatment, prevention or alleviation of diseases related to disorders or adverse conditions of the central nervous system (CNS), including affective disorders, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or

CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders, memory dysfunction, motion disorders, motor
 CC disorders, neurodegenerative diseases, Parkinson's disease and
 CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
 CC convulsions and epilepsy.

SO Sequence 897 AA;
 Query Match 95.7%; Score 4527.5; DB 22; Length 897;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 36 MKDYSGGRVILNSAARGDGLLIGRAATLGGGGGLRESRKGARMLLGPIS 95
 DB 1 MKDYSGGRVILNSAARGDGLLIGRAATLGGGGGLRESRKGARMLLGPIS 60
 QY 96 YTSOSCRNRYRVQVLYLVLEPRPGMAFYHAFVFLVFGCLLSVFSTIPEHTKL 155
 DB 61 YTSOSCRNRYRVQVLYLVLEPRPGMAFYHAFVFLVFGCLLSVFSTIPEHTKL 120
 QY 156 ASSCLLIEFVIVFGLFETIRWSAGCCCRYRGWGLRPAKPCVYDITVLASIA 215
 DB 121 ASSCLLIEFVIVFGLFETIRWSAGCCCRYRGWGLRPAKPCVYDITVLASIA 180
 QY 216 VVSAGKGNIFATSLRSLRFLQILRMVMDRGGTWKLLGSVYVHAKSELTAWTIGFL 275
 DB 181 VVSAGKGNIFATSLRSLRFLQILRMVMDRGGTWKLLGSVYVHAKSELTAWTIGFL 240
 QY 276 VLFSSFLVYLVEKDANKFSTYADALMWGTTTLTTIGYDGTPLTWLRLSAGALLG 335
 DB 241 VLFSSFLVYLVEKDANKFSTYADALMWGTTTLTTIGYDGTPLTWLRLSAGALLG 300
 QY 336 ISFFALPAGILGSGFALKVQOHROKHFEKRRNPANLIQCVRSYAADEKSVSIATWKP 395
 DB 301 ISFFALPAGILGSGFALKVQOHROKHFEKRRNPANLIQCVRSYAADEKSVSIATWKP 360
 QY 396 HLKALHTCSPT-----NQKLSFKERVRAASRGOSIKRSQASVGRBRSPSDITAE 446
 DB 361 HLKALHTCSPTKKQGGERSQKLSFKERVRAASRGOSIKRSQASVGRBRSPSDITAE 420
 QY 447 GSPTKYQKSWSFNDRTFRPSLRKSSQPKFVIDADTALGTDVYDEKQCCQCDVSVEDLT 506
 DB 421 GSPTKYQKSWSFNDRTFRPSLRKSSQPKFVIDADTALGTDVYDEKQCCQCDVSVEDLT 480
 QY 507 PRLKTYIRAIRIMKFNHAKKFKETLRPYDVKVDIEQYSAGHLMICRIKSLQTRVDQIL 566
 DB 481 PRLKTYIRAIRIMKFNHAKKFKETLRPYDVKVDIEQYSAGHLMICRIKSLQTRVDQIL 540
 QY 567 GKQGITSDKSKREKITAHEHTTDLMSLGRVYVKEKOVOSTESKIDCLDIYQOVLKRS 626
 DB 541 GKQGITSDKSKREKITAHEHTTDLMSLGRVYVKEKOVOSTESKIDCLDIYQOVLKRS 600
 QY 627 ASALALASFOIPEFECQTSQDYQSPVDSKDLGSAONSGCISRSTANISRLQETILPN 686
 DB 601 ASALALASFOIPEFECQTSQDYQSPVDSKDLGSAONSGCISRSTANISRLQETILPN 660
 QY 687 EFSAGOFYALSPMHSGATQVPISSQSGSANAATNTANQNTAPKPAPTTLQIPPLP 746
 DB 661 EFSAGOFYALSPMHSGATQVPISSQSGSANAATNTANQNTAPKPAPTTLQIPPLP 720
 QY 747 AIKHLRPRPETHLAPNPAAGLQESIDVTCLVASKENVOVAQSNLTPDRSMRKSFEWGGFTL 806
 DB 721 AIKHLRPRPETHLAPNPAAGLQESIDVTCLVASKENVOVAQSNLTPDRSMRKSFEWGGFTL 780
 QY 807 LSYCPVWPDLGSLVSQNLIRSTEELINLQSGSSSGSRGODEPYPMWRSEKLTITDEE 866
 DB 781 LSYCPVWPDLGSLVSQNLIRSTEELINLQSGSSSGSRGODEPYPMWRSEKLTITDEE 840
 QY 867 VGEETETDTPDAAPAPAREAFASDSLRTGRSSSOSICKAGESTDALSLPHVKLK 923
 DB 841 VGEETETDTPDAAPAPAREAFASDSLRTGRSSSOSICKAGESTDALSLPHVKLK 897

RESULT 6
AAE16599
ID AAE16599 standard; Protein: 897 AA.
XX
XX AAE16599;
AC
AC 09-APR-2002 (first entry)
DT
DT
XX
XX Human potassium channel polypeptide, KCNO5.
DE
XX Human: potassium channel polypeptide; KCNO5; pain; migraine; stroke;
KM dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
KM ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KM anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KM addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KM learning deficiency; cognitive disorder; motor disease; neuron disease;
KM neuropsychological disorder; neuropsychological disorder; asthma;
KM neuron cell death; brain tumour; gene therapy; antisense therapy;
KM synaptic transmission; electrical excitability.
KM
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH Region 191..209
FT /note= "pore region"
FT 265..285
FT Region /note= "S4 voltage sensor region"
XX
XX W0200192526-A1.
XX
XX 06-DEC-2001.
XX
XX 24-MAY-2001; 2001WO-US17314.
XX
XX 26-MAY-2000; 2000US-207389P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;
PI GriDKoff VK;
XX
XX WPI: 2002-122069/16.
DR N-PSDB: AAD27192.
XX
XX Novel potassium channel polypeptide, KCNO5 and polynucleotide encoding
PT it, for diagnosing, treating and identifying modulators useful in
PT treating neurological, neuropsychological and neuropsychological
PT diseases
XX
XX Claim 25; Fig 2; 128bp; English.
XX
XX The invention relates to potassium channel polypeptides referred to
CC as KCNO5 and nucleic acid molecules encoding such polypeptides. KCNO5
CC polypeptides are useful for identifying compounds that modulate their
CC biological activity. The compounds identified and KCNO5 polynucleotides
CC are useful for treating acute and chronic pain, migraine, acute stroke,
CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
CC disorders, depression, bipolar disorders, sleep disorders, eating
CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
CC memory loss, learning deficiencies, cognitive disorders and motor
CC neuron diseases. The nucleic acid molecules of the invention are
CC further useful for treating neuropsychological, neuropsychological,
CC disorders, asthma, neuron cell death and brain tumours. They are also
CC used in gene therapy and antisense therapy. KCNO5 polypeptides modulate
CC synaptic transmission and electrical excitability in the brain and are
CC useful for generating antibodies. They are also useful to affinity
CC purify biological effectors from biological materials e.g. disease
CC tissues or cells. The present sequence is human KCNO5 protein.
XX
XX Sequence 897 AA:
SQ

Query Match 95.7%; Score 4527.5; DB 23; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 36 MKDVESGRGRVLLNSAARGDGLLLTGRAATLGGGGGGLRESRRKGAGRNALGKPLS 95
DB 1 MKDVESGRGRVLLNSAARGDGLLLTGRAATLGGGGGGLRESRRKGAGRNALGKPLS 60
QY 96 YTSQSCRRNVKRRVONLYLVLEPRGNMFYTHAFVLLVFGLLISVSTIDEHKL 155
DB 61 YTSQSCRRNVKRRVONLYLVLEPRGNMFYTHAFVLLVFGLLISVSTIDEHKL 120
QY 156 ASSCLLLEFMIVVFGLEFIRIMSAGCCCRKMGQRLRFARKPCVIDITVILASIA 215
DB 121 ASSCLLLEFMIVVFGLEFIRIMSAGCCCRKMGQRLRFARKPCVIDITVILASIA 180
QY 216 VSAKTGNIPTATSLRSLRFLQILRMVMDRGGTWKLLGSVYVASHKELITANYIGFL 275
DB 181 VSAKTGNIPTATSLRSLRFLQILRMVMDRGGTWKLLGSVYVASHKELITANYIGFL 240
QY 276 VLIFFSFLVLYVEKDANKKESTYADALMWGTTTTTIGYGDKPTLWTIGRLISAGPALG 335
DB 241 VLIFFSFLVLYVEKDANKKESTYADALMWGTTTTTIGYGDKPTLWTIGRLISAGPALG 300
QY 336 ISFPALPAGILSGFALKVQEHOKHFEKRRNPANLIQCWRSYAADEKSVSIATWKP 395
DB 301 ISFPALPAGILSGFALKVQEHOKHFEKRRNPANLIQCWRSYAADEKSVSIATWKP 360
QY 396 HLKALHTCSPT-----NKLSEKERVMAASPRGOSIKSRQASVGDNRSPSDITAE 446
DB 361 HLKALHTCSPTKKEGEASSQKLSFKERVMAASPRGOSIKSRQASVGDNRSPSDITAE 420
QY 447 GSPTRKQKSWFNDRTPRPSLRKSSQPKPYIDADTLGTDVDYDEKCCQCDVSEDLT 506
DB 421 GSPTRKQKSWFNDRTPRPSLRKSSQPKPYIDADTLGTDVDYDEKCCQCDVSEDLT 480
QY 507 PPLKTVIRAIRIMFHVAKRKEKTELRPYDVADVEQYSAGHLDMLCRISLQTRVDQIL 566
DB 481 PPLKTVIRAIRIMFHVAKRKEKTELRPYDVADVEQYSAGHLDMLCRISLQTRVDQIL 540
QY 567 GKQGITSDKRSREKITTAEHETDDISLGRVYKVKQVQISKDLCLDIYQOVLKKS 626
DB 541 GKQGITSDKRSREKITTAEHETDDISLGRVYKVKQVQISKDLCLDIYQOVLKKS 600
QY 627 ASALALASFQIPEPCEQTSQVPSVDSKDSGSAQNSGCLSRSTANISRGLOFTLTPN 686
DB 601 ASALALASFQIPEPCEQTSQVPSVDSKDSGSAQNSGCLSRSTANISRGLOFTLTPN 660
QY 687 EFSAQTEFALSPTHSQATQVPISSQDSANVAATNTIANQINTAPKPAPTLQIPLPLP 746
DB 661 EFSAQTEFALSPTHSQATQVPISSQDSANVAATNTIANQINTAPKPAPTLQIPLPLP 720
QY 747 AIKHLPRETLHPNPAIGQESISDVTTCLVASKENVQVQASNLTKDRSKRKSMDGGETL 806
DB 721 AIKHLPRETLHPNPAIGQESISDVTTCLVASKENVQVQASNLTKDRSKRKSMDGGETL 780
QY 807 LSVCPMPVKDGLKSLSVONLIRSTEEINQLSGSESSGSGSGSODEFPKPKRESKLFITDEE 866
DB 781 LSVCPMPVKDGLKSLSVONLIRSTEEINQLSGSESSGSGSGSODEFPKPKRESKLFITDEE 840
QY 867 VGPETETDTDDAOPAREAFASDSLTGRSSRSQISCKAGESTDALSLPHVKIK 923
DB 841 VGPETETDTDDAOPAREAFASDSLTGRSSRSQISCKAGESTDALSLPHVKIK 897
RESULT 7
AAU09023
ID AAU09023 standard; Protein: 897 AA.
XX
XX AAU09023;
AC
AC 18-DEC-2001 (first entry)
DT

Human voltage gated potassium channel hKCNQ5-1 variant #2.

Human; voltage-gated potassium channel; hKCNQ5-1; noctropic; cerebroprotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder; psychotic disorder; seizure; learning disorder; memory disorder; stroke; pain; gene therapy; mutant; muten.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 50 /note= "Wild-type Ala substituted by Ser"

Region 343..640 /label= "Conserved region" /note= "This sequence is specifically claimed in claim 13"

MO200170759-A1.

27-SEP-2001.

20-MAR-2001; 2001WO-US09328.

21-MAR-2000; 2000US-190954P.

(ICAG-) ICAGEN INC.

Jegla TJ;

WPI; 2001-611467/70.

Polypeptides and polynucleotides of potassium channel KCNQ5 for identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ alpha subunits

Disclosure; Page - : 78pp; English.

The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modeling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraine, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a polymorphic variant of hKCNQ5-1.

Note: The present sequence does not appear in the specification but is based on hKCNQ5-1 sequence appearing as AA009020.

Query Match 95.6%; Score 4524.5; DB 22; Length 897;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 886; Conservative 2; Mismatches 0; Indels 9; Gaps 1;

36 MKDVESGRGVLLNSAARGDGLLLGTRATLGGGGGLRSRGRKGQARSILGKPLS 95

1 MKDVESGRGVLLNSAARGDGLLLGTRATLGGGGGLRSRGRKGQARSILGKPLS 60

96 YTSOSCRNVRKTRRVNNTLYNLEPRPGMAFYHAFFLVFGLILSVSTIDBTKL 155

61 YTSOSCRNVRKTRRVNNTLYNLEPRPGMAFYHAFFLVFGLILSVSTIDBTKL 120

156 ASSCLILEVMIVVFGLFIRISAGCCCRYGWGRLPARPCVIDIVILASTA 215

121 ASSCLILEVMIVVFGLFIRISAGCCCRYGWGRLPARPCVIDIVILASTA 180

216 VVSATQGNIFATSAISLRFLLRMVRMDRGSTWKLGSVYVYHAKELITANYIGFL 275

181 VVSATQGNIFATSAISLRFLLRMVRMDRGSTWKLGSVYVYHAKELITANYIGFL 240

276 VLISSFFLVYLVKDKANKERSTYADALMWGITLTITIGYGRKPTLWGLRSLAGFALLG 335

241 VLISSFFLVYLVKDKANKERSTYADALMWGITLTITIGYGRKPTLWGLRSLAGFALLG 300

336 ISFFALPAGILSGFALKVOEHRKHFEKRRNPAANLQCVMSYADEKSVSIATWKP 395

301 ISFFALPAGILSGFALKVOEHRKHFEKRRNPAANLQCVMSYADEKSVSIATWKP 360

396 HLKALHTCSPT-----NKLISFEKERYRMASSPRQSIKSKQASVGDRRSPSTDIYAE 446

361 HLKALHTCSPTKEGEASSSQKLSFEKERYRMASSPRQSIKSKQASVGDRRSPSTDIYAE 420

447 GSPTKQKSMSEFDRFRFRSLRLKSSQPRVIDADPALTGDVYDEKCCQCVSEDLT 506

421 GSPTKQKSMSEFDRFRFRSLRLKSSQPRVIDADPALTGDVYDEKCCQCVSEDLT 480

507 PLKTVIRAIRIMKFNVAKRREKTLRPYVKVDYEQYSAGHLMCLRIKSLQTVDDIL 566

481 PLKTVIRAIRIMKFNVAKRREKTLRPYVKVDYEQYSAGHLMCLRIKSLQTVDDIL 540

567 GKGQITSDKRSRKITAHEHTDLSMLGRVYKVKOVOSTIESKLDCLDITYOQVLRKS 626

541 GKGQITSDKRSRKITAHEHTDLSMLGRVYKVKOVOSTIESKLDCLDITYOQVLRKS 600

627 ASALALASFOIPPECEOTSDYOSPYDSKDLGSAONGCISRSTANISRGLOFTLPN 686

601 ASALALASFOIPPECEOTSDYOSPYDSKDLGSAONGCISRSTANISRGLOFTLPN 660

687 ESSAQTFFVALSPTMHSQATQVPIQSODGSAVAANTNTIANTINAPKPAAPTLLIIPPLP 746

661 ESSAQTFFVALSPTMHSQATQVPIQSODGSAVAANTNTIANTINAPKPAAPTLLIIPPLP 720

747 ATKHLPRPETLHPNPAGLQESTIDVTCLYASKENVOVAOSNLTFRKSMRKSFTMGGRTL 806

721 ATKHLPRPETLHPNPAGLQESTIDVTCLYASKENVOVAOSNLTFRKSMRKSFTMGGRTL 780

807 LSVCPMPKDLKSLSVQNLIRSTEELNQLSGSSSGSGSGSODFPKWRRSKLFITDEE 866

781 LSVCPMPKDLKSLSVQNLIRSTEELNQLSGSSSGSGSGSODFPKWRRSKLFITDEE 840

867 VGPETETDTPDAAPAPAREAAFPASPSLRTGRSSOSICKAGESTALSLPHVKL 923

841 VGPETETDTPDAAPAPAREAAFPASPSLRTGRSSOSICKAGESTALSLPHVKL 897

RESULT 8

AA009025 standard; Protein; 897 AA.

AA009025;

18-DEC-2001 (first entry)

Human voltage gated potassium channel hKCNQ5-1 variant #4.

Human; voltage-gated potassium channel; hKCNQ5-1; noctropic; cerebroprotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder;

FT Region 343..640
 FT /label="Conserved_region
 FT /note="This sequence is specifically claimed in
 FT claim 13"
 FT Misc-difference 446
 FT /note="Wild-type Ser substituted by Gly"
 PN WO200170759-A1.
 XX 27-SEP-2001.
 XX 20-MAR-2001; 2001WO-US09328.
 XX 21-MAR-2000; 2000US-190954P.
 XX (ICAG-) ICAGEN INC.
 PA Jegla TJ;
 PI WPI; 2001-611467/70.
 DR Polypeptides and polynucleotides of potassium channel KCNQ5 for
 XX identifying a compound modulating ion flux in eukaryotic cell or cell
 XX membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 PT
 PS Disclosure: Page - ; 78pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a polymorphic variant of hKCNQ5-1.
 CC Note: The present sequence does not appear in the specification but
 CC is based on hKCNQ5-1 sequence appearing as AAU09020.
 CC
 XX
 XX Sequence 897 AA:
 SQ
 Query Match 95.6%; Score 4523.5; DB 22; Length 897;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 886; Conservative 1; Mismatches 1; Indels 9; Gaps 1;
 OY 36 MKDVESEGGRVLSNAARGBGLLIGTRAATLGGGGGIGRESRRGKQGRMSLGRPLS 95
 DB 1 MKDVESEGGRVLSNAARGBGLLIGTRAATLGGGGGIGRESRRGKQGRMSLGRPLS 60
 OY YTSOSCSRANKYRVONYLVNLEPRGMATFYAHFVLVGCILISFSTIPETHTKL 155
 DB 61 YTSOSCSRANKYRVONYLVNLEPRGMATFYAHFVLVGCILISFSTIPETHTKL 120
 OY 156 ASSCLLLEFYVIVFGLEFIIRISAGCCCRYRGNGRLEFARKPCVDTIVLASIA 215
 DB 121 ASSCLLLEFYVIVFGLEFIIRISAGCCCRYRGNGRLEFARKPCVDTIVLASIA 180
 OY * 216 VVSAKTGGINFATISALSRFLQLILRMVAMDRGGTWKLGSVYVAHSEKLLITAWYIGFL 275

DB 181 VVSAKTGGINFATISALSRFLQLILRMVAMDRGGTWKLGSVYVAHSEKLLITAWYIGFL 240
 OY 276 VLIFFSFLVYLVEVDANKKESTYADALMWGITTLTIGYGDKTPLTWGRLLSAGFALLG 335
 DB 241 VLIFFSFLVYLVEVDANKKESTYADALMWGITTLTIGYGDKTPLTWGRLLSAGFALLG 300
 OY 336 ISFFALPAGILGSGFALKVOEHOHOKHEKRRNPANLITQCVRSYVADEKSVSTATWMP 395
 DB 301 ISFFALPAGILGSGFALKVOEHOHOKHEKRRNPANLITQCVRSYVADEKSVSTATWMP 360
 OY 396 HLKALHTCSPT-----NOKLSFKERVMAASPRGOSIKRSQASVGRSPSTDTAE 446
 DB 361 HLKALHTCSPTKRQGEASSSQKLSFKERVMAASPRGOSIKRSQASVGRSPSTDTAE 420
 OY 447 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPYADATLGDYDYDEKCGQCDVSVEDLT 506
 DB 421 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPYADATLGDYDYDEKCGQCDVSVEDLT 480
 OY 507 PPLKTVIRAIRIMKEFHAKRKEETLRPYDKVDVEQYSAGHLMICRTKSLQTRVDOL 566
 DB 481 PPLKTVIRAIRIMKEFHAKRKEETLRPYDKVDVEQYSAGHLMICRTKSLQTRVDOL 540
 OY 567 GKQITSDKKSREKITAHEHTTDDLMLGRVYKVEKQVQSIKSLDCLDIYQOVLARKGS 626
 DB 541 GKQITSDKKSREKITAHEHTTDDLMLGRVYKVEKQVQSIKSLDCLDIYQOVLARKGS 600
 OY 627 ASALALASFOIPPECCQTSYOSQPVDSKDLGSAQNSGCLSRSTSANISRGLOFLTPN 686
 DB 601 ASALALASFOIPPECCQTSYOSQPVDSKDLGSAQNSGCLSRSTSANISRGLOFLTPN 660
 OY 687 EFAQOTFYALSPMHQSATQVPISQDSQSAVAATNTINQINTAKPAPATLOIPPPAP 746
 DB 661 EFAQOTFYALSPMHQSATQVPISQDSQSAVAATNTINQINTAKPAPATLOIPPPAP 720
 OY 747 AIKHLRPEETLHPNPAQLQESISDVTTCVASKENYVQAQSNLTIKDRSMRKSFGMGGETL 806
 DB 721 AIKHLRPEETLHPNPAQLQESISDVTTCVASKENYVQAQSNLTIKDRSMRKSFGMGGETL 780
 OY 807 LSYCPVWPMDLGLSLSQNLIRSTEEINLQSGSESSSRSSQDPYPRWREKLTITDBE 866
 DB 781 LSYCPVWPMDLGLSLSQNLIRSTEEINLQSGSESSSRSSQDPYPRWREKLTITDBE 840
 OY 867 VGEETETDFFDAAPQPARAAFAASDSLRTGRSSQSGICAGESTDALSIPHYVK 923
 DB 841 VGEETETDFFDAAPQPARAAFAASDSLRTGRSSQSGICAGESTDALSIPHYVK 897
 RESULT 10
 AAU09022
 ID AAU09022 standard; Protein: 897 AA.
 AC AAU09022;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Human voltage gated potassium channel hKvN5-1 variant #1.
 DE
 XX Human; voltage-gated potassium channel, hKCNQ5-1; nocotropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 36
 FT /note="Wild-type Gly substituted by Ala"
 FT /label="Conserved_region
 FT /note="This sequence is specifically claimed in
 FT claim 13"

XX MO200170759-A1.
 XX 27-SEP-2001.
 XX 20-MAR-2001: 2001MO-US09328.
 XX 21-MAR-2000: 2000US-190954P.
 XX (ICAG-) ICAGEN INC.
 XX Jegla TJ;
 XX WPI: 2001-611467/70.
 XX
 XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 XX identifying a compound modulating ion flux in eukaryotic cell or cell
 XX membrane expressing the protein, comprises KCNQ alpha
 XX subunits
 XX
 XX Disclosure: Page - : 78pp: English.
 XX
 XX The invention relates to an isolated polypeptide comprising an
 XX alpha-subunit of a KCNQ potassium channel, with a subsequence having
 XX 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 XX sequence and forms a KCNQ potassium channel having the characteristic of
 XX voltage-gating with at least an additional KCNQ alpha subunit. Also
 XX included in the scope of the invention are the nucleic acids encoding
 XX hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 XX expression vectors encoding them, antibodies against them, the use of
 XX 3-dimensional computer modelling to identify molecules that bind to a
 XX KCNQ containing potassium channel and modulate ion flux through the
 XX channel. The KCNQ polypeptide is useful for identifying a compound that
 XX increases or decreases ion flux through a potassium channel expressed in
 XX an eukaryotic host cell or cell membrane. The compound (and the
 XX KCNQ nucleic acid when used in gene therapy) is useful as
 XX a pharmaceutical agent for treating diseases involving abnormal ion flux,
 XX such as disorders of the central nervous system, such as epilepsy,
 XX migraines, hearing and vision problems, psychotic disorders, seizures,
 XX learning and memory disorders, stroke and pain. The antibodies are
 XX useful for detecting a KCNQ5 polypeptide in a human tissue and the
 XX use of a nucleotide sequence of KCNQ5 to search computer databases to
 XX find variants of the sequence which are associated with disease states,
 XX is useful for screening mutations of KCNQ5. The present sequence is
 XX a polymorphic variant of hKCNQ5-1.
 XX Note: The present sequence does not appear in the specification but
 XX is based on hKCNQ5-1 sequence appearing as AA09020.
 XX
 XX Sequence 897 AA:
 SQ
 Query Match 95.5%; Score 4521.5; DB 22; Length 897;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 886; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

QY 336 ISFFALPAGTIGSGFALXVOEHRKHFERRRNPAAALIOCVWRVAADEKSVIATWKP 395
 DB 301 ISFFALPAGTIGSGFALXVOEHRKHFERRRNPAAALIOCVWRVAADEKSVIATWKP 360
 QY 396 HUKALHTCSPT-----NKLSEKERYRMA SPRGOSIKSRQASVGRDRSPSTDTTAE 446
 DB 361 HUKALHTCSPTKKKEGQASSQKLSFKEERYRMA SPRGOSIKSRQASVGRDRSPSTDTTAE 420
 QY 447 GSPTKVQKSWSENDRTFRPSLRKLSQPPVADADALGTDDYVDEKGCDDVSVDLT 506
 DB 421 GSPTKVQKSWSENDRTFRPSLRKLSQPPVADADALGTDDYVDEKGCDDVSVDLT 480
 QY 507 PLKTVIRAIRIKMFHAKRKFKETLLRPYDKVDIEQYSAGHLMCLCRKLSQTRVDDIL 566
 DB 481 PLKTVIRAIRIKMFHAKRKFKETLLRPYDKVDIEQYSAGHLMCLCRKLSQTRVDDIL 540
 QY 567 GKGOITSDDKSRREKITAHEHTDLSMIGRVYKVKOVQSIIESKLDCLLDIYOQVLKRG 626
 DB 541 GKGOITSDDKSRREKITAHEHTDLSMIGRVYKVKOVQSIIESKLDCLLDIYOQVLKRG 600
 QY 627 ASALALASFOIPPECEQTSDDYQSPVDSKDLSSAONSGCISRSTANISRLQFTLPN 686
 DB 601 ASALALASFOIPPECEQTSDDYQSPVDSKDLSSAONSGCISRSTANISRLQFTLPN 660
 QY 687 EFSNAGTFYALSPMHSAOTQVPIISDGSAAVAATNTIANQINTAPKPAPTTLOIPPLP 746
 DB 661 EFSNAGTFYALSPMHSAOTQVPIISDGSAAVAATNTIANQINTAPKPAPTTLOIPPLP 720
 QY 747 AIKHLRPETLHPNPAQLQESISDVTTCVASKENVOVAGNLTNRDSMRKSPDMGETL 806
 DB 721 AIKHLRPETLHPNPAQLQESISDVTTCVASKENVOVAGNLTNRDSMRKSPDMGETL 780
 QY 807 LSCVPMWPKDLGSLSVONLIRSTEEINLQSGSESSGRSODFPKWRSKLETTDEE 866
 DB 781 LSCVPMWPKDLGSLSVONLIRSTEEINLQSGSESSGRSODFPKWRSKLETTDEE 840
 QY 867 VGPETEETDTPDAAPAREAFASDSLRTGRSSOSICRAGESTDALSLPHVKL 923
 DB 841 VGPETEETDTPDAAPAREAFASDSLRTGRSSOSICRAGESTDALSLPHVKL 897

RESULT 11
 AAB24241
 ID AAB24241 standard; Protein: 846 AA.
 AC AAB24241;
 XX
 XX 07-FEB-2001 (first entry)
 XX
 XX Human KCNQ5 (KCN6q) protein sequence SEQ ID NO:3.
 DE
 XX Human: KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salia disease; ophthalmological; auditory; central nervous system;
 KW cardiocative; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200061606-A1.
 PN
 XX 19-OCT-2000.
 PD
 XX 10-APR-2000; 2000MO-US09587.
 PF
 XX 14-APR-1999; 99US-0129274.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Petruchin K, Caskey CT, Li W, Metzker ML;
 PI

XX WPI: 2000-647417/62.
 DR N-PSDB; AAC64370, AAC64371.
 XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Claim 8; Fig 2; 99pp; English.

CC The present sequence represents the human KCNQ5 (also called KCNQ6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.

SO Sequence 846 AA:

Query Match 90.2%; Score 4269.5; DB 21; Length 846;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 835; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

QY 87 MSLGKPLSTYSSOSCRRVKKRRQNYLYNLEPRGNAFYHAFVFLVFGCLISVF 146
 DB 1 MSLGKPLSTYSSOSCRRVKKRRQNYLYNLEPRGNAFYHAFVFLVFGCLISVF 60
 QY 147 STDEHTKLASSCLLIEFVIVFGLFIIIRMSAGCCCRYGMOGRLEFARKPFQVID 206
 DB 61 STDEHTKLASSCLLIEFVIVFGLFIIIRMSAGCCCRYGMOGRLEFARKPFQVID 120
 QY 207 TIVIASIAVVSATQGNIFATSLRSLRFLQILRNVDRDRGCTWKLGSVYVAHSEL 266
 DB 121 TIVIASIAVVSATQGNIFATSLRSLRFLQILRNVDRDRGCTWKLGSVYVAHSEL 180
 QY 267 ITAVYIGFLVLFSSFLVYVEKDKANKERSTADALMGTITLTITGSGKPLTWGRL 326
 DB 181 ITAVYIGFLVLFSSFLVYVEKDKANKERSTADALMGTITLTITGSGKPLTWGRL 240
 QY 327 LSAGFALLGISFFALPAGILSGFALKVQEHROKHFEKRRNPANLIDCVMSYADEK 386
 DB 241 LSAGFALLGISFFALPAGILSGFALKVQEHROKHFEKRRNPANLIDCVMSYADEK 300
 QY 387 SVSIAIWKPHLKALHTCSPT-----NOKLSREKRRVMASSPROGSIKSRQASVGD 437
 DB 301 SVSIAIWKPHLKALHTCSPTKKEGEASSOKLSFKERVRMASSPROGSIKSRQASVGD 360
 QY 438 SPSTDIRAEGSPKTVOKSWSFNDRTFRPRLSLKSSQRPVDAADALGTDVYDEKGCQ 497
 DB 361 SPSTDIRAEGSPKTVOKSWSFNDRTFRPRLSLKSSQRPVDAADALGTDVYDEKGCQ 420
 QY 498 CDVSVEELTPPLKIVYAIRIRMKHVAARKREKELRPYDVKYIEQYSAGHLDMLCRIS 557
 DB 421 CDVSVEELTPPLKIVYAIRIRMKHVAARKREKELRPYDVKYIEQYSAGHLDMLCRIS 480
 QY 558 LQTRVDIILKGQITSPDKSKREKITAHEHTDDLSMLGVYVEKQVQSIESTLDCLDLDI 617
 DB 481 LQTRVDIILKGQITSPDKSKREKITAHEHTDDLSMLGVYVEKQVQSIESTLDCLDLDI 540
 QY 618 YQOVLKRGASALALASFOIPEFCEQTSYOSPYDSKDLSSAONSGCLSRSTANISR 677
 DB 541 YQOVLKRGASALALASFOIPEFCEQTSYOSPYDSKDLSSAONSGCLSRSTANISR 600
 QY 678 GLOFIIITPNEFSQOTFALSPTHMSQATQVPISSQSGSAVAANTNTIANDINTAPKPAAPT 737
 DB 601 GLOFIIITPNEFSQOTFALSPTHMSQATQVPISSQSGSAVAANTNTIANDINTAPKPAAPT 660

QY 738 TLOIPPLPAIKHLPRPETLHPNAGLOESTDYVTCVASKENVOVQASNLTKDSMRK 797
 DB 661 TLOIPPLPAIKHLPRPETLHPNAGLOESTDYVTCVASKENVOVQASNLTKDSMRK 720
 QY 798 SFDWGGETLLSYCPMPVFKDLGKSLSVONLIRSTEEELNQLSSGSSGSGSODFYPKMR 857
 DB 721 SFDWGGETLLSYCPMPVFKDLGKSLSVONLIRSTEEELNQLSSGSSGSGSODFYPKMR 780
 QY 858 SKLFTIDEEVGPETETDTFDAPQAPAREAPASDSLRTGSRSSQSTICKAGESTDALSL 917
 DB 781 SKLFTIDEEVGPETETDTFDAPQAPAREAPASDSLRTGSRSSQSTICKAGESTDALSL 840
 QY 918 PHYKLK 923
 DB 841 PHYKLK 846

RESULT 12
 AAB01476
 ID AAB01476 standard; Protein: 695 AA.

AC AAB01476;

DE 08-NOV-2000 (first entry)

XX KCNQ4 Potassium channel protein.

KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
 deathness; probes; treatment; therapy; transgenic animal; antibody;
 agonist; antagonist; timulus; hearing loss; neonatal deafness;
 KVM presbycusis; affective disorder; Alzheimer's disease; anxiety;
 ataxia; cognitive deficits; compulsive behavior; dementia;
 depression; Huntington's disease; mania; memory impairment;
 motor disorder; neurodegenerative disease; Parkinson's disease;
 Pick's disease; psychosis; schizophrenia; spinal cord damage;
 stroke; tremor.

OS Homo sapiens.

XX W0200044786-A1.

XX 03-AUG-2000.

PF 19-JAN-2000; 2000WC-DK00024.

XX 26-JAN-1999; 99DK-0000076.

PR 19-MAY-1999; 99DK-0000693.

XX (NEUR-) NEUROSEARCH AS.

PA Jentsch TJ;

PI WPI: 2000-548813/50.

XX N-PSDB; AAA47618.

PT Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
 PT useful e.g. for treating timulus, deafness, Alzheimer's and
 PT Parkinson's diseases

PS Claim 8; Page 48-51; 65pp; English.

CC Mutations in 3 known genes of the KCNQ branch of the potassium
 CC channel gene family underlie inherited cardiac arrhythmia's, neonatal
 CC epilepsy and in some cases associated with deafness. KCNQ4 has been
 CC mapped to the DFNA2 locus for autosomal dominant hearing loss, and
 CC a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
 CC pedigree has been identified. KCNQ4 is the first potassium channel
 CC gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
 CC channels with other KCNQ channel subunits, especially KCNQ3.
 CC Nucleotides encoding the KCNQ4 protein and the protein itself may be
 CC used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate KCNQ4 expression. The nucleotides may
 CC also be used as DNA probes in diagnostic assays (e.g. polymerase

CC chain reactions (PCR) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function
 CC of KCNQ4 polypeptides and their role in metabolism, for example
 CC through the production of transgenic animals. The KCNQ4 polypeptides
 CC may be used as antigens in the production of antibodies and to
 CC identify modulators (agonists and antagonists) of KCNQ4 expression
 CC and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may
 CC also be used to down regulate KCNQ4 expression and activity. They may
 CC be used in this way to treat tinnitus, loss of hearing (especially
 CC progressive hearing loss), neonatal deafness and presbycusis
 CC (deafness of the elderly) and disease or adverse conditions of the
 CC central nervous system (CNS) such as affective disorder, Alzheimer's
 CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
 CC neurodegenerative illness, cognitive deficits, compulsive behavior,
 CC dementia, depression, Huntington's disease, mania, memory impairment,
 CC memory disorders and dysfunction, motion disorders, motor disorders,
 CC neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
 CC disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
 CC cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
 CC molecules may be administered to down regulate KCNQ4 expression by
 CC binding with the cells own KCNQ4 genes and-preventing their
 CC expression.

CC Sequence 695 AA;

Query Match 42.1%; Score 1991; DB 21; Length 695;

Best Local Similarity 57.8%; Pred. No. 8.1e-165;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

25 AAGGGRGSGMKVSGRGRVLLNSAARGDGLLLGTRAAITLGGGGGLRESRKGOG 84
 DB | | | | | : : : : : | | | | |
 2 AEAAPRLGLGPPGADARAEVALTAVOSEG-----EAGGGGSPR----- 43
 QY | | | | | : : : : : | | | | |
 85 ARMSLCKPL-----SYSSQSCRNVKRYRVOVLYLVLEPRGAFIT 130
 DB | | | | | : : : : : | | | | |
 44 -RLGLLSPLPGAPLPDPGSGSGSACGCRSSAAKRRYRLONWVYVLERGMAFYVH 102
 QY | | | | | : : : : : | | | | |
 131 AFVFLVPGCLISVFTIPHTKLASSCLILEFVMIVFGLFIRIRMSGCCCRYG 190
 DB | | | | | : : : : : | | | | |
 103 VFIFLVFSCVLSVSTIQEHLANCLLLEFVMIVFGLFIRIRMSGCCCRYG 162
 QY | | | | | : : : : : | | | | |
 191 WGRRLFAKRPFCVDTIVLISIAVSAKTOGNIFATSAKSLRQLIRVMRDRG 250
 DB | | | | | : : : : : | | | | |
 163 WGRFRFAKRPFCVDTIVLISIAVSAKTOGNIFATSAKSLRQLIRVMRDRG 222
 QY | | | | | : : : : : | | | | |
 251 TWKLLGSAVVAHSEKELITAWYIGFLVLFSSFLVYLVKEDANKESTYDALMGITITL 310
 DB | | | | | : : : : : | | | | |
 223 TWKLLGSAVVAHSEKELITAWYIGFLVLFSSFLVYLVKEDANKESTYDALMGITITL 282
 QY | | | | | : : : : : | | | | |
 311 TIGGDKPLTWLWGLRLSAGFALLGISFPALPAGILGSGFALKVORHOKHEKRRNPA 370
 DB | | | | | : : : : : | | | | |
 283 TIGGDKPLTWLWGLRLSAGFALLGISFPALPAGILGSGFALKVORHOKHEKRRNPA 342
 QY | | | | | : : : : : | | | | |
 371 ANLIQCVRSYAAD-EKSVSIATW----- 393
 DB | | | | | : : : : : | | | | |
 343 ANLIQCVRSYAAD-EKSVSIATW----- 393
 QY | | | | | : : : : : | | | | |
 394 -----KPHLKAHLT-----CSPTNOKLSFKRRVMAASRGOSISRQ--ASYGDR 436
 DB | | | | | : : : : : | | | | |
 403 PVPDPAPSRYPVAVACHRPSTSPFCGESSRMGIKRIRIGSSQRTGSGKQDLAPPTMP 462
 QY | | | | | : : : : : | | | | |
 437 RSPSTDIATAG-SPTKVOXSMGFNDPRTFRPSLRKSSQPPYIDATGATDVYDEKG 495
 DB | | | | | : : : : : | | | | |
 463 TSPSEQYGEATSPKVOXSMGFNDPRTFRPSLRKSSQPPYIDATGATDVYDEKG 516
 QY | | | | | : : : : : | | | | |
 496 CQCDVSVEDLPPLKTVIRAIRIMKFRVAKRKEKTLRPYDVQVTEQYSAGHLMGRI 555
 DB | | | | | : : : : : | | | | |
 517 YQCELTVDDIMPVAVTVIRISIRIKFLVAKRKEKTLRPYDVQVTEQYSAGHLMGRI 576
 QY | | | | | : : : : : | | | | |
 556 KSLQTRVDDIILGKQITSPKKSRE---KITAEHTDDLSMLGRVYKVEQVOSIESKLD 612
 DB | | | | | : : : : : | | | | |

DB 577 KSLQTRVDDIIVGNG--PGGRKAREKDKGSDAEVDEISMGRVYKVEQVOSIESKLD 634
 QY 613 CLLDIYQOYLKRSKASALATASFOIPPEECOTSDYQSPYDSKDLSSAQNGLSRSTS 672
 DB 635 LLIGFISRLKRSSTSA--SLGAVQVPLFDDIISDHPDHEDISVSAQTL--ISRSVS 691
 QY 673 ANI 675
 DB 692 TNM 694
 RESULT 13
 AAEL6621
 ID AAEL6621 standard; Protein: 695 AA.
 XX AAEL6621;
 AC
 DT 09-APR-2002 (first entry)
 XX
 DE Human potassium channel polypeptide, KCNQ4.
 KW Human: potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neuropsychological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; KCNQ4 protein;
 KW hearing loss.
 KW
 XX Homo sapiens.
 OS
 XX
 PN W0200192526-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17314.
 XX
 PR 26-MAY-2000; 2000US-207389P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Dwoletzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;
 XX Gribkoff VK;
 XX
 DR WPI: 2002-122069/16.
 XX
 XX Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
 PT it, for diagnosing, treating and identifying modulators useful in
 PT treating neurological, neuropsychological and neuropsychological
 PT diseases
 PS
 PS Disclosure; Fig 5; 128bp; English.
 XX
 XX The invention relates to potassium channel polypeptides referred to
 CC as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
 CC polypeptides are useful for identifying compounds that modulate their
 CC biological activity. The compounds identified and KCNQ5 polynucleotides
 CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for creating neuropsychological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease

QY 201 PCVIDITVLIAIAVAVSAKTQGNIFATLSRLFLQILRMVRRDRRGTKWLLGSVYV 260
 DB 167 PCVIDIMVLIAIAVAVSAKTQGNIFATLSRLFLQILRMVRRDRRGTKWLLGSVYV 226
 QY 261 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 286
 QY 321 TWIGRLLSAGFALLGISFFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCVWRS 380
 DB 287 TWNGRLLAATFTLLIGVSPFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCVWRS 346
 QY 381 YAAD-----EKSVSIATWK--PHLKALHTC-----SPT 406
 DB 347 YATNLSTRDLHSTWQYERTVTPMRLPLPNOLELRLNLKSKSGILATKROPPPEPSP- 405
 QY 407 NOKLSFKERVMAASPRGOSIKSROASVGD--RRSPSTDTAAGSPPTKYOKSWSFNDRTRF 464
 DB 406 SOKVSLKDRV-FSSPRGVAAKGKSPQAOVTRSPADSLDPSKVKPWSFGDRSRA 464
 QY 465 RPSLRKSSQPKPYIDADTALCTDGVYDEKGCOCVSVEDLTPPLKTVIRAIRIMKFNVA 524
 DB 465 RQAFRIKGAASRQNSE-EASLPGEDIVDCKSCPEFVEDLTPGLKVSIRAVCVMEFLVS 523
 QY 525 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGGOITSDKRSREKITAE 584
 DB 524 KRKFESLRPYDVMVIEOYSAGHLDMLCRISLQTRVDOILGGOITSDKRSREKITAE 582
 QY 585 HETTDLSMLGRVYKVEKOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPPECC- 642
 DB 583 AELPEDPMGMRLGKVEKOVLSMEKKLDPLVNIYMQ--RMG-----IPPTETEA 629
 QY 643 -----EQTSDYQSPVDSKDLSSGSAQNSGCLSRISNAISRLQIILIPNESAOFTVA 695
 DB 630 YFAGKEPPAPPYHSPEDSRE--HVDHRCCTVKTIVRSSSTG-----QKNASAP- 678
 QY 696 LSPTHMSOATQVPIOS-----DGSAAVTNTITANOINPAPKPAAPPTLOI----- 741
 DB 679 APP-----VQCPSTSMQPOSHPRQGHGTSPPVGDHSLVIRIPPAHERSLAYGSGNR 732
 QY 742 -----PP-----PLPAIKHLPRPETLHPNPAAGLOESISDVTTC 775
 DB 733 ASMEFLROEDPFGCRPEGLTLDSDTISIPSYVDH-----EELERSFSGF--SISQ----- 781
 QY 776 VASKENNOVAOS 787
 DB 782 --SKENDALANS 791
 RESULT 15
 ID AAY01530 standard: Protein: 722 AA.
 AC AAY01530:
 XX
 DE 16-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of murine KCNQ2/KvL1.
 XX
 KM KCNQ protein; nervous system-specific potassium channel;
 KM neuronal excitability; neurotransmitter release; KCNQ modulator;
 KM ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KM age-associated memory loss; learning deficiency; motor neuron disease;
 KM epilepsy; stroke.
 OS Mus sp.
 XX
 PN WO9907832-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 26-JUN-1998; 98WO-US13276.
 XX

PR 12-AUG-1997; 97US-0055599.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Blauar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 PI Little MA, Neubauer MG, Yang W;
 XX
 DR WPI: 1999-190047/16.
 DR N-PSDB: AAX26588.
 PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
 XX
 PS Claim 4; Fig 10A-D; 6app; English.
 XX
 CC The present sequence represents murine KCNQ2/KvL1. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.
 XX
 SQ Sequence 722 AA;
 Query Match 37.9%; Score 1792.5; DB 20; Length 722;
 Best local similarity 53.4%; Pred No. 5.2e-151;
 Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;
 QY 21 GAAAAAGGRIAGSGMKDVEGRVLLNSAARDGILLGTRATLGGGGGGRRESRR 80
 DB 9 GYVGTSGEKKLKVGFGLDPCA-----PDSTRGALLIAGSEAPK--RGSVLSKPT 59
 QY 81 GKQGRMSLKKPLSTSSQCRNRYKRYVNYLYNVEERRRGAFTYHAFVFLVFGC 140
 DB 60 GGAGA-----GKP-----PKRNAFYKILNFTYNERPRGMATYHAFVFLVESC 106
 QY 141 LILSVFTIPHTKLASCILILEFMYVFGLEFTRISAGCCCRYGWQGRFLPARK 200
 DB 107 LVLSVFTIKKEYKESGALYILEYTVYFGEVYFVRIMAGCCCRYGRWGRFLPARK 166
 QY 201 PCVIDITVLIAIAVAVSAKTQGNIFATLSRLFLQILRMVRRDRRGTKWLLGSVYV 260
 DB 167 PCVIDIMVLIAIAVAVSAKTQGNIFATLSRLFLQILRMVRRDRRGTKWLLGSVYV 226
 QY 261 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 320
 DB 227 AHSKELITAWYIGFLVLIFFSFLVLYVEKDANKKEPSTYADALMWGITLTITIGYGDPTL 286
 QY 321 TWIGRLLSAGFALLGISFFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCVWRS 380
 DB 287 TWNGRLLAATFTLLIGVSPFALPAGILGSGFALKVQBOHROKHFERKRNPAANLIQCVWRS 346
 QY 381 YAAD-----EKSVSIATWK--PHLKALHTC-----SPT 406
 DB 347 YATNLSTRDLHSTWQYERTVTPMRLPLPNOLELRLNLKSKSGILATKROPPPEPSP- 405
 QY 407 NOKLSFKERVMAASPRGOSIKSROASVGD--RRSPSTDTAAGSPPTKYOKSWSFNDRTRF 464
 DB 406 SOKVSLKDRV-FSSPRGVAAKGKSPQAOVTRSPADSLDPSKVKPWSFGDRSRT 464
 QY 465 RPSLRKSSQPKPYIDADTALCTDGVYDEKGCOCVSVEDLTPPLKTVIRAIRIMKFNVA 524
 DB 465 RQAFRIKGAASRQNSE-EASLPGEDIVDCKSCPEFVEDLTPGLKVSIRAVCVMEFLVS 523
 QY 525 KRKFETLRPYDKVIVIOYSAGHLDMLCRISLQTRVDOILGGOITSDKRSREKITAE 584
 DB 524 KRKFESLRPYDVMVIEOYSAGHLDMLCRISLQTRVDOILGGOITSDKRSREKITAE 582
 QY 585 HETTDLSMLGRVYKVEKOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPPECC- 642
 DB 583 TELPEDPMGMRLGKVEKOVLSMEKKLDPLVSIYTO--RMG-----IPPTETEA 629

OY 643 -----EQTSDYQSPVDSKDLSSAONSGC---LSRSTSANISRGLOFILTPNEFSAGT 692
 DB 630 YFGAKEPEPAPYPHSPEDSRD---HADKHGCIIVKIVSTSS-----TCGR 671
 OY 693 FYALSTPMHSQATQVPIPSOS 712
 DB 672 NYAAPPAI--PPAACPPTS 689
 RESULT 16
 ABG10644
 ID ABG10644 standard; protein; 912 AA.
 AC ABG10644;
 XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #10635.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 DR N-PSDB; AAS74831.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 20; SEQ ID No 41003; 103bp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantifying a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of drugs and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 912 AA;
 Query Match 37.8%; Score 1790.5; DB 22; Length 912;

Best Local Similarity 47.7%; Pred. No. 1,2e-150;
 Matches 411; Conservative 91; Mismatches 196; Indels 164; Gaps 25;
 OY 21 GAAAAAAGGGLGSGMGKDVESGRVULNSAARQDGLLTGTAATLGGGGGLRESRR 80
 DB 67 GYPPGSPGEEKKLKGVFGLDPGA-----PDSTRGALLIAGSEAK---RGSILKPR 117
 OY 81 GKQGARMSLCKPLSTYSQSCRVRVRYVNYLYNLERGMAFTYHAFVLLVFGC 140
 DB 118 GGAGA-----GKP-----PKRNFYRKLNFLNLYLERPRGMFIYHAFVLLVFGC 164
 OY 141 LILVFSTIPEHTKLASSCLLILEFVMTVEFGLFEFIRFTWSGCCCRYGMOGRLEFARK 200
 DB 165 LVLSVFSTIEKEKSSBGLALILEVTIVYVEFVRMAAGCCCRYGMRKLEFARK 224
 OY 201 PCFVIDITVLIASTAVVSAKTQGNIPATSALESLFLQILNVRMDRDRGTWKLGSVY 260
 DB 225 PCFVIDIMVLIASTAVVLAAGSQGNVFAFSALRSLFLQILNVRMDRDRGTWKLGSVY 284
 OY 261 AHSKELITAMVIGFLVLFSSFLVYVLEKDKNESTYADALMNGTITITIGYGTPL 320
 DB 285 AHSKELITAMVIGFLVLFSSFLVYVLEKDKNESTYADALMNGTITITIGYGTPL 344
 OY 321 TWLGRLLSAGFALLGISFALPAGILGSGFALKVQEOHRKHFEKRRNPAANILQVMS 380
 DB 345 TWNGRLLAATFTLIGVFEFALPAGILGSGFALKVQEOHRKHFEKRRNPAANILQVMS 404
 OY 381 YAAD-----EKSVIATWK-----PHLKALHTC----- 403
 DB 405 YATNLSRTDHSWYERYTYVPMYSQOTYGSRLPLPLNQLDELRLNLSKSLAER 464
 OY 404 -----SPTNOKLSFKERYRMASPROGSIKRSOASVGD--RRSPSTITAGSPTRYOK 454
 DB 465 KQPPPEPSP-SQAVSLKDRV-FSSPRGVAAGKSPQAQYVRKSSADQSLDSSPKVX 522
 OY 455 SMSFNDTRPRPLRLKSSQPKPVYIDATLGTDDYDEKQCCQDVSEDLTPPLKTYR 514
 DB 523 SMSFGDRSRAHQAFRIKGAASRQNSE-EASLPGEDIVDKCPCFEVETDLTPGLKVSIR 581
 OY 515 AIRIKKFNVAKKFKETLRPYDVYDEQVSAGHLMICRKSQIOTRDOIIGKQIISD 574
 DB 582 AYCVMRFVLSKRFKESLRPYDVMDVLEQVSAGHLMISRIKSLQSRVDQIVGRPAITD 641
 OY 575 KKSREKITAHEHTDLSMLGRVYVKEQVQISKLDCLDIYQOVLKGSASALALAS 634
 DB 642 -KDRTKGPAEALPEDEPSMVGRLGKQVLSMEKIDFLVNIYMQ--RMG----- 689
 OY 635 FQIPPEEC-----EQTSDYQSPVDSKDLSSAONSGCLSRSTSANISRGLOFILTP 685
 DB 690 --IPPEETAVYFGAKEPEPAPYPHSPEDSRD---HYDRHGCIIVKIVRSSSTG-----Q 738
 OY 686 NEFSAQTFYALSTPMHSQATQVPIPSOS-----DGSAAVATNTIANQINAPAPAPT 737
 DB 739 KNFSAPP--AAP-----VQCPPTSWMQPSHRQGHGSPVDGHSVLIPIPPAHER 790
 OY 738 TLQI-----PP-----PLPAIHLPRFTLHPNPAQLQ 765
 DB 791 SLTAVGAGNRASMEFLRQEDTPGCRPEETLRDSDTISIPSVH-----ELHMSFGSF 845
 OY 766 ESISDVTTCLVASKENVAQAS 787
 DB 846 -SISO-----SKENIDALINS 859
 RESULT 17
 AAY08347
 ID AAY08347 standard; protein; 930 AA.
 AC AAY08347;
 XX 22-JUL-1999 (first entry)
 XX Human mutant KCNO2 protein.
 DE

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myoclonic epilepsy;
 KW JM; Rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening.
 XX Homo sapiens.
 OS Synthetic.
 XX W09921875-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98WO-US22375.
 XX PR 24-OCT-1997; 97US-0063147.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Charlier C, Leppert MF, Singh NA;
 XX DR WPI: 1999-312938/26.
 XX DR N-PSDB; AAX57145.
 XX PT Nucleic acid encoding potassium channels KCNQ2 and 3
 PS Claim 1: Page 172-176; 195pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 CC
 XX Sequence 930 AA:
 SQ
 Query Match 37.8%; Score 1789.5; DB 20; Length 930;
 Best Local Similarity 43.9%; Pred. No. 1.5e-150;
 Matches 433; Conservative 109; Mismatches 246; Indels 199; Gaps 26;

DB 287 TWNGRLLAATFTLLIGVFALPAGILSGFALKVQEOHROKHFEKRRNPAGLLQSAWRF 346
 QY 381 YAAD-----EKSYIATWK-----PILKALHT----- 402
 DB 347 YATNLSTRLDHSWTWYERTVTPMYSQOTQYASRLIPLNOLLELRNLKSKGLAFR 406
 QY 403 -----CSP--TWOKLSFERVMAASPRGOSIKRQASVGD--RR 437
 DB 407 KDPPEPSPKSGRCRGLGCCCGGRSSQKSLNDRV-FSSPRGVAAGKSGSPQAOYRR 465
 QY 438 SPSPDITAEOSPPTVKQSWSPENDRTFRPRLSLKSSQPKPYIADTALGTDVDYDEKGCQ 497
 DB 466 SPADQSLDESPSKVPSKWSFGRSRAQAFRIKGAARQNSE-BASLPGEDIVDDKSCP 524
 QY 498 CDVSVEDLTPPLKTVYTRAIRIMKHVAKRKRETLRPVDVDTQYASGHIDMLCRKS 557
 DB 525 CEFTVEDLTPGLKVSIRAVCYMRFLVSKRKRESLRPYDMDVIEQYSGHIDMLSRKS 584
 QY 558 LQTRVDOLGQITSDKRSREKJTAEHETDLSMLGRVYVVEKOVOSIESKLDCLDI 617
 DB 585 LQSRVDQIVGRPAITD-KDRTKGAELDEDPSSMGRIGKVEKQVLSMEKKDLPLVNI 643
 QY 618 YQVYLKRGASALALASFOIPFEC-----EQTSDYQSPVDSKDLGSAQNSGCS 668
 DB 644 YMQ--RMG-----IPTEEAYFGAKEPEPAPPYHSPEDSRE--HYDRHCIV 687
 QY 669 RSTANISRGLQFLITPNEFSAQTLYALSPMHSAQTVPISQSGSANAATNTANQIN 728
 DB 688 KIVSSSSSTG-----QKN 700
 QY 729 TAPKPAFTTQIIPPL-----PAIKHLPETLH-----PNPAGLOESISPVTTCL 775
 DB 701 FSAPPAP-PVQCEPSTWQSHRQGHGSPVDHGSLVRLPPPAHERLSAAGCN 759
 QY 776 VASKEENVQVQASNLTK--DRSKRSFDMGGETLLSVCPWPKDLGKLSVQNLINSTEEL 833
 DB 760 RASMEFLRQEDTPGCRPEGNLRDS-----DTSISIPVDHDELSFSGFSISQSKENI 814
 QY 834 NIQLSGSSSSSGSGODFPKMRKSKLFTIDEV--GP-----ESTEDTTPAARQ 882
 DB 815 DALNSCIAVAAPCAKVRPTIAGESD--TDSDLCTPCGPPRRSATGEPPFDYGVAGIG 871
 QY 883 PAREAPASDSILRTGRSSRSQISCKAG 909
 DB 872 PGSEALG---QWTRPRPSSARCLRG 894
 RESULT 18
 ID AAY01529
 XX AAY01529 standard; Protein: 871 AA.
 AC AAY01529;
 DT 16-JUN-1999 (first entry)
 DE
 XX Amino acid sequence of human KCNQ2/KvL1.
 KW Human; KCNQ protein; nervous system-specific potassium channel;
 KW neuronal excitability; neurotransmitter release; KCNQ modulator;
 KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KW age-associated memory loss; learning deficiency; motor neuron disease;
 KW epilepsy; stroke.
 OS Homo sapiens.
 XX W09907832-A1.
 XX PD 18-FEB-1999.
 XX PF 26-JUN-1998; 98WO-US13276.
 XX PR 12-AUG-1997; 97US-0055599.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 914 AA;

Query Match 37.8%; Score 1788.5; DB 22; Length 914;

Best Local Similarity 45.6%; Pred. No. 1.7e-150; Indels 199; Gaps 27; Matches 420; Conservative 91; Mismatches 211;

```

QY 2 PRHAGGEGGAGAGLW-----VKSAAAAAGGRLGSGMKDVEGSGRGLVLSA----- 51
DB 5 PPRCGSGRPGGLG--WGRRRPRRSAPAPPEPDGRLPQGTWQKSNNGVYGPSEKKL 62
QY 52 -----AARGDCLLLGTRAAATLGGGGGLRESRGKQKAGMSLLGKPLSYTS 98
DB 63 KVFVGGLDPGAPADSTRDGLALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP----- 109
QY 99 SQRBRNRYKRYOVYLVNLERPRGMAFIYHAFVLVFGGLISVFSTIPEHTKLAS 158
DB 110 ---PKRNFYKFLQVNLVLERPRGMAFIYHAFVLVFGGLISVFSTIPEHTKLAS 166
QY 159 CLILFEYVIVFGLFIIRIWSAGCCCRYRGMOGRLEAPKPCVYIDTVLIASIAVVS 218
DB 167 ALYILEIYIVFVGEYEVIRIWAAGCCCRYRGMRGRLEAPKPCVYIDTVLIASIAVLA 226
QY 219 AKTGNINATISALSLRLQILIRMYRMDRGSTWKLISVYVAHSELTAMVIGFLVLI 278
DB 227 AGSGGNVATISALSLRLQILIRMYRMDRGSTWKLISVYVAHSELTAMVIGFLVLI 286
QY 279 FSSFLVYVVEKDANKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAGFALLGISF 338
DB 287 LASFLVYLAEGENHFDYDALMWGLTTLTIGYDGTPLTWLGRLLSAGFALLGISF 346
QY 339 FALPAGILSGFALVQEQHROKHEKRRNPAANLIQCYWRSTYAD-----E 385
DB 347 FALPAGILSGFALVQEQHROKHEKRRNPAANLIQCYWRSTYAD-----E 406
QY 386 KSVSIATMK-----PHKALHT----- 402
DB 407 RTVYVPMYSSTOTYVAGASRLPLPNOLELLRLNLSKSGLAFFKDPPEPSFGSPGRCR 466
QY 403 ---TNOKLSFEREYRMAAPRQOSIKSRQASVGD--RSPSTDTIAGSPTKQVS 455
DB 467 LCGCCPGRSQKQVSLKDRY-FSSPRGVAAKKGSPQAQVYRSPASQSLSDSPSKVPS 525
QY 456 WSENDTRPRSLRLKSSQPKVYIADIALGDDVYDEKCCQCDVSEDTLPKTYIRA 515
DB 516 IIRIMEFVAKRKEFTLRPYDVYDEQY SAGHLMICRKSLOTRVDOILLGQOITS 575
QY 555 VCVMEFLVSKRKFESLRPYDVYDEQY SAGHLMICRKSLOTRVDOILLGQOITS 643
DB 576 KSRKRIAEHETTDLSMLGRVYVKEVQVQIESKIDCLLDIYQOVLKKSASALASAF 635
QY 644 KORTGPAPAELEPDEPSMGRGKVEKQVLSMEKIDELVINIYMQ--RMG----- 691
QY 636 QIIPPEEC-----EOTSQVQSPVDSKDLSSAQNQSLSTANISRGLOFILPN 686
DB 692 -IIPPEEYFEGAKKEPEAPYPHSPEDSRK---HVDHRCIYIVKVRSSSG---OK 741
QY 687 EFSAQTFYALSPTMHSQATOVPISSQ-----DGSANAVATNTIANDINTAPKPAFTT 738
DB 742 NTSAPP--AAPP-----VQCPSTSMQPSHPRQGHGTSRPGVGHSLVIRPPPAHRS 793
QY 739 LOI-----PP-----PLPAIKHLPPPELTHPPAGIOE 766
DB 794 LSAVGGNRAAMEFLRQEDTPEGCRPEGNLRDSDTISISVDH-----EELERSFSG-- 847
QY 767 SISDVTTCLVASKENOVQAS 787
DB 848 SISQ-----SKENDALNS 861

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RESULT 20

AAV23215

ID AAV23215 standard; Protein: 854 AA.

XX AAV23215;

XX 25-AUG-1999 (first entry)

XX Human brain-derived potassium channel protein.

XX Human; brain-derived potassium channel; neurophysiology;

XX cognitive disorder; behavioural disorder; psychiatric disorder;

XX neurodegenerative disorder; developmental disorder; mental retardation;

XX asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;

XX Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;

XX amyotrophic lateral sclerosis; retinitis pigmentosa;

XX cerebellar degeneration; urinary incontinence; diabetes; asthma;

XX premature labour; hypertension; cardiac ischemia; arrhythmia;

XX autoimmune disease; cancer; graft rejection; inflammation; allergy;

XX proliferative disorder; anaemia; autoimmune disease;

XX type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;

XX Sjogren's syndrome; mixed connective tissue disease;

XX experimental allergic encephalomyelitis; rheumatoid arthritis.

XX Homo sapiens.

XX W09931232-A1.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-GB03720.

XX 13-DEC-1997; 97GB-0026339.

XX (ZENNE) ZENNECA LTD.

XX Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;

XX WPI: 1999-395178/33.

XX N-PSDB: AAX81547.

XX New isolated potassium channel polypeptide

XX Claim 6; Fig 3; 151pp; English.

XX The present sequence represents a human brain-derived potassium channel.

XX compounds that modulate the biological activity of a potassium channel

XX or neurophysiology. It is used as a method of treatment for patients

XX with conditions which are mediated by the biological activity of a

XX human potassium channel. Antagonists can be used in modulating cognitive,

XX behavioural, psychiatric, neurodegenerative and developmental disorders

XX (mental retardation) as well as asthma, migraine, epilepsy and stroke

XX and brain tumours. They can be used for treating diseases such as

XX Huntington's disease, Lou Gehrig's, neurodegeneration, multiple

XX sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis

XX pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,

XX asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,

XX autoimmune diseases, cancer, graft rejections, acute and chronic

XX inflammation, allergies, proliferative disorders, anaemias, as well as

XX neurodegenerative diseases with immunological components, as well as

XX autoimmune diseases including rheumatoid arthritis, type-1 diabetes

XX mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's

XX syndrome, mixed connective tissue disease, and experimental allergic

XX encephalomyelitis (EAE).

XX Sequence 854 AA;

XX Query Match 37.7%; Score 1786; DB 20; Length 854;

XX Best Local Similarity 47.7%; Pred. No. 2.6e-150;

XX Matches 411; Conservative 91; Mismatches 196; Indels 164; Gaps 25;


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QY 381 YAAD-----EKSYIATWK-----PHLKALHT-----402
D 347 YATNLSFTDLHSTWQYERYVTWPMYSQOTQYASRLIPLNQLELLNLKSKSGLAFR 406
QY 403 -----CSP--TNQKLSFEKRVEMASPGOSIKSRQASVGD--RR 437
D 407 KDPPEPSPKSGPCRCRGLCCGCCGRSQQKYSIKMRV--FSSPRGVAANKGSPQAQTVAR 465
QY 438 SPSTDTAEGSPYTVOKSMWFSNDRTFRPSRLKSKSQPKPVADTALCTDDVYDEKGCQ 497
D 466 SPASDQSLIEDSPSKYKPSKMSFGDSRSRAQAFRIKGAASRQNSE--EASLPGEDIVDKSCP 524
QY 498 CDVSEVELPLPLKVIRAIRIMKPHVAKRKKEETLRPDVKVITQYSAGHIDMLCRIS 557
D 525 CEVTEDELTPGLKVSIRAVCVARFLVSKRKRESLPPYDQVMDVIEQYSGHIDMLSRIS 584
QY 558 LQTRVDDQLLKGQITSDKRSREKITYAEHTTDDLMLGRVYVEKOVQSIKSLDCLDI 617
D 585 LQSHVDQIVGRPAITD--KDRTKGPAEALPEDPMSMGRLGKVEKQVLSMEKKLDPLVNI 643
QY 618 YQOVLKRGASALALASFOIRPEEC-----EQTSYQSPVDSKDLSGSQRNSGCLS 668
D 644 YMQ--RMG-----IPPTTEAYFGAKEPEPPAPYHSPEDSRE--HYDRHGCIY 687
QY 669 RSTGANISRGLOFILPNEFSQOTFYALSPTMHSQATQVPIQS-----DGSAYVAT 720
D 688 KIVSSSSSTG-----QKNFSAPP--AAP-----VQCPPTSMQPSHPRQGHGTSY 733
QY 721 NTIANQINTAPKPAAPTLLQI-----PP-----PLPAT 748
D 734 GDHDSLVIRIPPPAHERSLSAYGGNRRASMEFLRQEDTGCRRPEGNLRDSDTSISIPSV 753
QY 749 KHLPRPELHNPAGLQESISDVYTCVASKENVOYAS 787
D 794 DH---EELERSFSGF--SISQ-----SKENLDALNS 819

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RESULT 22

AA08345

AA08345 standard: Protein: 757 AA.

```

AC AAY08345;
AC AAY08345;
DT 22-JUL-1999 (first entry)
DE Mouse partial KCNQ2 protein.
DE KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
DE benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
DE JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
DE detection; gene therapy; drug screening.
OS Mus musculus.
PN MO9921875-A1.
XX 06-MAY-1999.
XX 23-OCT-1998; 98WO-US22375.
XX 24-OCT-1997; 97US-0063147.
XX (UTAH) UNIV UTAH RES FOUND.
XX Charlier C, Leppert MF, Singh NA;
XX WPI; 1999-312938/26.
XX DR N-PSDB; AAX57140.
XX Nucleic acid encoding potassium channels KCNQ2 and 3
XX PS Claim 1, Page 156-159; 195pp; English.
XX

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CC This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 or KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent the forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.

Sequence 757 AA;

Query Match 37.2%; Score 1761; DB 20; Length 757;
 Best Local Similarity 51.8%; Pred. No. 3.7e-148;
 Matches 395; Conservative 77; Mismatches 200; Indels 90; Gaps 18;

```

21 GAAAAAGGGRILGSGMKDVEGRCGRVLLNSAARGDGLLTGTRATILGGGGGLRESR 80
9 GYVGTGSEXXLLKTVGVLDPG-----XPXSTRGKLLILAGSEAPK---RGXLLSKPRT 59
81 GKQGRMSLKLKPLSTYSQSCRNVKRRVONYLYNVLERRGNAFYIHAFFVLLPFC 140
60 GGAGG-----GKPPX-----RNAFYKILQNFYLVIERGKAFYIHAFFVLLPFC 106
141 LILVSESTIPRHTKLASSCLLLEFVMYVFGLEFIRIWSAGCCCRYGMGRFLPARK 200
107 LVLSVFSTIKYEKSEBAGALVLEIYTVVEFVEFVRIMAGCCCRYGMGRFLPARK 166
201 PCVYIDTVILASIAVVSAGTQGNIFATSAISLRFLOILRVNRDRDRCGTWKLGSVY 260
167 PECVIDIVVLASIAVLAAGSGVNFATSLRSLRFLQILRIMRDRDRCGTWKLGSVY 226
261 AHSKELTAWYIGFLVLFSSFLVYLVEKDAKKESTVDALIMWGITLTITGGYKPTL 320
227 AHSKELTAWYIGFLVLFSSFLVYLVEKDAKKESTVDALIMWGITLTITGGYKPTL 286
321 TWLGRLLSAGFALGISEFPALPAGILGSGFALKVQEOHOKHFEKRRNPAANLIQCVMS 380
287 TWNGRLLAATFLIIGVSFPALPAGILGSGFALKVQEOHOKHFEKRRNPAANLIQCVMS 346
381 YAADKESVSI--ATWK-----PHLKALHTGSPNTOK--LSRK 413
347 YATNLSFTDLHSTWQYERYVTWPMYSQOTQYASRLIPLNQLELLNLKSKSGLTFR 406
414 ERYR---WASPRGOSIKSRQASVGD--RSPSTDTAEGSPYTVOKSMWFSNDRTFRPSL 468
407 KEQPEPSPSPRGMAKAGSGPQAQTVRSFASDQSLDPSKVPKMSFGDSRSRQAF 466
469 RLKSSOPKPVADADALGTDVYDEKGCQDVSEVELPLPLKVIRAIRIMKPHVAKRK 528
467 RIKGAASRQNSEASLIPGEDIYEDNKSCEFTEDLTGKKSIRAVCMRFLVSKRK 526
529 KETLRPDVKVIEQYSGHIDMLCRIKSLQTRVDDILKGOQITSDKRSREKITYAEHTT 588
527 KESLRPDVMDVIEQYSGHIDMLCRIKSLQTRVDDIVRGPTITD--KDRTKGPAETELP 585
589 DDLMLGRVYVEKOVQSIKSLDCLDIYQVLKRGASALALASFOIRPEECQTSY 648
586 EDPMSMGRLGKVEKQVLSMEKKLDPLVSIYTO--RMGIDPAETEAIFGAK--EPEPAPPY 641
649 GSPVDSKDLSGSQRNSGCL--LSRSTANISRGLOFILPNEFSQOTFYALSPTMHSQAT 705
642 HSPEDSRD---HADKHGCIITKIVRSST-----TGQRNVAAAPA----- 677
QY 706 QVPISQDSGSAVAATNTIANQINTAPKPAAPTLLQIPPLPA 747

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Db          678 -IPPAQCPFS--TSMRSHQHRCRHSPPGHDGLVRLT-PPLPA 715

RESULT 23
ABGI0645
ID   ABGI0645 standard; Protein; 942 AA.
XX
AC   ABGI0645;
XX
DT   13-FEB-2002 (first entry)
XX
DE   Novel human diagnostic protein #10636.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001MO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
XX   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   MPI: 2001-639362/73.
XX   N-PSDB; AAS74832.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity
XX
PS   Claim 20; SEQ ID NO 41004; 103pp; English.
XX
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ   Sequence 942 AA;

Query Match          36.2%; Score 1711.5; DB 22; Length 942;
Best Local Similarity 47.1%; Pred. No. 1.4e-143;
Matches 396; Conservative 90; Mismatches 214; Indels 141; Gaps 24,
21 GAAAAAAGCGRIGSGMKDVEESGRCGRVLLNSAARGDGLLIGTRATYLGCGGGGARERR 80
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
9 GVGVPGESEKTLKTFVGVDIGA-----PSTRGALLINSESPK--RSTLISKPPA 59

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QY	81	GKQAMRSLILGKPLSTYSQSQRNRYKVRNQNLYVLEPRGMATYNAFVLLVGGC	140
Db	60	GGAGA-----GKR-----PKRMATRYKLQNFVLYLERPRGMATYNAFVLLVESC	106
QY	141	LILSVSTIPERTKLASSCLLIEFVMIIVFGLEFIIRISAGCCCRGMQGRLPARK	200
Db	107	LVLVSSTIKEYEKSSGALYILIEIVIVVEGVEYFVRIMAGCCCRGMGRGLPARK	166
QY	201	PECVITFLVIAIAVYSAKTOGNIFATSLRSIRFQILRMVMDRGGTWWLLGSVY	266
Db	167	PECVIDIMVLIAIAVLAAGSQGNVRTSALRSIRFQILRMIMDRGGTWWLLGSVY	226
QY	261	ANSKELITAMYIGFVLVLPSSFLVYLVKDNANKEFSTYADALMWGITLLTLYGDKTPL	320
Db	227	ANSKELITAMYIGFLLCLILASFLVYLVAEKENDEHFDYADALMWGITLLTLYGDKYPO	286
QY	321	TWLGRLISAGFALISFPAIRPGILIGSGFALVVOOHROKHKEKRRNPANILQCYMS	380
Db	287	TWNGRLILATFTLLIGSFALRPGILIGSGFALVVOEDHROKHKEKRRNPAGILQSAWRF	346
QY	381	YAAD-----EKSVSLATWK--PHLKALHTCSPTNOK--LSF-KEEVIRMA SPR	422
Db	347	YATNLSTRDLHSTWQYERTVTPVPMRYRLPLNQLELRLNLSKSGLAFLRKDDPPRSPS	406
QY	423	GGSIKSRQASVGDNRSPSTDITAE-----GSPTVQKQSWMSNDNTRRPPSLRLKSSOP	475
Db	407	QPPRRGCGGEGVAPGPDCEAVTQRRPRRPPRPPARCPSWSPGDSRRARQAFRIRIGAS	466
QY	476	KFVIDADTALGTDDVYDEKGCOCODVSEDLTPRLKIVIRAIRIMKRFHVAKRKRETLRPY	535
Db	467	RQNSE-EASLPGEDIVDKSCPEFTEDELTLGLKYSIAVQCYMRFLVSKRKKESLRPY	525
QY	536	DYKDVIIEQYSAHLDMLCRKIKSLQTVVDOLILGKQITSPKRSREKITAETHETDLSMLG	595
Db	526	DVMDVIEQYSAHLDMLSRKIKSLQSHVDQIVGRPAITD-KORTKPAEAELPRDPSMNG	584
QY	596	RYVVKTEKQOYISIESKLDCLDIYQVLRKKSASALALASFOIIPFPFC-----EQTS	646
Db	585	RLGKVEKQVLSNEKKLDELVLNLYMQ--RMG-----IPPTTEAYFGAKKEPPAP	631
QY	647	DYQSYVDKDLSSGAKNSGCLSRSTISANISRLGLQTLTPNEFSAQTFVALSPTMHSQATQ	706
Db	632	PRHSEDSRE---HYDRHGCIYKIVRSSSSSTG-----OKNSAPR--AAP-----VQ	674
QY	707	VPISGS-----DGSAAVAAENTIANQNTAPKPAAPTLDI-----	741
Db	675	CPSPSTSMQPOSHPRQHGHSIPVGDHGSIVLRIPPRAHENSLAYGGGNASMEFLROEDT	734
QY	742	-----PP-----PLPAIKHLPRPETHLPNPAIGLOESISDYVTTCLVASKENYQVAQ	786
Db	735	PGCRPEEGTLRDSITSISIPSYDH-----EELERSFSGF-----SKENDALN	781
QY	787	S 787	
Db	782	S 782	
RESULT 24			
ID AAY08344			
AAV08344 standard; Protein; 872 AA.			
XX AAY08344;			
DT 22-JUL-1999 (first entry)			
XX Human KCNQ3 protein.			
DE			
KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;			
benign familial neonatal epilepsy; BFNE; juvenile myoclonic epilepsy;			
KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;			
detection; gene therapy; drug screening.			
XX			

OS Homo sapiens.
 XX W09921875-A1.
 XX 06-MAY-1999.
 XX 23-OCT-1998; 98MO-US22375.
 XX 24-OCT-1997; 97US-0063147.
 PR (UTAH) UNIV UTAH RES FOUND.
 XX Charlier C, Leppert WF, Singh NA;
 XX WPI; 1999-312938/26.
 DR N-PSDB; AAK57059.
 XX Nucleic acid encoding potassium channels KCNQ2 and 3
 PS Claim 1; Page 136-139; 1999pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 CC
 XX Sequence 872 AA:
 S0 Query Match 34.2%; Score 1620.5; DB 20; Length 872;
 Best Local Similarity 42.2%; Pred. No. 1.8e-135;
 Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;
 QY 7 GGEBCGAAGLWVKGAAAGGRLGSGMDVSGRGR-----VLNSAARCGLL 60
 DB 14 GGGGGGGG-----GGAANPAGGDAAGADEERKVLAFGDVEQVTLAAGADKDGTL 68
 QY 61 LGTRAAATLGGGGGGLRESRKGOGARMSLLGK-PLSTYSQSGRRVVKYRRVQNYLYNVL 119
 DB 69 L-----EGGGRDEGGRTPQG--TGLAATPLSRPVK---RNNAKTRRIOTLTLYDAL 115
 QY 120 ERPRGMFAVFAFVLWFGCLLSVFTIPEHTKLASSCLILEFVMVFGLEFIRI 179
 DB 116 ERPRGMALYHALVFLVILGCLLAVLTFFKRYEYVSGWMLLLEFFALFIFEAEALRI 175
 QY 180 WSAGCCCTYRKGQGLRPARKPFVYDITVLASTAVSAKQGNFATLSLRFLQI 239
 DB 176 WAAGCCCTYRKGRLKFAKRLKMLDIFVLASVAVVAVGQGNVLAIS-LRSLRFLQI 234
 QY 240 LRMVMDRGGTGWKLGSVVAVSHKELTAVTIGFVLFFSSFLVVLVEDA----- 291
 DB 235 LRLMDRGGTGWKLGSVICHASKELTAVTIGFVLFFSSFLVVLVEDA----- 294
 QY 292 --NKEESTYADALMWGITLTITIGYGDKPTLWGLRLSAGFALLGISFPALPAGILSG 349
 DB 295 EKKEEFETYADALMWGITLTITIGYGDKPTKTEWGLIATFSLIGVSFPALPAGILSG 354
 QY 350 FALKVOEORHKKHFEKRRRPAANLIQCVKRSAADEKSVS-TATWK-----PHIKAL 400
 DB 355 FALKVOEORHKKHFEKRRRPAELIQAAWRYATNPNRIDLVTWTRFYESVSPFPRKE 414

QY 401 HTCSPTNOKLSFEKRYVMASPRQSLKRSOASVGRDRSPSTDTIAEGSPTRKQKSWISFND 460
 DB 415 QLEAASSQKGLDRVRLNSPRGSNTK-----GKLFPLNVDALIEESPSEKRPVGLNN 468
 QY 461 RTFRPSLRK-----SSQPKYIDADLTALGTDVYDEKGCQCDVSDVETLPLKTYIR 514
 DB 469 KERFRTRAFRMKAVAFWQSSSE-----DAGTG---DPMEDRGYGDPLIEDMIPILKAIR 520
 QY 515 AIRIMKFAKRRKFEKTLRPYDVYDEOXSAGHLDMICRKSLOTNRDQILGQOTSND 574
 DB 521 AVRILQRLYKKKFKETLRPYDVAVDIOYSAGHLDMISRKTYQTRIDMLFTPEPSTP 580
 QY 575 KKSRR-----EKITAEHTT--DDLMSLGRVAVKQVOSIESKLDCL 615
 DB 581 KHKKSQKSAFTPPSQGSFPRNEPVARPTSEIDQSMGKFKVAKEROVQDMGKLDPLV 640
 QY 616 DTYQOYLR-----KGSALALASFOJPPPECEDTSDYQSVDSKDLGSGMKN 663
 DB 641 DMHMHMERLOVOYTEYPTPKGTSS-----PAEAERKENRYS-DKTTIICNTSE 689
 QY 664 SGCLSRSTSANISGLQFILTPEFSQTFYALSPMTMSQATQVPIQSQSGAVATWTI 723
 DB 690 TGPEPEPSFH-----QVTDKVSPIGFRAHD-----VNLPRGSPSSGKVAT-- 733
 QY 724 ANQINTAPKPAAPTLLQIPPLPAIKLPRBETLHPNPAGQESIDVTTCLVASKENVQ 783
 DB 734 -----PPSATTYVERPVLPTLLTLDNSVSCG-SQADLQGPYSD-----RIS 775
 QY 784 VAQSNLTKDSMKRSFDMGCTLLSCVPMVKDLKSLSYONLIRSTELNQLSGSES 843
 DB 776 PRQ-----RRSITRDSPTPLT-----MSVNH-----BELERSPSGFSIS 810
 QY 844 GSRGODEFP-----KWRSEKLFITDEYGPETETDTE 877
 DB 811 QDRDYYFGPNGGSSMKREKRYLAE--GETDTIDPF 845
 RESULT 25
 ID AAE16620 standard; Protein: 872 AA.
 AC AAE16620;
 DT 09-APR-2002 (first entry)
 XX
 DE Human potassium channel polypeptide, KCNQ3.
 XX
 KW Human; potassium channel polypeptide; KCNQ3; pain; migraine; stroke;
 KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis;
 KW ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
 KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
 KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
 KW learning deficiency; cognitive disorder; motor disease; neuron disease;
 KW neurophysiological disorder; neuropsychological disorder; asthma;
 KW neuron cell death; brain tumour; gene therapy; antisense therapy;
 KW synaptic transmission; electrical excitability; KCNQ3 protein.
 OS Homo sapiens.
 XX W0200192526-A1.
 XX 06-DEC-2001.
 XX 24-MAY-2001; 2001WO-US17314.
 XX 26-MAY-2000; 2000US-207389P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;
 PI Gribkoff VK;
 DR WPI; 2002-122069/16.

CC diseases, epilepsy, and stroke.

XX Sequence 854 AA;

Query Match 33.9%; Score 1603.5; DB 20; Length 854;
Best Local Similarity 42.7%; Pred. No. 5,8e-134;
Matches 393; Conservative 109; Mismatches 252; Indels 167; Gaps 29;

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20 SGAAGGAGG--GRLSGMKDYESGGRVLLNSAARGDGLLLGTRATLGGGGGLRE 77
DB 11 AGDAAAGDEERKVGCLAPDVEQ---VTALGAGADKDTLL-----EGCGREG 59
QY 78 SRGKGARMSLLGK-PLSTYSOSCRNRYRRQNTLVNLEPRGMATFYHAFVFL 136
DB 60 QRRTPQG--IGLAKTPLSRPVK--RNNAKYRRQTLIDALERPRGALLVHALVFL 114
QY 137 VEGCLISVFSTIEPHRTKLASSCLLIEFVMIIVVGFELIRMSAGCCCRYRGNQRLR 196
DB 115 VLGLLILAVLTTEFEYEVSGDWMLLLETFALIFGAFALRIMAGCCCRKMGRLK 174
QY 197 FARRPCVIDITVLIAIVAVSANTQNIETASLRSLFLOILNVRMDRGCTWKLIG 256
DB 175 FARRPLCMLDIFVLIAVYVAVGNQNLATS--LRSLRFLQILRMLRMDRGCTWKLIG 233
QY 257 SVVYAHSEKITAVYIGFLVLFSEFLVYLVEKDA-----NKESTYADALMNGT 306
DB 234 SAICAHSEKITAVYIGFLVLFSEFLVYLVEKDAPEVDAGCEMKEEFTYADALMNGL 293
QY 307 ITLTITIGDKTPTLWLGRLSAGFALLGISFALPAGILGSGFALKVOEHRKHFERR 366
DB 294 ITLTATIGGDKTPTWEGRLIAATFSLIGVSFALPAGILGSGFALKVOEHRKHFERR 353
QY 367 RNPANLILQCVRSYADEKVS--IAWK-----PLKALHTCSPLNOKLSFEERR 417
DB 354 RKPAAELIQAMRYATNPRIIDLVATWRFEYSVSFPFPEREOLAAASOKLGLDRVR 413
QY 418 MASRGSIKSRQASVGRSPSTDTAEGSPTKQKSMSPDRTRFERSRLRK----- 471
DB 414 LSNRGSMWK-----GKLTPLNDALEESPSKEPKPGLNKEKFRFAFRKAAFAWQ 467
QY 472 SSQPKPVADATAGTDVYDEKGCOCVSVEDLTPPLKTVIRAIRIMKFAVAKRFEET 531
DB 468 SSE-----DAGTG--DMAEDRGYGNDFIEDMITLKAATRAVRIILOFRLTKKRFET 519
QY 532 LRPDVKNVIOYSGHLMCRISLQTRVQIILKGQITSDKSR----- 578
DB 520 LRPDVKNVIOYSGHLMCRISLQTRVQIILKGQITSDKSR----- 578
QY 579 ----EKTAHEHTT--DDLMLGRVYKVEKQVQIESKLDCLDIYQVLR----- 623
DB 580 SPRNEPYVARPSTSEIDQSMAGKFKYKVRQYQDMCKKIDLVDMQHMNERLOVTEY 639
QY 624 ---KGSASALALASFQIPPECEQTSYQSPVDSKDLSSAONSGLSNSTANISRLG 680
DB 640 YPTKQTS-----PAEAKEKEDNRY--DLKTIICNYSETGPPEPPYSPH----- 682
QY 661 FILTPNESAOTFYALSPMHQAQOVPISQSDGSAVAANTNTIANINTAPKRAAPTTL 740
DB 663 -QVITDKVSPYGEFAHP-----VNLPRGSSSGKVQAT-----PPSSATTIYE 725
QY 741 IPPPLPAKHLPRPETLHPNAGLQESISDVTTCLVASKENYVAQSNILTKDSMRKSF 800
DB 726 RPTVPIILTLDSRSCH--SQADLQGYSD-----RISPRQ-----RISIT 765
QY 801 MGGFTLLVCPWVPKDLKSLSVQNLIRSTEELNIOSSGSSGSRGSDFTY----KWR 856
DB 766 RQSDPLSLT-----MSVNH-----EELERSPSGISQDRDQVYFGPGSSSM 809
QY 857 ESKLFTDEVGPEETETDTF 877
DB 810 REKRILAE---GETDTIDTDF 827

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RESULT 27

AY08346

ID AY08346 standard; Protein: 870 AA.

XX AY08346;

XX 22-JUL-1999 (first entry)

XX Mouse KCNQ3 protein.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;

XX benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;

XX JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;

XX detection; gene therapy; drug screening.

XX Mus musculus.

XX W09921875-A1.

XX 06-MAY-1999.

XX 23-OCT-1998; 98WO-US22375.

XX 24-OCT-1997; 97US-0063147.

XX (UTAH) UNIV UTAH RES FOUND.

XX Charlier C, Leppert MF, Singh NA;

XX WPI; 1999-312938/26.

XX N-PSDB; AAX57141.

XX Nucleic acid encoding potassium channels KCNQ2 and 3

XX Claim 1; Page 164-167; 195pp; English.

This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. CC Antibodies specific for mutant or wild-type proteins are used as CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are CC useful in rational design of drugs and therapeutically (in replacement CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and CC 3 sequences can now be diagnosed early (before symptoms are manifest), CC and better treatment options will be available.

XX Sequence 870 AA;

Query Match 33.2%; Score 1570.5; DB 20; Length 870;

Best Local Similarity 41.6%; Pred. No. 5,4e-131;

Matches 388; Conservative 109; Mismatches 273; Indels 163; Gaps 28;

7 GGEAGGAGLWVKSAAAAAGG-----RLGSGMKDYESGGRVLLNSAARGG 57

DB 12 GGEAGGAGG-----GGAANPAGDSAVAGDEERKVGOLAPDVEQ---VTALGAGADKDG 63

QY 58 LLLLTGTRATLGGGGGRLSRGOGAMSLGK-PLSTYSOSCRNRYRRQNTLVNLEPRGMATFYHAFVFL 116

DB 64 TLLT-----EGGREGGQRRTPQG--IGLAKTPLSRPVK--RNNAKRRIITGLY 110

QY 117 NVLERPRGMATFYHAFVFLVFGCLILSVSTPIPHETKLASSCLLIEFVMIIVFGLEFL 176

DB 111 DALERPRGMATFYHAFVFLVFGCLILAVLTTFKEYEVSGDWMLLLETFALIFGAEFA 170

QY 177 IRMSAGCCCRKRGQGRLEFARRKPCVIDITVLIAIVAVSAKTQGNIFATSLSLRF 236

QY 400 LHTCSPTNOKLSFEKERVMASSPGOSIKRSQASVGDNRSPSDITAEPSPTKQKWSFN 459
 Db 415 EOLEAASSOKLGLDRLVLSNPRGSNTK-----GKLFPLVNDALIESPSKEPKVGLN 468
 QY 460 DRTFRPSLRK-----SSQPKPVIDADTALGTDDVYDEKGCOCQDVSEDLPLPLKTVI 513
 Db 469 NKEFRFTRFMRKAYAFWQSS-----DAGTG---DPMADRGYGNDFIEDMPTLKAAI 520
 QY 514 RAIRIKKPHVAKRKKEKTELPRYDKVYIEOVSAGHLDMLCRISLQTRVDQILGKQITS 573
 Db 521 RAVRILOFRLYKKKKEKTELPRYDKVYIEOVSAGHLDMLCRISLQTRVDQILGKQITS 580
 QY 574 DKRSREKITAHE-----ETTDLSMLGRVVK-VEKOVQSIESTK 610
 Db 581 PKHKEVFRKGGHFTFPSSQSSRGLNHNKXARPSTSEIEDORHXWKGKFKVSKLGVOGLGRK 640
 QY 611 LDCLDIYQOVLK-----KGSASALALASFOIPECEQTSYQSPVSDKLS 658
 Db 641 LDPLVDMHMQHMERLQOVTEYTPKGTSS-----PAEAKKEDNRYS-DLKTIL 689
 QY 659 GSAONSGLSSTSNISRGLOFILTPNEFSQOTFALSPMTMSQATQVPISQSDSAYA 718
 Db 690 CNYSETGPEPPYSFH-----QVTIDVSPYGFPAHD-----VNLPRGGSPSGKVQ 736
 QY 719 ATNTIANQINTAPKPAAPTLTQIPPLPAIKHLPRPETLHPNAGLOESISDVTTCIVAS 778
 Db 737 AT-----PPSSATTYVERPYVPLITLLDSRVSCH-SQADLQGPYSD----- 777
 QY 779 KENVQVQASNLTKRDSMRKSFDMGCELTLLSCPMVKDLGKLSYONLIRSTEELNIQLS 838
 Db 778 --RISPRQ-----RRSITRDSPTLSL-----MSVNH-----EELERSPS 810
 QY 839 GSESGSGSGQDFY---KMRSEKLFITDEVEYPEETENDTF 877
 Db 811 GFSISQDRDDYVFGPGSGSSMMREKRYLAE---GETTDTPDPF 830

RESULT 29

ABG19734
 ID ABG19734 standard. Protein; 1375 AA.

AC ABG19734;
 XX 18-FEB-2002 (first entry)
 DT XX
 DE Novel human diagnostic protein #19725.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSB-) HYSBQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS83921.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnosis, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX

PS Claim 20; SEQ ID No 50093; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1375 AA;
 Query Match 32.6%; Score 1544; DB 22; Length 1375;
 Best Local Similarity 41.0%; Pred. No. 2,7e-128;
 Matches 387; Conservative 109; Mismatches 269; Indels 178; Gaps 30;
 QY 7 GGEEGAAGLWVKSAAAAAGGRLGSGMKVDSGRG-----VLNSAARGCILL 60
 Db 83 GGGDGGGG-----GGAANPAGDAAAGADEERKGLAPGDVEOVTALGAGDKGCTLL 137
 QY 61 LGTRATILGGGGGLRESRKGARMSLIGK-PLSYTSQSCRNVKRYRVOYNYLV 119
 Db 138 L-----EGGGRDEGQRTPDG--TGLAKTPLSPVK---RNNAKTRRIOTLIYDAL 184
 QY 120 EPRGMATYHAFVFLVFGCLLSYFTSTPETHKLASSCLLIEFVIMVFGLEPIRTI 179
 Db 185 EPRGMALLYHAFVFLVFGCLLAVLTFFKEEYVSGDWLLLEFPAIFGAEFALRI 244
 QY 180 WSAGCCCRKRGWGRIRFAKRPCCVDTIVLIASIVVSAKNGINFATSLASIRLOI 239
 Db 245 WAAAGCCCRKRGWGRIRFAKRPCCVDTIVLIASIVVSAKNGINFATSLASIRLOI 303
 QY 240 LRMVR-MDRRGSTWKLGSVVAHSHKELTAVYIGFLVIFSSFLVYVEKDA----- 291
 Db 304 LRLMDGPEGGTWWKLSAICAHSHKELTAVYIGFLVIFSSFLVYVEKDPVENDAG 363
 QY 292 ---NKEFSYADALMMGTTLTITGYGDKTPTLWLGRLSAGFALLGISFPALPAGILGS 348
 Db 364 EEMKEFEFYADALMMGTTLTITGYGDKTPTLWLGRLSAGFALLGISFPALPAGILGS 423
 QY 349 GFALVYEOHOKHFEKRRNPAANLIQCVRSTAADEKYS-IATWK-----PILKA 399
 Db 424 GLALKVYEOHOKHFEKRRNPAANLIQCVRSTAADEKYS-IATWK-----PILKA 483
 QY 400 LHTCSPTNOKLSFEKERVMASSPGOSIKRSQASVGDNRSPSDITAEPSPTKQKWSFN 459
 Db 484 EOLEAASSOKLGLDRLVLSNPRGSNTK-----GKLFPLVNDALIESPSKEPKVGLN 537
 QY 460 DRTFRPSLRK-----SSQPKPVIDADTALGTDDVYDEKGCOCQDVSEDLPLPLKTVI 513
 Db 538 NKEFRFTRFMRKAYAFWQSS-----DAGTG---DPMADRGYGNDFIEDMPTLKAAI 589
 QY 514 RAIRIKKPHVAKRKKEKTELPRYDKVYIEOVSAGHLDMLCRISLQTRVDQILGKQITS 573
 Db 590 RAVRILOFRLYKKKKEKTELPRYDKVYIEOVSAGHLDMLCRISLQTRVDQILGKQITS 649
 QY 574 DKRSREKITAHE-----ETTDLSMLGRVVK-VEKOVQSIESTK 610
 Db 650 PKHKEVFRKGGHFTFPSSQSSRGLNHNKXARPSTSEIEDORHXWKGKFKVSKLGVOGLGRK 709

D	b		641	FLVYMHQHMRRLQGVTEYPTKTS-----PAEKEDKNYS-DLKTIION	689
O	y		661	AQNSGCLSRSTSANISRGLQLPILTPNEFSACOTFYALSPMHSQAQVPPISSDGSVAAT	720
		:	:	: : : : : :	:
D	b		690	YSEFPEPPPSFHF-----QVTIDKVSYPGFFAHDP-----VNLPRGCPSSGKVQAT	736
O	y		721	NTIANQITAPKKPAPTLOIPPLPAIKHLRPETLHPNPAGLGESIDVYTCLVASKE	780
		:	:	: : : : : :	:
D	b		737	-----PPSATTYVERFTVLPIFLTLDLRVSCH-SQADLOGPYSD-----	775
O	y		781	NVOYAQSMLTKDRSMRKSFDMGGETLLSGCPWPVKDLGKSLSQVNLIRSTEELNQLSGS	840
		:	:	: : : : : :	:
D	b		776	RISRQ-----RSRTIDSDFPLSI-----MSVNH-----ELERPSPGF	810
O	y		841	ESSGRSGSQDFP---KWRESKLFTDEEGPEETDTDF	877
		:	:	: : : : : :	:
D	b		811	SISODRDQDYVGPNGSSMMREKRYLAIE--GETDTDDPF	848
 RESULT 31 AAW14282 ID AAW14282 standard; Protein; 393 AA. XX XX AAW14282; XX AC XX DT 09-JAN-1998 (first entry) XX DE Human K+ channel protein sequence. XX KW Human K+ channel protein sequence. XX KM Human; neuroblastoma; K+ channel; glioma; probe; diagnosis; detection; XX tumor. XX OS Homo sapiens. XX PN JP09191882-A. XX PD 29-JUL-1997. XX PF 16-JAN-1996; 96JP-0004726. XX PR 16-JAN-1996; 96JP-0004726. XX PA (NITSB) JAPAN TOBACCO INC. XX DR WP1; 1997-429182/40. XX DR N-PSDB; AAT85964. XX PT DNA encoding new human K+ channel protein - useful for detecting XX PT glioma(s) and tumours XX PS Claim 1; Page 10-12; 14pp; Japanese. XX CC This is the amino acid sequence of a novel human K+ channel protein XX CC which is expressed on human glioma cells. The encoding gene was isolated XX CC from a 3' directed cDNA library prepared from human neuroblastoma cell XX CC line CHP134. The screen isolated a clone designated GS008740 whose XX CC insert contained the coding sequence and the 5' and 3' sequences of the XX CC gene (AAT85964-6 respectively). Expression of the gene was detected in XX CC neuroblastoma cell lines. Oligonucleotides derived from the sequence of XX CC the K+ channel gene can be used as probes for diagnosing human gliomas, XX CC and in the detection of new tumours. XX SQ Sequence 393 AA;					
Q	y		Query Match	25.9%; Score 1227.5; DB 18; Length 393; Best Local Similarity 64.8%; Pred. No. 7.7e-101; Matches 243; Conservative 37; Mismatches 72; Indels 23; Gaps 5	
D	b		21	GAAAAAGGGRGSGMKDVESGRGYVLNSAAARGDGLLTGRAATTGGGGGLRESRR	80
		:	:	: : : : : :	:
D	b		9	GVYPPSPSGKKLVGFGVGLDPCA-----PDSTRDGALLIAGEAPK---RGSLISKPR	59
		:	:	: : : : : :	:
O	y		81	GKGGRMSLIGKPLISTTSSQSCRNNKYTRVQNYLYNLERPGMAFIYHAFFLVGC	140

[illegible]

CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.

XX Sequence 807 AA:

Query Match 25.1%; Score 1188; DB 20; Length 807;
 Best Local Similarity 37.7%; Pred. No. 8,7e-97;
 Matches 285; Conservative 118; Mismatches 186; Indels 166; Gaps 22;

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QY 75 LRESRRGKOGARMSLGLKPLSTSSOSCRNRKRVONLYNLERPGW-AFTYHAFV 133
DB 77 LADSEGNR-KMSLGGKPLTY--KNYRDFORFRMKNMHNLEPRGMKAATYHAY 131
QY 134 FLVVGCLLSEVSTPEHTKLASSCLLEFWMIVVFGLEFLIRMSAGCCRRGNOG 193
DB 132 LFMVLMCLALSVSTPDEPVNATIVLYLEIVFLATEYICRWASGCRSRKRGISG 191
QY 194 RLRFARKEPCVIDITVLIASIAVSAKTGNIPTASRLRFLQILRMVMDRRGTWK 253
DB 192 RIRFATSACVADIIVLASIVLIGATGVFAASAIRGRFQ-LRMLRIDRAGATWK 250
QY 254 LIGSVYVAHSEKELITRMVIGFLVLISSFLVYVEKANKFEETADALMWGTTLTIG 313
DB 251 LIGSVYVAHROELITVYVIGFLVLISSFLVYVEKANKFEETADALMWGTTLTIG 310
QY 314 YGDKTPLMVLGRSLSGFALLGISFALPAGIISGSGFALVQEDHROKHFEKRRPANA 373
DB 311 YGDKTPEWPGKITIAFCALLGISFALPAGIISGSGFALVQEDHROKHFEKRRPANA 370
QY 374 IQCVRSYAADEKSVSIATWKR--LKALHTCSP--TNOKLSFKERVMASPRGOSIK 427
DB 371 IQCLMRHYSAPESSTSLATWIKHLABELPRIVKTLPLGSNNATGLINLRQSTKRTPLN 430
QY 428 SRQASVGRDRS-----PSTDT-----AEG-----SPTVQKWS 457
DB 431 NQMLAVNSQATSKNLSVPRVNRHDTISLSTDISIEIOLGALGFSLGWKSXKYGSGSK 490
QY 458 FND-----RFRFRPSL-----RLKSOPKPVIDADTALG-- 486
DB 491 ATDSDVLOSRLAPSAHLDMDMRSRRSASLCRVVNTGHLRLQDRSTISDSGVITDY 550
QY 487 -----TDDVYD-----ERGCQC 498
DB 551 SLMAPIYOWCEOMYORNSTPGEQVWSQSLSQTLTTCATRTREDISDGEDEAVGYQ- 609
QY 499 DVSVEDLPPKTYVIRAIIMKFNHAKRKPELTPVDVDFEYASGHTDMLCRITSL 558
DB 610 PQTIEFTPALNCVRAIRIQLVARKKFKALKPRVDVLEIYOSAGHVDLOSRAKTV 669
QY 559 QTRVDOLIGKQITSDKRSREKITAETHETDLSMLGRVVKVEKOVOSIESKLDLDIY 618
DB 670 QAKIDFIG-----KNIETIEPK-----ISMFRITLETFTVCKMKKDLDMWL 715
QY 619 QOVLKGSASALALASFOIPECEQTSYQSPVDSKLSGSAONSCLSRSTANSIRG 678
DB 716 M-----GQASQGRVFSQNTSP-----RGEFSEPTSAQO-----DLFRSRSSWSTD 756
QY 679 LOFLITPNEFSAQTFYALSPTMHSOATQVPISSD 713
DB 757 MEM-----YIARSH-----SPGYHGDARPI-IAQID 781

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RESULT 33
 AAB82236 ID AAB82236 standard: Protein: 676 AA.

XX AAB82236;
 XX 21-JUN-2001 (first entry)
 XX Human KVLQ1 mutant S566F.
 XX DE

KW KVLQ1: Long QT syndrome; LQTS: cardiovascular disease;
 KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
 KW diagnosis; prognosis; therapy; drug screening; mutant; mutenl.

XX Homo sapiens.

XX WO200124681-A2.

PD 12-APR-2001.

PF 09-AUG-2000; 2000WO-0521660.

PR 09-AUG-1999; 99US-0147488.

PR 17-MAR-2000; 2000US-0190057.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

PI WPI; 2001-290564/30.

PT New KVLQ1 and SCN5A genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome -

PS Claim 6; Page -: 76pp; English.

CC The present sequence is that of the claimed S566F mutant of the
 CC human KVLQ1 protein. The mutant is encoded by a KVLQ1 mutant
 CC gene in which a C/T mutation alters codon 566 from TCC to TTC.
 CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:
 CC Y110C, E160K, R174H, G179S, A194P, R243C, W248R, I266P, V307SP,
 CC V310I, S349W, Q356K, R366Q, T391I, P448R, O530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX Sequence 676 AA:

Query Match 23.3%; Score 1104; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2.2e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

```

QY 98 SSQSCRNRKVR-RVQNTLYNLERPGW-AFTYHAFVLLVFGCLLSVSTIDEHTKL 155
DB 92 SITSTRPPLARHVOGRVYNFLERPGMKCFYHFAVFLIVLCILSVLSITQYAL 151
QY 156 ASSCLLIEFVMIVVGELEFLIRMSAGCCCRRYGWCGRLEFARKEPCVIDITVLIASIA 215
DB 152 ATGTLMEVLEVLVFEETEVRLMSAGCRKYVGLMRLRPARPISITIDLVVASV 211
QY 216 VVSAKTGNIFATSLRSLRFLQILRMVMDRRGTWKLSVYVAHSEKELITVAYIGFL 275
DB 212 VLVGSKQGVFAISAIRGIRFLQILRLMHDROGTWRLLSVYFIHQELITTYIGTL 271
QY 276 VLISSFLVYLVKDA-----NKESTYADALMWGTTLTIGYGDKTPFLWGLRLSAG 330
DB 272 GLIFSSYFVYLAEKDAVNESGRVFEYSADALMWGVVYVTIGYGDKVPQFTWVGKIASC 331
QY 331 FALGISFALPAGIISGSGFALVQEDHROKHFEKRRPANAIIQCVRSYAADEKSVSI 390
DB 332 FSVFAISFALPAGIISGSGFALVQEDHROKHFEKRRPANAIIQCVRSYAADEKSVSI 390

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QY 391 ATWKPLKAL---HT-CSPFNOKLSFKERYRMASPRGOSIKSROASVGDRRSPSTDITAE 446
 DB 391 -TWKIYIRKAPRSHLTLSFSPKP---KSYVYVKKKKFKLDKNDGVTEGKMLTYPHITCD 446
 QY 447 GSPTRVQKQKMS---FNDRTFRFSLRLKSSQPKPVIDADATGALGDVYDEKGCOCDSVE 503
 DB 447 PPEERLDFHFSVDGYDSSVAKSPPTL-LEVSMFH-----FMRINSFAD-----LDLEGE 494
 QY 504 DLTPPL-----KTVIRAIRIMKFNHAKRKFETLRYDYKDYIEQYSAGHLMIC 553
 DB 495 TLTPTTHISOLREHNRATIKVIRRMQFYAKKKFQOARKPYDRDYIEQYSOGLNLMV 554
 QY 554 RIKSLQTRVDQILGKQ---ITSDKSREKITAETHETDLSMLGRVYVKEKOVOSIESKL 611
 DB 555 RIKEIQRRLDQFSGPSLFTSVSEKSKDR-----GSNTIGARLNKRVEDKTYQLDQRL 606
 QY 612 DCLLDIYQGVL-----RKGS-----SALALASFOIPEE 641
 DB 607 ALITDMLHQLLSLHGSGTPGSGGPPREGGAHITQPCGSGGSVDPDLPLPSNTLPTYE 663

RESULT 34

AAB82229

ID AAB82229 standard; Protein; 676 AA.
 AC AAB82229;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Human KVLQ1 mutant V310I.

XX KVLQ1; Long QT syndrome; LQTS; cardiovascular disease;
 KM Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
 KM diagnosis; prognosis; therapy; drug screening; mutant; mutain.

XX Homo sapiens.
 PN WO200124681-A2.
 XX
 PD 12-APR-2001.

XX 09-AUG-2000; 2000MO-US21660.
 PF
 XX

XX 09-AUG-1999; 99US-0147488.
 PR
 XX 17-MAR-2000; 2000US-0190057.

XX (UTAH) UNIV UTAH RES FOUND.
 PA

XX Keating MT, Splawski I;
 PI

XX WPI; 2001-290564/30.
 DR

XX New KVLQ1 and SCNSA genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome
 PS
 XX
 PS Claim 6; Page -: 76pp; English.

XX The present sequence is that of the claimed V310I mutant of the
 CC human KVLQ1 protein. The mutant is encoded by a KVLQ1 mutant
 CC gene in which a G/A mutation alters codon 310 from GTC to ATC.
 CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:
 CC V310I, S349W, Q356R, R366Q, T391I, P448R, Q530X, S566F, V307SP,
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human

CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the Sequence Listing
 CC (see AAB82229).

XX SQ Sequence 676 AA;

Query Match 23.3%; Score 1103; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 2,7e-69;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSQSCRNVKVR-RVQNYLYNVLPRGW-AFTYHAFVLLVPGCLLSVSTIPEHTKL 155
 DB 92 SYSTRRPVLAETHVQGRVYNLEPRTGKCFYHFAVFLIVLCLFVSSTIEQYAL 151
 QY 156 ASSCLILFEVMIYVGLFEITRIWAGCCCRGMGRIRFARKPCVIDTIVLSIA 215
 DB 152 ATGTLEFMEIVLVEFGTEVVRVWLSAGCSKTVGLMGRIFARKPISITDLVAVASV 211
 QY 216 VVSATQGNIFATSALESRLFLQILRMVMDRGRGTWKLGSVYVASHKELITAMYIGFL 275
 DB 212 VLVGSKGVFATSAIRGIRFLQILMLHVDROGRTWRLLSGVFTIHRQELITLYIGFL 271
 QY 276 VLFSSFLVYVVEKDA-----NKESTYADALMWGTTITITIGYDKTPLTWIGRLISAG 330
 DB 272 GLFSSYFYVLAEKDAVNESGVEFGSYADALMWGVTTITITIGYDKVPQTWIGKTIASC 331
 QY 331 FALIGSFALPAGILGSGFALKVOEHOHQHKEKRNPAANLIQCWRYADDEKSVSI 390
 DB 332 FSVFALSFALPAGILGSGFALKVOOKOROKHNRROIIPAASLIQTMARCYAAENPDSS- 390
 QY 391 ATWKPLKAL---HT-CSPFNOKLSFKERYRMASPRGOSIKSROASVGDRRSPSTDITAE 446
 DB 391 -TWKIYIRKAPRSHLTLSFSPKP---KSYVYVKKKKFKLDKNDGVTEGKMLTYPHITCD 446
 QY 447 GSPTRVQKQKMS---FNDRTFRFSLRLKSSQPKPVIDADATGALGDVYDEKGCOCDSVE 503
 DB 447 PPEERLDFHFSVDGYDSSVAKSPPTL-LEVSMFH-----FMRINSFAD-----LDLEGE 494
 QY 504 DLTPPL-----KTVIRAIRIMKFNHAKRKFETLRYDYKDYIEQYSAGHLMIC 553
 DB 495 TLTPTTHISOLREHNRATIKVIRRMQFYAKKKFQOARKPYDRDYIEQYSOGLNLMV 554
 QY 554 RIKSLQTRVDQILGKQ---ITSDKSREKITAETHETDLSMLGRVYVKEKOVOSIESKL 611
 DB 555 RIKEIQRRLDQFSGPSLFTSVSEKSKDR-----GSNTIGARLNKRVEDKTYQLDQRL 606
 QY 612 DCLLDIYQGVL-----RKGS-----SALALASFOIPEE 641
 DB 607 ALITDMLHQLLSLHGSGTPGSGGPPREGGAHITQPCGSGGSVDPDLPLPSNTLPTYE 663

RESULT 35

AAV57368

ID AAV57368 standard; Protein; 676 AA.
 AC AAV57368;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human KVLQ1 protein.
 XX
 KM KVLQ1; KCNE1; Long QT syndrome; LQT syndrome; minK protein;
 KM antiarrhythmic; gene therapy; human.
 XX
 OS Homo sapiens.
 PN WO200006600-A1.
 XX
 PD 10-FEB-2000.
 PF
 XX 06-OCT-1998; 98WO-US17838.
 XX


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Db      272 GLIFSSYFYVLAEKDAVNESGRVEFGSVADALMWGVVTTTIGYGDVPGQTMVGKTIASC 331
QY      331 FALIGISFFALPAGILSGFALKVOEQHROKHFEKRRNPANLIOCVRSTAADEKSVSI 390
Db      332 FSVFAISFFALPAGILSGFALKVOEQHROKHFEKRRNPANLIOCVRSTAADEKSVSI 390
QY      391 ATKRPHLKAL---HT-CSPFNQKLSFKERVRMASPRGOSISRSQASVGDNRSPSDITAE 446
Db      391 -TWKTIYIRKAPRSHHTLSPSPKP---KRSVYVKKKKFKLDKNGVTPPEKMLTVPHITCD 446
QY      447 GSPTKVKQSWMS---FNDTRFRPRLRLKSQPKPVIDADTALGDDVYDEKGCOCQDVSYE 503
Db      447 PPEERRLDHFESVDGSSVRKSPIL-LEVSMPH-----FMRTNSFAED-----LDLEE 494
QY      504 DLTPPL-----KTVIRAIRIMKFNHAKKFKETLRPYDVADVEQYSAGHLDMIC 553
Db      495 TLLRPITHISQLRHHRATIKVIRMOYFVAKKFKQARKPDVADVEQYSQGHILNMY 554
QY      554 RIKSLQTRVDOILGKGQ--ITSDDKSREKITAHEHTTDLMLGRVVKERKVOGSIESTL 611
Db      555 RIKELORLDDOSIGKPSLFISSVSEKSKDR-----GSNTIGARLNREVEDKVTQLDORL 606
QY      612 DCLLDIYQOVL-----RKGS-----SALALASFQIPPE 641
Db      607 ALITDMLHQLSLHSGSTPGSGGPPREGGAHITOPCGSGSVDPPELFLPSNLTPTYE 663

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RESULT 37
AAB82220
ID AAB82220 standard; Protein: 676 AA.

AC AAB82220:

DT 21-JUN-2001 (first entry)

DE Human KVLQ1 protein.

XX KVLQ1: Long QT syndrome; LQTS; cardiovascular disease;

KM Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

KW diagnosis; prognosis; therapy; drug screening.

OS Homo sapiens.

XX WO200124681-A2.

PN 12-Apr-2001.

XX 09-AUG-2000; 2000WO-US21660.

XX 09-AUG-1999; 99US-0147488.

PR 17-MAR-2000; 2000US-0190057.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX MPI: 2001-290564/30.

DR N-PSDB: AAF30824.

XX New KVLQ1 and SCN5A genes, which contains alterations or mutations,

XX useful in diagnostic/prognostic or drug screening methods, particularly

XX in mutational analyses for screening individuals with or at risk for

XX long QT syndrome -

XX Claim 6; Page 59-61; 76pp; English.

XX The present sequence is that of the protein encoded by the human

XX KVLQ1 gene. This gene is implicated in Romano-Ward syndrome, the

XX autosomal dominant form of long QT syndrome (LQTS), and in Jervell

XX and Lange-Nielsen syndrome, a form of LQTS associated with deafness,

XX a phenotype abnormality inherited in an autosomal recessive fashion.

XX Novel mutations have been identified in the gene using single strand

XX conformation polymorphism analysis. These result in the following

CC amino acid alterations: Y111C, E160K, R174H, G179S, A194P, R243C,
CC W248R, L266P, V307SP, V310I, S349W, Q356X, R366Q, T391I, P448R,
CC Q530X, S566F, R583C and R594Q. Isolated human polypeptides
CC comprising such a mutation (see AAB82221-39) are claimed.
CC Knowledge of the mutations provides means for assessing a risk
CC in a human subject for LQTS, for diagnosing a mutation which
CC causes LQTS, and for screening for drugs useful in treating a
CC human having a mutation in the KVLQ1 gene.

XX Sequence 676 AA;

Query Match 23.3%; Score 1102; DB 22; Length 676;

Best Local Similarity 41.9%; Pred. No. 3.3e-89;

Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

```

QY      98 SSOSCRNNVYR-RVQNTLVNVERPRGW-AFTIHAFELLVPGCLISVSTPEHKKL 155
Db      92 SYSTRRPVLAIRHVGQRYVNFELRPFGWKCEVHFVFLVLVCLIFSVLSTIEQVIAL 151
QY      156 ASSCLILEFVMIYVGFLEFIRISAGCCCRYGMOGRLEPARKPCVIDITVLIASIA 215
Db      152 ATGTFEMELIVLVFPGTEYVRLMSAGCRSKYVGLMGRLEPARKPISIIDIVVASVY 211
QY      216 VVSATQGNIPANSALSLRFLQILRMVMDRGGTWSLVVYASHKELTAYIGFL 275
Db      212 VLCVSGKQVFATSAIRGIRFLQILRMVMDRGGTWSLVVYASHKELTAYIGFL 271
QY      276 VLFSSFLYVLEKDA-----NKEFSYADALMGMGTITLTITIGYDGTPTLWGRLLSAG 330
Db      272 GLIFSSYFYVLAEKDAVNESGRVEFGSVADALMWGVVTTTIGYDVKPQTMVGKTIASC 331
QY      331 FALIGISFFALPAGILSGFALKVOEQHROKHFEKRRNPANLIOCVRSTAADEKSVSI 390
Db      332 FSVFAISFFALPAGILSGFALKVOEQHROKHFEKRRNPANLIOCVRSTAADEKSVSI 390
QY      391 ATKRPHLKAL---HT-CSPFNQKLSFKERVRMASPRGOSISRSQASVGDNRSPSDITAE 446
Db      391 -TWKTIYIRKAPRSHHTLSPSPKP---KRSVYVKKKKFKLDKNGVTPPEKMLTVPHITCD 446
QY      447 GSPTKVKQSWMS---FNDTRFRPRLRLKSQPKPVIDADTALGDDVYDEKGCOCQDVSYE 503
Db      447 PPEERRLDHFESVDGSSVRKSPIL-LEVSMPH-----FMRTNSFAED-----LDLEE 494
QY      504 DLTPPL-----KTVIRAIRIMKFNHAKKFKETLRPYDVADVEQYSAGHLDMIC 553
Db      495 TLLRPITHISQLRHHRATIKVIRMOYFVAKKFKQARKPDVADVEQYSQGHILNMY 554
QY      554 RIKSLQTRVDOILGKGQ--ITSDDKSREKITAHEHTTDLMLGRVVKERKVOGSIESTL 611
Db      555 RIKELORLDDOSIGKPSLFISSVSEKSKDR-----GSNTIGARLNREVEDKVTQLDORL 606
QY      612 DCLLDIYQOVL-----RKGS-----SALALASFQIPPE 641
Db      607 ALITDMLHQLSLHSGSTPGSGGPPREGGAHITOPCGSGSVDPPELFLPSNLTPTYE 663

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RESULT 38
AAB82234
ID AAB82234 standard; Protein: 676 AA.

AC AAB82234:

DT 21-JUN-2001 (first entry)

DE Human KVLQ1 mutant P448R.

XX KVLQ1: Long QT syndrome; LQTS; cardiovascular disease;

KM Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

KW diagnosis; prognosis; therapy; drug screening; mutant; mutein.

XX Homo sapiens.

XX WO200124681-A2.

XX 12-APR-2001.
 PD 09-AUG-2000; 2000MO-US21660.
 XX 09-AUG-1999; 99US-0147488.
 XX 17-MAR-2000; 2000US-0190057.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Keating MT, Splawski I;
 XX MPI: 2001-290564/30.
 DR
 XX
 XX New KVLQT1 and SCN5A genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome -
 XX
 XX
 PS Claim 6; Page -: 76pp; English.
 CC
 CC The present sequence is that of the claimed P488R mutant of the
 CC human KVLQT1 protein. The mutant is encoded by a KVLQT1 mutant
 CC gene in which a C/G mutation alters codon 488 from CCA to CGA.
 CC Mutations of the KVLQT1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of Long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormally inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQT1 gene
 CC lead to the following amino acid alterations in the KVLQT1 protein:
 CC Y111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307SP,
 CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQT1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQT1 sequence given in the Sequence Listing
 CC (see AAB82220).
 CC
 XX
 XX Sequence 676 AA:
 SO
 Query Match 23.3%; Score 1102; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 3,3e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
 QY 98 SSOSCRNKKYR-RVONTLYNLEPRGM-AFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
 DB 92 SIYSTRPVLARTHVQGRVYNLEPRGKCEVYHRAVLIYVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLLLEFVIVVEGLEFIIRMSAGCCCRYRGMOGRLEFRARKPCVITIVLASIA 215
 DB 152 ATGTLFMEIYLVVEFGTEYVRLMSAGCRSKYVGLMGRLEFRARKPCVITIVLASIA 211
 QY 216 VSAKTOGNIFATSAIRLRLQILRMVMDRGGTWMKLGSSVYVHAKSKELLTAWIYGL 275
 DB 212 VLVGSGGVFAITAIRKIRLQILRMVMDRGGTWMKLGSSVYVHAKSKELLTAWIYGL 271
 QY 276 VLIFFSFLVYLVKEDA-----NKEFSYADALMNGTITITIGYGDKTLLWLGRLISAG 330
 DB 272 GLIFFSYFYVLAEDKDAVNESGRVEGVSADALMNGGVITITIGYGDKTLLWLGRLISAG 331
 QY 331 FALLGIFEFALPAGILSGFYLKVOEHOHROKHEKRRNDPAANLQCVMSYADEKSVST 390
 DB 332 FSVFAISFFPALPAGILSGFYLKVOEHOHROKHEKRRNDPAANLQCVMSYADEKSVST 390
 QY 391 ATMKPHKAL---HT-CSPTNOKLSFKERVRMARSPRGOSIKRQASVGRBSSTDTITAE 446
 DB 391 -TWKIYIRKAPRSGITLSPSPK---KSSVYVKKKKFKLDKNGYTPGKMLTVPHITCD 446
 QY 447 GSPTKYOKSMS---FNDTRFRPSLRKSSOPKPVYIDATLGTDDVYVEKGCQCQDVSE 503
 DB 447 PREERIRLDHFSVDDGYSSVRKSPTL-LEVSMPH-----FWRTNSFAD-----LDLEGE 494

QY 504 DLTPPL-----KTVIRAIRMKFHVAKRKRKPELLRPVDVQVIEOYSAGHDMIC 553
 DB 495 TLTPPIHISQLRHHNRATTVIRMOYFVAKKFOAKRPYDVQVIEOYSAGHDMIC 554
 QY 554 RIKSLQTRVDOLIGKO--ITSDKRSREKITAHEHTTDLISMAGVYVEKQVQSIKSL 611
 DB 555 RIKELQRRLDQSIGKPSLFIYSVSEKSKDR-----GSNTIGARLNREDKVTQDQRL 606
 QY 612 DCLLDIYQOVL-----RKGA-----SALALASFOIPPE 641
 DB 607 ALITDMHLHLSLHGSGTSGSGPPREGAHITOPCGSGSGSVDPETFLPSNTLPYE 663
 RESULT 39
 AAB49494
 ID AAB49494 standard; Protein: 676 AA.
 XX
 AC AAB49494;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Human KVLQT1.
 XX
 KW Human; KVLQT1; antiarrhythmic; cardiact; gene therapy;
 KW cardiac potassium channel; Jervell and Lange-Nielsen syndrome; JLN;
 KW chromosome 11p15.5; long QT syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US6150104-A.
 XX
 PD 21-NOV-2000.
 XX
 PE 17-AUG-1998; 98US-0135021.
 XX
 PR 29-JUL-1998; 98US-0094477.
 PR 13-JUN-1997; 97US-0874655.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Keating MT, Splawski I;
 XX
 DR MPI: 2001-060013/07.
 DR N-PSDB; AAC89911.
 XX
 PT DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
 PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
 PT or diagnosing or prognosing JLN -
 XX
 PS Example 4; Columns 59-64; 58pp; English.
 CC
 CC The present sequence is wild-type human KVLQT1. KVLQT1 is a cardiac
 CC potassium channel and mutations in the KVLQT1 gene cause Jervell and
 CC Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome 11p15.5. The
 CC present invention relates to a mutant KVLQT1 coding sequence (see
 CC AAC89914). The mutant KVLQT1 coding sequence is useful in the diagnosis
 CC of long QT syndrome and in screening humans for the presence of KVLQT1
 CC gene variants which cause JLN syndrome.
 CC
 XX
 SO Sequence 676 AA:
 Query Match 23.3%; Score 1102; DB 22; Length 676;
 Best Local Similarity 41.9%; Pred. No. 3,3e-89;
 Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;
 QY 98 SSOSCRNKKYR-RVONTLYNLEPRGM-AFIYHAFVLLVFGCLLSVFSTIPEHTKL 155
 DB 92 SIYSTRPVLARTHVQGRVYNLEPRGKCEVYHRAVLIYVCLIFSVLSTIEQYAL 151
 QY 156 ASSCLLLEFVIVVEGLEFIIRMSAGCCCRYRGMOGRLEFRARKPCVITIVLASIA 215
 DB 152 ATGTLFMEIYLVVEFGTEYVRLMSAGCRSKYVGLMGRLEFRARKPCVITIVLASIA 211

CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:
 CC V111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307SP,
 CC V310I, S349W, R356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX Sequence 676 AA:

Query Match 23.3%; Score 1101; DB 22; Length 676;

Best Local Similarity 41.9%; Pred. No. 4e-89;

Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

156 ASSCLLLEFVMIVFGLFETIRIMSAGCCCRYGMOGRLARARPCFVIDIVILASIA 215
 152 ATGTLFEMELVAVFEGTEYVRLMSAGCRSKRYGLMGRRLARPKPISIDILVAVASV 211
 216 VSAKTGNIENFATSLRFLQILRVNMDRGGTWNLSVVAHSKELITAVYIGFL 275
 212 VLVGSGQGVFAISAIKIRFLQILRLMLHVDROGTWLLSVFIHQELITTYIGFL 271
 276 VLIFFSFLVLYLVENDA-----NKEFSYADALMVGITITLTIGYDGTPTLWGLRLSAG 330
 272 GLIFFSYFYVLAEDAVNESGRVFGSYADALMVGIVVTITIGYDGTPTWVGRTIASC 331
 331 FALIGISFFALPAGILSGFALKVOEORHOKHFEKRRRPAANLIDCWRSVADEKSVSI 390
 332 FSVFAISFFALPAGILSGFALKVOEORHOKHFEKRRRPAANLIDCWRSVADEKSVSI 391
 391 ATKMPHILKAL--HT-CSPTNQKLSFKERVMASPRGOSIKRSQASVGDRRSPSTDI7AE 446
 392 --WRIYIRKAPRSHLTLLSPKPK--KKSYYVKKKKFKLMDKNGVTPGKMLTVPHITCD 446
 447 GSPTKVKOKMS--FNDRTFRPSIRLKSOPKPYIDADTALGTDVYIDEKGCQCDVSYE 503
 447 PPEERRLDHFSVDGSDSVSRKSPPL-LEVSMPH-----FWRTNSFAED---LDLEGE 494
 504 DLPPPL-----KTVIRAIRIMKPHVAKRKFKETLRPDVDVIEQYSAGHIDMC 553
 495 TLLPTIHHISQLRHHRRATIKVIRMOYFVAKKFKQAKRPDVADVIEQYSGHINLAW 554
 554 RIKSLQTRVDQILKGO--ITSDDKSRREKITAHEHTTDLISMLGRVAVKEKQVOSIESKL 611
 555 RIKLQRLRDQISIKPILFISVSEKSKR-----GSNTIGARLNREDEKVTYQLDQYL 606
 612 DCLLDITVQOYL-----RKGSA-----SALALASQIPPE 641
 607 ALITDMLHQLSLHSGSTPGSGPPREGGAHITOPCGSGSVDPLELPSNLTPLYE 663

RESULT 43

AAB82238 standard; Protein; 676 AA.

XX AAB82238;

XX 21-JUN-2001 (first entry)

XX Human KVLQ1 mutant R594Q.

XX

KW KVLQ1; Long QT syndrome; LQTS; cardiovascular disease;
 KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
 KW diagnosis; prognosis; therapy; drug screening; mutant; mutein.
 OS Homo sapiens.
 XX MO200124681-A2.
 PN 12-APR-2001.
 PD 09-AUG-2000; 2000WO-US21660.
 PF 09-AUG-1999; 99US-0147488.
 PR 17-MAR-2000; 2000US-0190057.
 XX (UTAH) UNIV UTAH RES FOUND.
 PA Reating MT, Splawski I;
 PI WPI; 2001-290564/30.
 DR

XX New KVLQ1 and SCN5A genes, which contains alterations or mutations,
 PT useful in diagnostic/prognostic or drug screening methods, particularly
 PT in mutational analyses for screening individuals with or at risk for
 PT long QT syndrome -
 XX Claim 6; Page -, 76pp; English.

CC The present sequence is that of the claimed R594Q mutant of the
 CC human KVLQ1 protein. The mutant is encoded by a KVLQ1 mutant
 CC gene in which a G/A mutation alters codon 594 from CGA to CAA.
 CC Mutations of the KVLQ1 gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
 CC deafness, a phenotype abnormality inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQ1 gene
 CC lead to the following amino acid alterations in the KVLQ1 protein:
 CC V111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307SP,
 CC V310I, S349W, R356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594Q. Knowledge of the mutations provides means for assessing a
 CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human
 CC having a mutation in the KVLQ1 gene.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQ1-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX Sequence 676 AA:

Query Match 23.3%; Score 1101; DB 22; Length 676;

Best Local Similarity 41.9%; Pred. No. 4e-89;

Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

98 SSOSCRNNVYR-RVQNYLYNVLERPRGW-AFIYHAEVLLVFGCLLSVSTIPEHKL 155
 92 SISTRPVLARPHVQGRVYVFLERPGWKCFVHFVAVFLVLCILSVSLSTIQYAL 151
 156 ASSCLLLEFVMIVFGLFETIRIMSAGCCCRYGMOGRLARARPCFVIDIVILASIA 215
 152 ATGTLFEMELVAVFEGTEYVRLMSAGCRSKRYGLMGRRLARPKPISIDILVAVASV 211
 216 VSAKTGNIENFATSLRFLQILRVNMDRGGTWNLSVVAHSKELITAVYIGFL 275
 212 VLVGSGQGVFAISAIKIRFLQILRLMLHVDROGTWLLSVFIHQELITTYIGFL 271
 276 VLIFFSFLVLYLVENDA-----NKEFSYADALMVGITITLTIGYDGTPTLWGLRLSAG 330
 272 GLIFFSYFYVLAEDAVNESGRVFGSYADALMVGIVVTITIGYDGTPTWVGRTIASC 331
 331 FALIGISFFALPAGILSGFALKVOEORHOKHFEKRRRPAANLIDCWRSVADEKSVSI 390
 332 FSVFAISFFALPAGILSGFALKVOEORHOKHFEKRRRPAANLIDCWRSVADEKSVSI 390

QY 391 ATWKPRLKAL---HT-CSPPTNOKLSFEKERYMASPRGQSIKSRQASVGDRRSPSTDITAE 446
 Db 391 -TWKIIRKAPRSHHTLSPSPK---KSSVYVKKKKFKLDKNDGVTPTEGKMLTVPHTICD 446
 QY 447 GSPTVQKWS---FNDRTFRPSLRKSSQPKPYIDADALGDDVYDEKGCDCVSYE 503
 Db 447 PPEERLRDHFSDVGDSSVRSKSPTL-LEVSMPI-----FMRTNSPSED---LDLEGE 494
 QY 504 DLTPPL-----KTVIRAIRIMKFNHAKRKFKETLRPYDVKDVEQYSAGHLDMIC 553
 Db 495 TLLPPTHTHSQLEHHNRATIKVIRMOYFAKKKFKQARKPYDVADYIEQYSQGLNLNAV 554
 QY 554 RIKSLQTRVDILGKQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEKQVQSIKSL 611
 Db 555 RIKELDRRLDOSIGKPSLFTSVSEKSKDR-----GSNTIGARLNQVEDKVTQLDQRL 606
 QY 612 DCLLDIYQOVL-----RKGS-----SALALASFOIPPE 641
 Db 607 ALITDMLHQLLSLHGSGTPSGSGPREGGAHITQPCGSGSVDPDLFSPNTLPYTE 663

RESULT 44

ID AAB82228 standard; Protein; 676 AA.

AC AAB82228;

DT 21-JUN-2001 (first entry)

DE Human KVLQTL mutant L266P.

KM KVLQTL; long QT syndrome; LQTS; cardiovascular disease;

KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

OS diagnosis; prognosis; therapy; drug screening; mutant; muten.

XX Homo sapiens;

XX MO200124681-A2.

PD 12-APR-2001.

PE 09-AUG-2000; 2000WO-US21660.

PR 09-AUG-1999; 99US-0147488.

XX 17-MAR-2000; 2000US-0190057.

PA (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

XX WPI; 2001-290564/30.

XX WPI; 2001-290564/30.

XX Claim 6; Page -: 76pp; English.

CC The present sequence is that of the claimed L266P mutant of the
 CC human KVLQTL protein. The mutant is encoded by a KVLQTL mutant
 CC gene in which a T/C mutation alters codon 266 from CTG to CCG.

CC Mutations of the KVLQTL gene are implicated in Romano-Ward syndrome,
 CC the autosomal dominant form of long QT syndrome (LQTS), and in
 CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with

CC deafness, a phenotype abnormally inherited in an autosomal
 CC recessive fashion. Mutations newly discovered in the KVLQTL gene
 CC lead to the following amino acid alterations in the KVLQTL protein:

CC Y111C, E160K, R174H, R194P, R243C, W248R, L266P, V307SP,
 CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
 CC R594O. Knowledge of the mutations provides means for assessing a

CC risk in a human subject for LQTS, for diagnosing a mutation which
 CC causes LQTS, and for screening for drugs useful in treating a human

CC having a mutation in the KVLQTL gene.

CC Note: The present sequence is not shown in the specification but is
 CC derived from the KVLQTL-1 sequence given in the Sequence Listing
 CC (see AAB82220).

XX SQ Sequence 676 AA;

Query Match 23.2%; Score 1100; DB 22; Length 676;

Best local Similarity 41.9%; Pred. No. 4.9e-89;

Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16;

QY 98 SSQSCRNNVYR-RVQNYLVNLEPRGW-AFIYAFVLLVFGCLLSVFSTIBETRL 155
 Db 92 SIYSTRPVLARHVGGRVYNFLERPGMKCFYHFAVFLVYLCILSFSLTBQYAL 151
 QY 156 ASSCLLEFVMVLPLEFIIRMSAGCCCRKGMORLRFARPCVIDIVLASIA 215
 Db 152 ATGTLFMETLVLFEGTEYVVRILMSAGCRSKYGLMGRLFARPISTIDLVVAVSV 211
 QY 216 VSAKTQGNIFATLSALSLRFLQILRMVRMDRGGTWSLVVYVANSKELITANYIFL 275
 Db 212 VLVGSKGVYFATSAIIGIRFLQILRMHVDROGTWLLSVYFIHQELTTPYIGL 271
 QY 276 VLIFFSFLVYLVKDA-----NKEFSYADALMWGTTITLTIGYGDKTPPLWLGRLSAG 330
 Db 272 GLIFSSFYVYLAERKDAVNEGSRVFGSYADALMWGVVITITIGYGDKVPQTVWGTIASC 331
 QY 331 FALGTSFALPAGILGSGFALKVQEOHROKHFERRRANLLOCVRSYADEKSVSI 390
 Db 332 FSVEAISFFALPAGILGSGFALKVQOKOROKRFPNQPAAASLTQTAARCYAAENPDS- 390
 QY 391 ATWKPRLKAL---HT-CSPPTNOKLSFEKERYMASPRGQSIKSRQASVGDRRSPSTDITAE 446
 Db 391 -TWKIIRKAPRSHHTLSPSPK---KSSVYVKKKKFKLDKNDGVTPTEGKMLTVPHTICD 446

QY 447 GSPTVQKWS---FNDRTFRPSLRKSSQPKPYIDADALGDDVYDEKGCDCVSYE 503
 Db 447 PPEERLRDHFSDVGDSSVRSKSPTL-LEVSMPI-----FMRTNSPSED---LDLEGE 494

QY 504 DLTPPL-----KTVIRAIRIMKFNHAKRKFKETLRPYDVKDVEQYSAGHLDMIC 553
 Db 495 TLLPPTHTHSQLEHHNRATIKVIRMOYFAKKKFKQARKPYDVADYIEQYSQGLNLNAV 554

QY 554 RIKSLQTRVDILGKQ--ITSDDKSREKITAHEHTDLSMLGRVYVKEKQVQSIKSL 611
 Db 555 RIKELDRRLDOSIGKPSLFTSVSEKSKDR-----GSNTIGARLNQVEDKVTQLDQRL 606

QY 612 DCLLDIYQOVL-----RKGS-----SALALASFOIPPE 641
 Db 607 ALITDMLHQLLSLHGSGTPSGSGPREGGAHITQPCGSGSVDPDLFSPNTLPYTE 663

RESULT 45

ID AAB82237 standard; Protein; 676 AA.

AC AAB82237;

DT 21-JUN-2001 (first entry)

DE Human KVLQTL mutant R583C.

KM KVLQTL; long QT syndrome; LQTS; cardiovascular disease;

KW Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;

OS diagnosis; prognosis; therapy; drug screening; mutant; muten.

XX Homo sapiens.

XX MO200124681-A2.

PD 12-APR-2001.

PF 09-AUG-2000; 2000WO-US21660.

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PR    09-AUG-1999:      99US-014748B .
PR    17-MAR-2000; 2000US-0190057 .
PA
PA    (UTAH ) UNIV UTAH RES FOUND.
PI
PI    Keating MT, Splawski I;
XX
XX
DR    WPI; 2001-290564/30.
PT
PT    New KVLQT1 and SCN5A genes, which contains alterations or mutations,
PT    useful in diagnostic/prognostic or drug screening methods, particularly
PT    in mutational analyses for screening individuals with or at risk for
PT    long QT syndrome _
PS
PS    Claim 6; Page -: 76pp; English.
CC
CC    The present sequence is that of the claimed R583C mutant of the
CC    human KVLQT1 protein. The mutant is encoded by a KVLQT1 mutant
CC    gene in which a C/T mutation alters codon 583 from CGC to TGC.
CC    Mutations of the KVLQT1 gene are implicated in Romano-Ward syndrome,
CC    the autosomal dominant form of Long QT syndrome (LQTS), and in
CC    Jervell and Lange-Nielson syndrome, a form of LQTS associated with
CC    deafness, a phenotype abnormality inherited in an autosomal
CC    recessive fashion. Mutations newly discovered in the KVLQT1 gene
CC    lead to the following amino acid alterations in the KVLQT1 protein:
CC    Y111C, E160K, R174H, G179S, A194P, R243C, M248R, S266P, V307SP,
CC    V310I, S349W, Q356X, R366Q, T391I, P448R, Q530X, S566F, R583C and
CC    R594Q. Knowledge of the mutations provides means for assessing a
CC    risk in a human subject for LQTS, for diagnosing a mutation which
CC    causes LQTS, and for screening for drugs useful in treating a human
CC    having a mutation in the KVLQT1 gene.
CC
CC    Note: The present sequence is not shown in the specification but is
CC    derived from the KVLQT-1 sequence given in the Sequence Listing
CC    (see AAB82220).
SO
SQ    Sequence      676 AA:

Query Match          23.2%; Score 1099; DB 22; Length 676;
Best Local Similarity 41.9%; Pred. No. 6.le-89;
Matches   250; Conservative 104; Mismatches 165; Indels   78; Gaps   16;

OY     98 SSOSCRRAVKKR-KVNLTLYLVLEPRRW-AFIHAAPFLVFGLLSYSTIPERKL 155
DB     92 SIYSRRRPVLAKTHVGKVNFLEPTMKCFVYHFAEFLTVCLLSYSTLEVRYAL 151
OY     156 ASSCLILEFMVIYVFGLFEIRIRSAGCCCRYRMGQRLEFPARKFCVIFIVLASIA 215
DB     152 ATGTLFMMEIYLVPFFGEYYVRILMSACRSKRYVGMKRRLRKARPISILLDIYVASMV 211
OY     216 VSATOGNIFATSALSLRFQLDIRMYBMDSRGSTMKLGSVVYAHSKEELITAMVIGEL 275
DB     212 VLCAVSQGQVAFSAIRGIREFLOILRMHLVDPROGGTWRLLGSVFRIHQEELTYLGFL 271
OY     276 VIIFSFFVLYVENKA-----NKESYAADLMIMGITTLTTGYGDKPPLMLGRLLSG 330
DB     272 GLIESFYVYLAEKDAVNESGRVEGSTADALMGCVIYTITIGDYDKPKQTIWGKTIASG 331
OY     331 FALLGISFFPALPGILGSGFALKVOEHROKHFERKRRNPANLIQCWRSTAADERSVSI 390
DB     332 FSVFASFEPFALPGILGSGFALKVOOKORHKFNFOIPAASLIIOTARCVAENPDSS- 390
OY     391 ATKRHKLAL---HT-GSPTNOKLSFKFRVMAASPARGQS IKSROASVGBDNRSPNDITAE 446
DB     391 -TWKIYIKRAPSRSHLLSPSPK--KTSVAVKKKKREKLDKNGVTPGEMKITPVHIICD 446
OY     447 GSPTTRVORSK----PNDRTRFRPSLRILSSOPKPYIDALTALGTDVYDEKGCCOCVSE 503
DB     447 PEERRLDHFSVDGSDSVRSKSPTL-LEVSMFH-----FRTNSPAD---DLIEGE 494
OY     504 DLTPPL-----KYIVAIRIMKEFVNAKRKKETLRPPDVADVITYEQSAGHDIMLC 553
DB     495 TLPTLTITNISOLREHHRAIKIVIRMOGFVAKKCKOOAQRPADVADVITYEQSGHNINLAW 554
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OY 554 RIKSLQTRVDDIILKGO--ITSDDKSKSEKITAHEFTDDLMLGCRVYKVKOVQSIESTKL 611
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 555 RIKELQRLRLDSDISGKPSLFLISVSEKSD-----CGSNITGARLNKVRDEKVTQLQRL 606
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 612 DCLLDIYQGVV-----RKGS-----SALALASFOIPPE 641
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 607 ALITDMLHQLSLHGGSTPGSGGPPREGAHIITPOCGSGSVDEPLFLPNTLPTYE 663
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 46
AAB82222
ID AAB82222 standard; Protein: 676 AA.
AC AAB82222;
DT 21-JUN-2001 (first entry)
DE Human KVLQTL mutant E160K.
XX KVLQTL; Long QT syndrome; LQTS; cardiovascular disease;
XX Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
XX diagnosis; prognosis; therapy; drug screening; mutant; mutain.
XX Homo sapiens.
XX OS
XX WO200124681-A2.
XX PN
XX 12-APR-2001.
XX PD
XX 09-AUG-2000; 2000MO-US21660.
XX PF
XX 09-AUG-1999; 99US-0147488.
XX PR 17-MAR-2000; 2000US-0190057.
XX PA
XX (UTAH ) UNIV UTAH RES FOUND.
XX PI
XX Keating MT, Splawski I;
XX WPI; 2001-290564/30.
XX DR
XX
XX New KVLQTL and SCN5A genes, which contains alterations or mutations,
XX useful in diagnostic/prognostic or drug screening methods, particularly
XX in mutational analyses for screening individuals with or at risk for
XX long QT syndrome -
XX PT
XX
XX Claim 6; page -: 76pp; English.
XX PS
XX
XX The present sequence is that of the claimed E160K mutant of the
XX human KVLQTL protein. The mutant is encoded by a KVLQTL mutant
XX gene in which a G/A mutation alters codon 160 from GAG to AAG.
XX Mutations of the KVLQTL gene are implicated in Romano-Ward syndrome,
XX the autosomal dominant form of Long QT syndrome (LQTS), and in
XX Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
XX deafness, a phenotype abnormally inherited in an autosomal
XX recessive fashion. Mutations newly discovered in the KVLQTL gene
XX lead to the following amino acid alterations in the KVLQTL protein:
XX C111C, E160K, R174H, G179S, A194P, R243C, W248R, I266P, V307SP,
XX V310T, S346W, Q355X, R366Q, T391I, P448R, Q530X, S566P, R583C and
XX R594Q. Knowledge of the mutations provides means for assessing a
XX risk in a human subject for LQTS, for diagnosing a mutation which
XX causes LQTS, and for screening for drugs useful in treating a human
XX having a mutation in the KVLQTL gene.
XX CC Note: The present sequence is not shown in the specification but is
XX derived from the KVLQTL-1 sequence given in the Sequence Listing
XX (see AAB82220).
XX
XX Sequence 676 AA:
XX
XX Query Match 23.2%; Score 1098; DB 22; Length 676;
XX Best Local Similarity: 41.7%; Pred. No. 7.5e-89;
XX Matches 249; Conservative 106; Mismatches 164; Indels 78; Gaps 16;

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QY 98 SSQSCRNNKYR-RVONYLYNVLPRGW-AFIYHAFVLLVFGCLLSVFSTIEPHTKL 155
DB 92 SIYSTRRPVLARHNVQGRVYNFLERPTGKCFYVHFAVLVLCLIFSISTIEQYAL 151
QY 156 ASSCLLLEFVMIVVGLFETIRIWSAGCCCRYRGWGRRLFAKRPFCVIDTIVLAIASIA 215
DB 152 AGCTLFEMKIVLVFEGTEVYVRLMSAGCRSKYVGLMGRLFAKRPISIIDLIVVASAV 211
QY 216 VVSATQGNIFATLSALRSLEFLOLRVNRDRRGSTWKLISVYVAHSEKELITAVYIGFL 275
DB 212 VLVGSKGQVAFATSAIRGIFLOLRHLDROGSTRRLGSVYFIHQDELITTYIGFL 271
QY 276 VLISSFLVYLVKDA-----NKEFSYADALMGWITITTYIGYDGTPTLWGLRLSAG 330
DB 272 GLIFSSYFYVLAKEKDAVNESGRVFEFSYADALMGWVYVITTYIGYDGVPTWVGKRTIASC 331
QY 331 FALGISFPALPAGILSGFALKVQEOHROKHFEKRRNPANLIQCVRSYAADKSVSI 390
DB 332 FSVFAISFPALPAGILSGFALKVQOKOROKHFNROIPAAASLIQTAWRCYAAENPDSS- 390
QY 391 ATWKPHLKAL---HT-CSPTNOKLSFERVYMASPRGOSIKSROASVGDERSPTDITAE 446
DB 391 -TWKITYIRKAPRSHLTLSPPKPR--KKSYYVKKKKFKKLDKNDGVTEGKMLVPHITCD 446
QY 447 GSPTVQKWS---FNDRTFRFSLKSSQPKPVIDADTALGTDVYDEKGCQCDVSE 503
DB 447 PPEERLDHFVSDYSSVAKSPPL-LEVSMPH-----FMRTNSFAD-----LDLGE 494
QY 504 DLTPPL-----KTVIRAIRIMKEHVAKRREKTELRYDYDKVIEQYSAHLDMLC 553
DB 495 TLTPITTHISQLEHNRATIKYIRMOYFAKKKFOQARKPYDVEDVIEQYSGHNLNAV 554
QY 554 RIKSLQTRVQDILGKQ--ITSDDKSREKITAETHETDLSMLGRVYVKEKOVOSIESKL 611
DB 555 RIKELQRRLDQSIGKPSLFSVSEKSKDR-----GSMITGARLNRVEDKVIQDLQRL 606
QY 612 DCLLDYQOVL-----RKGS-----SALMASQIPEE 641
DB 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGSVDPDELPLPSMTLPTYE 663

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RESULT 47
AAB82223
ID AAB82223 standard: Protein; 676 AA.

AC AAB82223;
XX
XX 21-JUN-2001 (first entry)
XX
XX
XX Human KVLQTL mutant R174H.
XX
XX KVLQTL; Long QT syndrome; LQTS; cardiovascular disease;
XX Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;
XX diagnosis; prognosis; therapy; drug screening; mutant; mutain.
XX
XX Homo sapiens.
XX
XX W0200124681-A2.
XX
XX 12-APR-2001.
XX
XX
XX 09-AUG-2000; 2000WO-US21660.
XX
XX
XX 09-AUG-1999; 99US-0147488.
XX PR 17-MAR-2000; 2000US-0190057.
XX
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Keating MT, Splawski I;
XX WPI; 2001-290564/30.
XX
XX
XX New KVLQTL and SCN5A genes, which contains alterations or mutations,

PT useful in diagnostic/prognostic or drug screening methods, particularly
PT in mutational analyses for screening individuals with or at risk for
PT long QT syndrome -

PS Claim 6; Page -; 76pp; English.

CC The present sequence is that of the claimed R174H mutant of the
CC human KVLQTL protein. The mutant is encoded by a KVLQTL mutant
CC gene in which a G/A mutation alters codon 174 from CGC to CAC.
CC Mutations of the KVLQTL gene are implicated in Romano-Ward syndrome,
CC the autosomal dominant form of Long QT syndrome (LQTS), and in
CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
CC deafness, a phenotype abnormality inherited in an autosomal
CC recessive fashion. Mutations newly discovered in the KVLQTL gene
CC lead to the following amino acid alterations in the KVLQTL protein:
CC V111C, E160K, R174H, G179S, A194P, R243C, W248R, L266P, V307S,
CC V310I, S349W, Q356X, R366Q, T391I, P448R, Q350X, S566F, R583C and
CC R594Q. Knowledge of the mutations provides means for assessing a
CC risk in a human subject for LQTS, for diagnosing a mutation which
CC causes LQTS, and for screening for drugs useful in treating a human
CC having a mutation in the KVLQTL gene.
CC Note: The present sequence is not shown in the specification but is
CC derived from the KVLQTL-1 sequence given in the Sequence Listing
CC (see AAB82220).

CC Sequence 676 AA;

Query Match 23.2%; Score 1097; DB 22; Length 676;

Best Local Similarity 41.7%; Pred. No. 9.2e-89;

Matches 249; Conservative 105; Mismatches 165; Indels 78; Gaps 16;

```

QY 98 SSQSCRNNKYR-RVONYLYNVLPRGW-AFIYHAFVLLVFGCLLSVFSTIEPHTKL 155
DB 92 SIYSTRRPVLARHNVQGRVYNFLERPTGKCFYVHFAVLVLCLIFSISTIEQYAL 151
QY 156 ASSCLLLEFVMIVVGLFETIRIWSAGCCCRYRGWGRRLFAKRPFCVIDTIVLAIASIA 215
DB 152 AGCTLFEMKIVLVFEGTEVYVRLMSAGCRSKYVGLMGRLFAKRPISIIDLIVVASAV 211
QY 216 VVSATQGNIFATLSALRSLEFLOLRVNRDRRGSTWKLISVYVAHSEKELITAVYIGFL 275
DB 212 VLVGSKGQVAFATSAIRGIFLOLRHLDROGSTRRLGSVYFIHQDELITTYIGFL 271
QY 276 VLISSFLVYLVKDA-----NKEFSYADALMGWITITTYIGYDGTPTLWGLRLSAG 330
DB 272 GLIFSSYFYVLAKEKDAVNESGRVFEFSYADALMGWVYVITTYIGYDGVPTWVGKRTIASC 331
QY 331 FALGISFPALPAGILSGFALKVQEOHROKHFEKRRNPANLIQCVRSYAADKSVSI 390
DB 332 FSVFAISFPALPAGILSGFALKVQOKOROKHFNROIPAAASLIQTAWRCYAAENPDSS- 390
QY 391 ATWKPHLKAL---HT-CSPTNOKLSFERVYMASPRGOSIKSROASVGDERSPTDITAE 446
DB 391 -TWKITYIRKAPRSHLTLSPPKPR--KKSYYVKKKKFKKLDKNDGVTEGKMLVPHITCD 446
QY 447 GSPTVQKWS---FNDRTFRFSLKSSQPKPVIDADTALGTDVYDEKGCQCDVSE 503
DB 447 PPEERLDHFVSDYSSVAKSPPL-LEVSMPH-----FMRTNSFAD-----LDLGE 494
QY 504 DLTPPL-----KTVIRAIRIMKEHVAKRREKTELRYDYDKVIEQYSAHLDMLC 553
DB 495 TLTPITTHISQLEHNRATIKYIRMOYFAKKKFOQARKPYDVEDVIEQYSGHNLNAV 554
QY 554 RIKSLQTRVQDILGKQ--ITSDDKSREKITAETHETDLSMLGRVYVKEKOVOSIESKL 611
DB 555 RIKELQRRLDQSIGKPSLFSVSEKSKDR-----GSMITGARLNRVEDKVIQDLQRL 606
QY 612 DCLLDYQOVL-----RKGS-----SALMASQIPEE 641
DB 607 ALITDMLHQLLSLHGSGTPSGGPPREGGAHITQPCGSGSVDPDELPLPSMTLPTYE 663

```

RESULT 48

CC Jervell and Lange-Nielsen syndrome, a form of LQTS associated with
CC deafness, a phenotype abnormally inherited in an autosomal
CC recessive fashion. Mutations newly discovered in the KVLQT1 gene
CC lead to the following amino acid alterations in the KVLQT1 protein::
CC Y111C, E160K, R174W, S191G, A194P, W248R, L266P, V307Snp.
CC S340I, S349V, Q356X, R366Q, T391I, P448R, Q530X, S566F, R553C and
CC R554Q. Knowledge of the mutations provides means for assessing a
CC risk in a human subject for LQTS, for diagnosing a mutation which
CC causes LQTS, and for screening for drugs useful in treating a human
CC having a mutation in the KVLQT1 gene.
CC Note: The present sequence is not shown in the Specification but is
CC derived from the KVLQT-1 sequence given in the Sequence Listing
CC (see AAB82220).

SQ Sequence 676 AA;

Query Match	23.2%	Score 1096;	DB 22,	Length 676;
Best Local Similarity	41.7%	Pred. No. 1,1e-88;		
Matches 249;	Conservative 105;	Mismatches 165;	Indels 78;	Gaps 16

OY		98	SSOSORBNKKY- RPNQNTLVNLEPERGM-AFTIYAFVFLVYGCILLSFSTIPETTKL	153
Db		92	SITYSRPRPLANTHVOGRVYNPLERTGKCEFYHHAVFLIVLCIFSVSLSTEQYAAL	151
OY		156	ASSCLLIIEFNVIIVFGLEEPIIRIMSAGCCCRBYRGOGRLRFARKEPCVDTVLVASIA	215
Db		152	ATGLTFMMEIYLVVEFGTEYVRWMSASRSRKRYGVLMGRILFRFKKISTIDLIVVAASKV	211
OY		216	VYSATQGNIEFTSALRSIRFLQIILRMVMDRRGGTWKLGSVVAAHSELLIMAYIGFL	275
Db		212	VLCVSGSKGOVFMTSAIRGIRFLQIIRMLHVDRDROGGTWRMLGVSVFTHREOLLTYIIGFL	271
OY		276	VLIFFSFVUYLYEKA-----NKESTVDALMMGHTITLTJTJGSGKPTLTWIGRLISAG	330
Db		272	GIIFFSYEVYLAIEKRAVNESGKVFECSYADALMMGVYVTITGTGDVKPQTWVGKTIASC	331
OY		331	FALLGISFPALPAGILSGFALKVOEQNRKHHEKRKNPAANLIDCWMSYADEKSVS1	390
Db		332	FSVFATSEFPALPAGILSGFALKVOOKQRKHHPNRQIPAAASLDIQAMRCYAAENDDSS-	390
OY		391	ATWKRHIAL--HT-CSPTNCKLSFEKENVPMAASPFGOSIKSRQASVDPDRSPSTDITAE	446
Db		391	-TWKYIKRAPRSHTLLSPSPKP---KKSVMVKKKKFKDKONGVYPGEKMILVPHITCD	446
OY		447	GSPTRVQKWS--FNDRTRPFRPSLRILKSOPKPYVIDADALTGTDVYDEKGQCQCVSYE	503
Db		447	PPEERLDHFVSVDGDSVVRKSPTL-LEVSMH-----FMRTNSFAED---IDLEBE	494
OY		504	DLTPPL-----KTVIRAIRIMKFNHVARRKRETLPDYDVKDIVEOYSAGHLDMIC	553
Db		495	TLLPRITISOLREHNRIATIKVIREMQYFVAKKPFQAQAPRDVDRVIEQYSQHNLNAV	554
OY		554	RKISLOTVPDIOILKQG--ITSDDKSREKITAHNETDDLMSLGVRVYKEKOVSIESLK	611
Db		555	RIKELQRLRSDSIGKPSLFISVEXSKOR-----GSNTIGARINRVEDVTOLODRL	606
OY		612	DCLLDIYOQVL-----RKISA-----SALALASFQIPPE	641
Db		607	ALITDMCHQLLSLHGSGTPSGSGPRREGAHTIQPGSGSGSVDPDELFLPSNLLPYTE	663
<hr/>				
RESULT 50				
AAB82230	ID	AAB82230	standard; Protein: 676 AA.	
XX	AAB82230;			
XX				
DT	21-JUN-2001	(first entry)		
XX				
DE	Human KVLQTI mutant S349W.			
KM	KVLQTI; Long QT syndrome; LQTS; cardiovascular disease;			
KM	Romano-Ward syndrome; Jervell and Lange-Nielsen syndrome; deafness;			

KW diagnosis; prognosis; therapy; drug screening; mutant; muteln.
XX

OS Homo sapiens
XY

PN WO200124681-A2

PD 12-APR-2001.

PF 09-AUG-2000; 2000WO-US21660.

PR 09-AUG-1999; 99US-0147488.

XX

XX

Department of

[illegible]

PT useful in diagnostic/prognostic or drug screening methods, particularly with new AML and SCNA genes, which contains alterations or mutations,

PT long QT syndrome -
 P1 in mutational analyses for screening individuals with or at risk for

aa
PS
XX

Claim 6; Page -: 76pp; English.

CC The present sequence is that of the claimed S349W mutant of the
CG human KVIOT1 protein. The mutant is encoded by a KVIOT1 mutant

CC gene in which a C/G mutation alters codon 349 from TCG to TGG.

the autosomal dominant form of Long QT syndrome (LQTS), and in Jervell and Lange-Nielsen syndrome, a form of LQTS associated with

SQ Sequence 676 AA;

Query Match	23.1%;	Score 1095;	DB 22,	Length 676;
Best Local Similarity	41.7%;	Pred. No. 1.4e-88;		
Matches 249;	Conservative 105;	Mismatches 165;	Indels 78;	Gaps 16

QY	98	SSOCRRNVRKR-RVONTLYANVLBBPRG-ATLYAHFVLLVAGCCLLSFNSIPRETKL	15
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	92	SIYTRRPVLARHVOGRYNEFLBPTGCKCVHHFAVLVLVCLIFSVLSTEDYAL	15
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	156	ASSCLLLEFMYIVFGEFTIRIMSAGCCCFYRGWGRRLRPAKCEVDITVLASIA	215
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	152	ATGTLFWMEIYLVVEEGTEYVRLMSAGRSXYVGLMGLRRARKISITIDLIVVASWY	211
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	216	VSAKKTGNGNFATASLRSLRLQILRMVBMRRGGTWKLGSVVAHSHKELLTAWYIGFL	275
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	212	VLCVSGSGVAFATSAIRGIRFLQILRMHVDROGGTWRLLGSVFEIHRBELITLYIGFL	271
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	276	VLFSSFLYLVLEVDA----NKERSTADALLMWGITLITLTIGYGKPTLWTWGRLLSAG	330
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	272	GLIFSTFVYLAEADVANSERVEGSTADALMWGVVITLTIGYGKVPQTWMTKIASC	331
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	331	FALLGISFFPALGILSGFALKVOEHRQKHFEKRRNPANDLICVWRSYADEKSVSI	390
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	332	FSVAFISFFPALGILSGFALKVOQRKQKHFNQIPRAASLIQTAWMCYAAENDDSS	390
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	391	ATKPHKAL---HT-CSPNTOKLSFEKERVMSRPGOSIKRSQASVGDGRSTDTITAE	446
		: : : : : : : : : : : : : : : : : : : : : : : : :	

```

Db      391 -TWKIYIRKAPRSHHTLSPSPKP---KKSvvvKKKKFKLDKNGVTPGEGMLTPPHITCD 446
QY      447 GSPTKVOKSWS--FNDTRFRPRLKKSOPKPYIDATALGTDDVDYDEKGCQCDVSYE 503
Db      447 PPEERLDHFVSDGVDSSVRKSPPL-LEVSMH-----FMRTNSFAD---LDLEGE 494
QY      504 DLTPPL-----KTVIRAIRIMKPFHAKRKFKETLRPYDVKDVIEQYSAGHLMVC 553
Db      495 TLLPTPIHISOLREHHRATIVIRRMQYFVAKKFFQAKRPYDVRDVIQYSGHLMNV 554
QY      554 RIKSLQTRVDOILGKGQ--ITSDDKSREKITAHEHTDDLSMLGRVVKYKQVQSIESTKL 611
Db      555 RIKELQRRLDOSIGKPSLFIYSVEKSKDR-----GSNTIGARLNREDEKVTQLDQRL 606
QY      612 DCLLDIYQOVL-----RKGSA-----SALALASFOIPPE 641
Db      607 ALITDMLHQLSLHSGSPGSGPPREGGAHITOPCGSGGSVDPPELFLPSNTLPTYE 663

```

Search completed: June 14, 2003, 17:42:35
 Job time : 87 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:31 ; Search time 48 Seconds
(without alignments)
1848.585 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRNHAGGEGGAAGLVWS.....SICKAGESTDALSPHWLK 923

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1227.5	25.9	393	2	JC5275
2	1226	25.9	744	2	T34116
3	950	20.1	645	2	T27186
4	423.5	8.9	664	2	T28852
5	291.5	6.2	858	2	S31761
6	289	6.1	853	1	CHRTD1
7	279	5.9	857	2	I56529
8	272	5.7	802	2	JH0595
9	251	5.3	769	2	I56546
10	248.5	5.3	528	2	T34417
11	248.5	5.3	924	2	B41359
12	245	5.2	984	2	T24238
13	245	5.2	581	2	S17150
14	243.5	5.1	679	2	A42073
15	242.5	5.1	490	2	T26983
16	242	5.1	624	2	A39402
17	242	5.1	624	2	S22703
18	241.5	5.1	625	2	E90564
19	241.5	5.1	625	2	S13919
20	241	5.1	263	2	A12384
21	238	5.0	654	2	S11049
22	237	5.0	523	2	A38101
23	237	5.0	525	2	A43531
24	235.5	5.0	660	2	S24125
25	235	5.0	924	2	S12746
26	234	4.9	643	2	S00480
27	234	4.9	653	2	A39922
28	233.5	4.9	656	2	JH0193
29	232	4.9	528	2	I84205

30	230	4.9	280	2	E75470	probable ion trans
31	230	4.9	495	2	B39113	potassium channel
32	230	4.9	511	2	A46020	potassium channel
33	230	4.9	511	2	S07095	potassium channel
34	229.5	4.8	495	2	I57680	potassium channel
35	228	4.8	651	2	A39372	potassium channel
36	227.5	4.8	630	2	JU0271	voltage-sensitive
37	227	4.8	585	2	A39395	delayed rectifier
38	226.5	4.8	558	2	T23991	hypothetical prote
39	225	4.8	495	2	A40090	potassium channel
40	223.5	4.7	602	2	JH0166	potassium voltage-
41	222.5	4.7	490	2	A53312	potassium channel
42	221.5	4.7	295	2	C72692	probable potassium
43	220.5	4.7	597	2	S51212	BAK5 protein - bov
44	219	4.6	361	2	S19552	potassium channel
45	215.5	4.6	460	2	T27759	hypothetical prote
46	214.5	4.5	280	2	C82490	probable potassium
47	214.5	4.5	455	2	A70461	potassium channel
48	214.5	4.5	489	2	I51532	potassium channel
49	214.5	4.5	602	2	A49507	shaw protein - Cal
50	214	4.5	489	2	JC4787	potassium channel
51	213	4.5	598	2	S66669	potassium channel
52	212.5	4.5	499	2	I77466	potassium channel
53	212.5	4.5	499	2	A48672	delayed rectifier
54	212.5	4.5	499	2	I84204	potassium channel
55	212.5	4.5	499	2	A33814	potassium channel
56	211.5	4.5	476	2	S21144	potassium channel
57	211.5	4.5	613	2	A56031	potassium channel
58	211	4.5	278	2	AD0651	probable membrane
59	211	4.5	498	2	A41359	potassium channel
60	211	4.5	776	2	T20896	hypothetical prote
61	207	4.4	514	2	C49507	potassium channel
62	207	4.4	530	2	JH0167	potassium channel
63	206.5	4.4	494	2	JC5919	potassium channel
64	203	4.3	482	2	T15828	hypothetical prote
65	200.5	4.2	499	2	JH0313	potassium channel
66	199.5	4.2	513	2	JC5920	potassium channel
67	199	4.2	529	2	S12787	potassium channel
68	198.5	4.2	491	2	T19635	hypothetical prote
69	196	4.1	297	2	A82682	ion transporter Xf
70	193	4.1	491	2	JE0276	voltage-gated pota
71	191.5	4.0	236	2	I57681	potassium channel
72	184.5	3.9	247	2	AC1332	voltage-gated pota
73	184.5	3.9	497	2	JE0275	probable potassium
74	181.5	3.8	283	2	B83459	hypothetical prote
75	180	3.8	209	2	C64317	potassium channel
76	176.5	3.7	247	2	AC1703	potassium channel
77	168	3.5	160	2	S60172	potassium channel
78	167.5	3.5	428	2	A82873	potassium channel
79	162.5	3.4	256	2	C97062	potassium channel
80	162.5	3.4	731	2	T09172	probable calcium-a
81	159.5	3.4	421	2	F90073	hypothetical prote
82	158	3.3	265	2	T29789	hypothetical prote
83	157	3.3	265	2	C95885	probable ionic voi
84	151.5	3.2	5327	2	T13564	microtubule-assoc
85	146.5	3.1	338	2	DB4067	potassium channel
86	145.5	3.1	1390	2	T18883	hypothetical prote
87	145.5	3.1	1910	2	H88124	protein T12C9.3 f1
88	144.5	3.1	985	2	T27083	hypothetical prote
89	144	3.0	1539	2	T30037	hypothetical prote
90	144	3.0	2206	2	JC5280	voltage-dependent
91	142.5	3.0	1891	2	T43262	calcium channel at
92	142	3.0	2212	2	A41098	calcium channel pr
93	141.5	3.0	256	2	E69166	conserved hypothet
94	141	3.0	2161	2	JH0564	calcium channel al
95	140.5	3.0	2223	2	A47447	calcium channel pr
96	140	3.0	815	2	T08450	hypothetical prote
97	139	2.9	2251	2	B54972	voltage-dependent
98	139	2.9	2336	2	A45386	omega-conotoxin-se
99	138.5	2.9	2262	2	T30890	calcium channel at
100	136.5	2.9	2272	2	C54972	voltage-dependent
101	135.5	2.9	1112	2	T43383	probable calcium-a
102	135	2.9	1610	2	A46227	voltage-dependent

103	133	2.8	1175	2	JH0697	potassium channel
104	134	2.8	1148	2	T09073	splicing factor Si
105	131.5	2.8	723	2	T14765	hypothetical prote
106	131.5	2.8	1547	2	JQ0096	hypothetical 176k
107	131.5	2.8	2270	2	A54972	voltage-dependent
108	130.5	2.8	1483	2	E86143	rFf3.12 protein -
109	130.5	2.8	1646	2	JH0422	voltage dependent
110	130	2.7	710	2	P86290	hypothetical prote
111	130	2.7	1097	2	A56138	transcription fact
112	129.5	2.7	783	2	T38891	hypothetical prote
113	129.5	2.7	925	2	T18747	probable potassium
114	129	2.7	1136	2	T26953	hypothetical prote
115	129	2.7	2688	2	I49477	hypothetical prote
116	128.5	2.7	1184	2	A39800	alpha-A-crystallin
117	128	2.7	375	2	E70011	calcium-activated
118	128	2.7	397	2	S74890	potassium channel
119	128	2.7	411	2	T39236	hypothetical prote
120	128	2.7	793	2	S67070	GAC1 protein - yea
121	128	2.7	1494	2	T26452	hypothetical prote
122	127.5	2.7	668	2	S64123	hypothetical prote
123	127.5	2.7	1008	2	T41244	SEC14 protein homo
124	127.5	2.7	2178	2	S29237	calcium channel pr
125	127.5	2.7	2259	2	S29236	calcium channel pr
126	127.5	2.7	2339	2	A42566	omega-conotoxin-se
127	127.5	2.7	3968	2	A44265	tRitroXa homology
128	127	2.7	140	2	B86739	potassium channel
129	127	2.7	793	1	S60735	splicing factor SF
130	127	2.7	1938	2	A59233	skeletal myosin he
131	126.5	2.7	2253	2	T30336	nuclear/mitotic ap
132	126	2.7	57	2	S09042	potassium channel
133	125.5	2.7	636	2	A84252	Htr1s transducer [
134	125.5	2.7	1284	2	T13168	probable potassium
135	125.5	2.7	1687	2	S41742	calcium channel al
136	125.5	2.7	2756	2	T30183	hypothetical prote
137	125	2.6	609	2	T38596	calcium-activated
138	125	2.6	985	2	S59330	Na+/H+-exchangng
139	125	2.6	1102	2	T17367	potassium channel
140	125	2.6	1113	2	S62904	calcium-regulated
141	125	2.6	1184	2	I49017	calcium-activated
142	125	2.6	1196	2	A48206	calcium-activated
143	125	2.6	1783	2	T37258	probable voltage-d
144	125	2.6	2143	2	JH0427	voltage-dependent
145	125	2.6	2222	2	A37490	calcium channel pr
146	124.5	2.6	1852	2	A37860	calcium channel pr
147	124.5	2.6	2562	2	T14266	xin protein - chic
148	124	2.6	1375	2	S48375	hypothetical prote
149	124	2.6	1518	2	S37928	probable purine nu
150	123.5	2.6	1154	2	S69206	regulator protein

ALIGNMENTS

```

RESULT 1
JC5275
voltage-gated potassium channel protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C:Accession: JC5275
R:Yokoyama, M.; Nishii, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A:Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A:Reference number: JC5272; MIMD:97191543; PMID:9039501
A:Contents: neuroblastoma cell
A:Accession: JC5275
A:Molecule type: mRNA
A:Residues: 1-393 <YOK>
A:Cross-references: DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:dt102224; PID:g1841341

Query Match          25 9%;   Score 1227 5;   DB 2;   Length 393;
Best Local Similarity 64.8%;   Pred. No. 3.5e-74;
Matches 243;   Conservative 37;   Mismatches 72;   Indels 23;   Gaps 5;

```

QY	21	GGAAAAAGGGRIGSSKKMDVSGGGRVLLNSAAARGDGLLITGTAAATLIGGGGGGGRRESR	80
Db	9	GYPPGSGSEKKLVGVGVGLDPGA-----PDSTRDGLADPSAPK---RGSLSKPRA	59
QY	81	GGGAGMSLLGRPLSTYSQSCRNNKYRRVQNYLVYLERPRQMAFYAFAVELVYGC	14
Db	60	GGAGA-----GKR-----PKRNFYRKLQNFVYLERPRQMAFYAHAYVELLVYSC	10
QY	141	LILSVSTIPEHTKTLASSCLLLEFYIVVFGLEFIIRISAGCCCRYRGQGRLEARK	20
Db	107	LVLVSFTIKEYEKSESGALYILIEIYIVVEGYEYFRIWAAGCCCRYRGGRGLKEARK	16
QY	201	PCVCIDTYILNISIAVYSAKTQGNIRATSLRSLRFQIIRMYMDRDRGGYWKLLGSVY	26
Db	167	PCVCIDIMVLNISIAVLAGSQGNVPTSLRSLRFQIIRIMRMDRGGYWKLLGSVY	22
QY	261	AHSEKLTAMYIGTFLVLFSSFEVYVEKPKANKEFSTYAADLMMGTTLTITIGYGDTP	32
Db	227	AHSEKELVAMYIGTFLCLLILASFLYVLAKEGNENHFDYADALMMGLTLTITIGYGDTP	28
QY	321	TWLGRLLSAGFALLGISFPALPAGILGSGFALVQEQHROKHFEKRRNPANLIGCYWRS	38
Db	287	TWNGRLLATFYLIGSFPALPAGILGSGFALVQEQHROKHFEKRRNPAGILQISAMRF	34
QY	381	YAADKESVI-ATWK 394	
Db	347	YATINLSRFDLHSTWQ 361	

RESULT 2

Voltage-gated potassium channel *klq-1* - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T34116
 R:Milcox, L.
 Submitted to the EMBL Data Library, December 1995
 A:Description: The sequence of C. elegans cosmid C25B8.
 A:Reference number: Z21479
 A:Accession: T34116
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-744 <Mile>
 A:Cross-references: EMBL:U41556; PIDN:AAC70874.1; GSPDB:GN00028; CESP:C25B8.1
 A:Experimental source: strain Bristol N2; clone C25B8
 C:Genetics:
 A:Gene: *klq-1*; CESP:C25B8.1
 A:Map position: X
 A:Introns: 31/3; 64/1; 81/3; 131/2; 161/3; 204/1; 262/3; 304/3; 341/3; 402/2; 426/1

[illegible]

Db 305 FLVCLVGLFIACTFOAANTQISVGLTLMMEENKNOQINRLNLAASITQCMWRHILA - 362
 QY 386 KSVSIATKTP---HKALHTC-----SPTNOKLSPEKERVMAAPPGOSISKROASVGD 435
 Db 363 -----TNKKPPRRRYFVHVCKLYTEERINONRVLAKKRLRELEKRPILKKK--SLTH 415
 QY 436 RRSSTDTITAGS---SPTRVOKSWSPNDTRFRPSRLKLSQPKPYIDADTALGTDVY 491
 Db 416 QNSVYAEILKFGFGKMAKPMLEKODSF--DKAEKISLR---RTRKRVLFABAR--NSSVE 469
 QY 492 DEKGQCVQSVEDLPPPLKTVIRAIRIMKFNHAKRKFET-----LRPVDVADVIEQY 544
 Db 470 TSMSSVDVS-----ELETFEITNLFQONDELSSKNGSGSKLLMKPGSGTLAOTQR 523
 QY 545 SAGHLDML-----CRKSLQTRVDQILGKGQTSDDKSRREKITAHEHTDLS 592
 Db 524 IAGOLMIEALAEERENONQMKLEALILLETGKPTVSPFPDSSGK-----LS 573
 QY 593 MLGRVYKVKOVQSTESKIDCLDI 617
 Db 574 IIERLEFCEKRMEDLEKTDALNEI 598

RESULT 5

S31761
 potassium channel protein DRK1 - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S31761
 R:Albrecht, B.; Lott, C.; Stocker, K.; Pongs, O.
 submitted to the EMBL Data Library, September 1992
 A:Description: Cloning, expression and chromosomal localization of the delayed rectifier
 A:Reference number: S31761
 A:Accession: S31761
 A:Residues: 1-858 <DNA>
 A:Molecule type: DNA
 A:Cross-references: EMBL:X68302; NID:g30892; PIDN:CAA48374.1; PID:g30893
 C:Genetics:
 A:Gene: GDB:KCNB1; KV2.1; DRK1
 A:Cross-references: GDB:128081; OMIM:600397
 A:Map position: 20q13.2-20q13.2
 C:Superfamily: potassium channel protein drk1

Query Match 6.2%; Score 291.5; DB 2; Length 858;
 Best Local Similarity 20.2%; Pred. No. 36-11;
 Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33;
 QY 115 LYNVLEPRGMA---FIFYHAFVLLVFGCLISVSPSTIEHRYL-----ASSCLILE 164
 Db 175 LMDLEKPNSSVAAKILAIISIMFVLTSLSL--NTLPELOSLDEFGOSTDNPQLAHVE 233
 QY 165 FVMIVFGLFEFIRISAGCCCRYGWQGRLEFARKPCVVIDIVLAIASIAVVSATQGN 224
 Db 234 AVCIAMFTMEYLFLLFLLSP-----KKW-----KFKGPIALIDLLALPYV-----T 276
 QY 225 IFATSAIRSL-----RFLQILIRYRMDRGSTWKLIGSVVYAHSEL--ITAW 270
 Db 277 IFLESKSVYQFQONVRVQVIFRMRILIRIKLARHSTGLSGITLRSYNELGLIL 336
 QY 271 YIGFLVIFSSFLVYLVKEDA--NKEFSYADALMGITITLITGYGDKPDLMTGLRLSA 329
 Db 337 FLAMGIVIFSS--LVFFAKEDDDTKFKSI PMSFWATTITVTGVDIYPKTLGKIVGG 395
 QY 330 GFALLGISFPALGAILGSGFALKVOEOROKHFEKRRNPANLILQCVWRSYADEKSVS 389
 Db 396 LCCIAGVLYALPIPIIVNNSEFYKEQKROKAIKR-----EALERARRNGS 444
 QY 390 IATMKPILKALHTOSPTNOKLSFEKRYVM---ASPRGOSISROASVGDRRSPSDTITA 445
 Db 445 IVS-----NMKDAFARISIMMDIVVEKNGENMKKDKVQDNHLSPNKMKWT 491
 QY 446 EGSPTKVKQSWSPNDTRFRPSRLKLSQPKPYIDADTALGTDVYDEKGCQCDVVEDL 505

Db 492 KRTILESTSSKSFETKEQSGPEKARSSSPQHL-----NVQOEDMY NKMA----- 537
 QY 506 TPPLKTVIRAIRIMKFNHAKRKFETLRPYVQKVDIEQYSAGHLMCLCRKSLQTRVDQI 565
 Db 538-----KTQSOPILNTKESAOSKPRKEELMESIPS-----PVAPLPRTTEGV 579
 QY 566 LKGQITSDKRSREKITAHEHTDLSMLGVRVYKVKOVQSTESKIDCLDIYQOVLKRG 625
 Db 580 I-----DMRS-----MSISDTISCATD--FPEATRRS 605
 QY 626 SASALALASFOIPPECEQTSQVSPVDSKDLSSAQNQSGCLSRSTANISGLOFILPP 685
 Db 606 HSPILTSIPS-----KTGSGTAP--EVMGRALGASG--GREVEANPS-----P 644
 QY 686 NESASQTFYALSP-----TMSQATQVPISSD-----GSAYAA 719
 Db 645 DASQHSFFLESRSKSKTNPNPLRLKLVFMGSDPSPLLPVIGMYHDPILNRNSAANA 704
 QY 720 T-----NTIANQINTAPKPAAPPTLQIPPLPAIKHLPRPTLHPN-----PAGQESTS 769
 Db 705 VAGLEGATLIDKRAVLSPSSSIYTTASAKTP-----PRSEKHTAIAFNFAAGVHQYI- 756
 QY 770 DYTCLVASKENYVAQSNLTQDRSMKRSFDMGGETLLSYCPWPVKDLGSLSYQNLIRS 829
 Db 757 DADT-----DDEGQLLYSVDSPPKSLPSTSPK----- 785
 QY 830 TEELNTQLSGSSSGSGSGQDFYPKMKRESKLFITDEVEGPETETDTPDAQPARAEAF 889
 Db 786 -----FSTGRSEKNHF-----BSSPLPTSPKFLRNQCT 814
 QY 890 ASDSLTRGSRSSQSISCKAGE--STDALSLP 918
 Db 815 YSTEALTGKPSQGEKCKLENHISPDVRLVP 845

RESULT 6

CHRTDI
 potassium channel protein drk1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
 C:Accession: S05448; A44838
 R:Frech, G.C.; Vandongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
 Nature 340, 642-645, 1989
 A:Title: A novel potassium channel with delayed rectifier properties isolated from ra
 A:Reference number: S05448; MUID:89365157; PMID:2770868
 A:Accession: S05448
 A:Molecule type: mRNA
 A:Residues: 1-853 <PRE>
 A:Cross-references: EMBL:X16476; NID:g57785; PIDN:CAA34497.1; PID:g57786
 A>Note: It is uncertain whether Met-1 or Met-17 is the initiator
 R:Frech, J.A.; Verna, S.; Frech, G.; Joho, R.H.
 J. Neurosci. 12, 538-548, 1992
 A:Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from d
 A:Reference number: A44836; MUID:92156897; PMID:1740650
 A:Accession: A44838
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 'MPAG', 1-571 <DRE>
 A:Cross-references: GB:M81783; NID:g205038
 A:Experimental source: brain
 A>Note: sequence extracted from NCBI backbone (NCBIP:81768)
 C:Genetics:
 A:Gene: drk1
 C:Superfamily: potassium channel protein drk1
 C:Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembra
 F:1182/Domain: Intracellular #status predicted <INT1>
 F:183-204/Domain: transmembrane #status predicted <TM1>
 F:225-245/Domain: transmembrane #status predicted <TM2>
 F:256-276/Domain: transmembrane #status predicted <TM3>
 F:291-312/Domain: transmembrane #status predicted <TM4>
 F:327-348/Domain: transmembrane #status predicted <TM5>
 F:389-410/Domain: transmembrane #status predicted <TM6>
 F:411-853/Domain: Intracellular #status predicted <INT2>

F:279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.18; Score 289; DB 1; Length 853;
Best Local Similarity 19.78; Pred. No. 4.4e-11;
Matches 176; Conservative 134; Mismatches 269; Indels 316; Gaps 37;

```

115 LYNVLEPRGMA---FYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLILE 164
171 LMDLLEKPNSSVAKILAITISIMEIVLSTALSL-NLPELOSIDERGOSTDNQOLAHVE 229
165 FVMIVVGEFTIRISAGCCCRVGMGRLEFARKPCVDTIVLILASIAVSAKTQGN 224
230 AVCIAMFTMEYLRLFLSSP-----KKW-----KEFKGPLNAIDLAILPYV-----T 272
225 IFATSLARSL-----RFLQILRMVRMDRGGTKLLGSVVAHAKSEL-ITAW 270
273 IFLETSKSVLQONVARRVQIFRIMRLRLKLARSTGLQSGFTLRSYNELGLLIL 332
271 YIGFVLIFESSFLVYLVEKDA-NKESTYADALMMGTTTLTGIGDKTPLTWLGRLLSA 329
333 FLAMGIMIEFS-LVFEAKEDDDTKFKSIPASFMAITMTTGVGDIYPTLLGKIYVG 391
330 GFALLGISFPALPAGILGSPALKVQOHROKHEKRRNPANLIQCVRSTYADEKSVS 389
392 LCCIAGLVIALPILPIIVNNESEFYKQKROEKAIKRR----- 429
390 IATWKPALKALHNCSPINOKLSFKERYRMAASPRQSIKRSQASVGDRRSPSTDITAEQSP 449
430 -----EALERAKRNGSIV----- 442
450 TKVQKWSFNDRTFRPSRLKSSQKRPVIDADTALGTDVYDEKGCOCOVSVEDLTPL 509
443 -----SMMKDAFARSIEH-----MDIYVEKNG----- 465
510 KTYIRAIRIMKFNVAKKFKETLRPYDVKYIEQYSAGHLDMLCRISLQTRVDOILGK 569
466 ESIAKKKQKVDNHLSPKMKWT-----KRALSETSSS-----KSPEK----- 503
570 QITSDDKSRREKITAHEHTDLSMLGRVYKVEKQVQSIKSLDCLDIYQVLRKGSAGA 629
504 EGSGPEKARSSSPQH-----LNVOOLE-----DMYSKAKQIOSQPI 540
630 L---ALASFOIPPECEGTSIDYQSPVDSKDLGSAONSGCLSRSTANSIRGLQFTLPN 686
541 LNTKEMAPQSKPPELEMS-MPSVAPL---PARTGVIDMRGMSSID---SFTSCAT 592
687 EFSAGTYIALSP-TMHSQATQVPLSQ-----SDGSAVAATNTIANQINT-----AP 731
593 DFPATRRSHSPLASLSSKAGSSTAPEVGMGALGASGRLETNPITPSTRSGFEVESP 652
732 KPAAPPTLQIP-----PLPAIKHLPRPETLHPNP-----AGLQESIS 769
653 RSSKATNNPKLRALKVNFVEGDDPTPLPSL---GLYHDLPLRNKGAAVAAGL-ECAS 707
770 DVTTCVLASKENVOVQNSLTKDRSMRK-----SFDMG-----GETLLSYCP 811
708 LLDKPVLSPESSITYTASARTPPRSPEKHTAIAFNFEAGVHHYIDTDDDEQOLLYSVDS 767
812 MVRPDLGKSLVQNLIRSTEELINTQLSGSESSGSRGSDQFPYKWRSKSLFTIDEVGPPE 871
768 SPPKSLHGSTSPK-----FSTGAR----- 786
872 TETTFDAPOPAR-----EAAFAASDLRTGRSRSSQISCKAGEST---DALSLP 918
787 TEKNHFESSPLPTSKFLRPNCVYSSEGL-TCKGPGAOEKCKALENTPPDVHMLP 840

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RESULT 7

156529

potassium channel protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 20-Aug-1999

C:Accession: I56529

R: Pak, M.D.: Covarrubias, M.; Ratcliffe, A.; Salkoff, L.

J. Neurosci. 11, 869-880, 1991

A:Title: A mouse brain homolog of the Drosophila Shab K⁺ channel with conserved delay

A:Reference number: I56529; MIMD:91162315; PMID:2002364

A:Accession: I56529

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-857 <RES>

A:Cross-references: GB:M64228; NID:g200975; PIDN:AAA0112.1; PID:g200976

C:Genetics:

A:Gene: Shab

C:Superfamily: potassium channel protein drkl

Query Match 5.9%; Score 279; DB 2; Length 857;

Best Local Similarity 20.4%; Pred. No. 2.1e-10;

Matches 181; Conservative 124; Mismatches 280; Indels 304; Gaps 37;

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115 LYNVLEPRGMA---FYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLILE 164
175 LMDLLEKPNSSVAKILAITISIMEIVLSTALSL-NLPELOSIDERGOSTDNQOLAHVE 233
165 FVMIVVGEFTIRISAGCCCRVGMGRLEFARKPCVDTIVLILASIAVSAKTQGN 224
234 AVCIAMFTMEYLRLFLSSP-----KKW-----KEFKGPLNAIDLAILPYV-----T 276
225 IFATSLARSL-----RFLQILRMVRMDRGGTKLLGSVVAHAKSEL-ITAW 270
277 IFLETSKSVLQONVARRVQIFRIMRLRLKLARSTGLQSGFTLRSYNELGLLIL 336
271 YIGFVLIFESSFLVYLVEKDA-NKESTYADALMMGTTTLTGIGDKTPLTWLGRLLSA 329
337 FLAMGIMIEFS-LVFEAKEDDDTKFKSIPASFMAITMTTGVGDIYPTLLGKIYVG 395
330 GFALLGISFPALPAGILGSPALKVQOHROKHEKRRNPANLIQCVRSTYADEKSVS 389
396 LCCIAGLVIALPILPIIVNNESEFYKQKROEKAIKRR-----EALERAKRNGS 444
390 IATWKPALKALHNCSPINOKLSFKERYRMA---ASPRQSIKRSQASVGDRRSPSTDITAE 445
445 IYS-----NMKDAFARSIEHMDIYVEKNGEYAKKQKVDNHLSPKMKWT 491
446 EGSPYKQKWSFNDRTFRPSRLKSSQKRPVIDADTALGTDVYDEKGCOCOVSVEDL 505
492 KRALSETSSSKSPFTKQSGPEKARSSSPQH---NVQOLQDYSK---NAKTQS 541
506 TPPLKTYIRAIRIMKFNVAKKFKETLRPYDVKYIEQYSAGHLDMLCRISLQTRVDO 565
542 QPILNT-----KEMAFQSQPELEMS-----MPSVAPLPTRTGCV 579
566 LGKQITSDDKSRREKITAHEHTDLSMLGRVYKVEKQVQSIKSLDCLDIYQVLRKG 625
580 I-----DMRS-----MSSIDSFISCATDP----- 598
626 SASALALASFOIPPECEGTSIDYQSPVDSKDLGSAONSGCLSRSTANSIR 677
599 -----PEATRRSHSPLAS---LSGSGSSTAPEVGMGALGASGR--- 636
678 GLQFTLPNP---EFSAGTYIALSP-----TMHSQATQVPLSQ-----AGLQESIS 726
637 LMENPILPASRSQGFVEYSSKMTNNPKLRALKVNFLESGD----- 679
727 INTAPKPAAPPTLQIPPELPAIKHLPRPETLHPNP-----AGLQESISDVTTL 775
680 -----PT-----PLPAL-----GLYHDLPLRNKGAAVAAGL-ECASLDPK 717
776 VASKENVOVQNSLTKDRSMRK-----SFDMG-----GETLLSYCPMVPRDL 817
718 LSPSSITYTASARTPPRSPEKHTAIAFNFEAGVHHYIDTDDDEQOLLYSVDSILPKSL 777
818 GKSLSVQNLIRSTEELINTQLSGSESSGSRGSDQFPYKWRSKSLFTIDEVGPPEETD 877
778 HGSTSPK-----FSLGAR-----TEKNHF 796

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QY 878 DAADPAR-----BAFASDSLRTGRSSRSOSICKAGEST--DALSLP 918
 Db 797 ESSPLPSPKFLRPNOCVYASEGL-PSKGPAGQCKCKENTSTPDVHMLP 844

RESULT 8

JH0595
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 20-Aug-1999
 C:Accession: JH0595
 R:Hanng, P.M.; Glatz, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H.
 Neuron 6, 473-481, 1992
 A:Title: A novel K⁺ channel with unique localizations in mammalian brain: molecular clon
 A:Reference number: JH0595; MUID:92198655; PMID:1550672
 A:Accession: JH0595
 A:Molecule type: mRNA
 A:Residues: 1-802 <HNA>
 A:Cross-references: GB:M77482; NID:g2033395; PIDN:AAA40905.1; PID:g2033396
 A:Experimental source: circumvallate papillae
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; phosphoprotein; transmembrane protein
 F:191-212/Domain: transmembrane #status predicted <TM1>
 F:233-254/Domain: transmembrane #status predicted <TM2>
 F:265-286/Domain: transmembrane #status predicted <TM3>
 F:289-320/Domain: transmembrane #status predicted <TM4>
 F:335-356/Domain: transmembrane #status predicted <TM5>
 F:397-418/Domain: transmembrane #status predicted <TM6>
 F:187-287, 419, 446/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:448,500/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 5.7%; Score 272; DB 2; Length 802;
 Best Local Similarity 24.4%; Pred. No. 5.5e-10;

Matches 121; Conservative 82; Mismatches 191; Indels 102; Gaps 21;

QY 115 LYNVLEPRGMA---FIYHAEVLLVFGCLLSVSTPE-----HTKASSC 159
 Db 179 LMDLEPNSSVAAKIATVILFTVLTALSTL-NTLPQLQENDEFGOPSDRKLAH- 235
 QY 160 LLILEFMIIVFGLFEIRIRMSAGCCCRMGQRLRPAKPCVDTIYLASIAVVA 219
 Db 236 ---VEAVCIAMFTMEYLLRFLSS-----PNKMKFKGPLNVIDLALILYYV- 279
 QY 220 KTQGNITATSLRL------RFLQILRMVMDRRGGTWKLLGSVVYAHSKEL 266
 Db 280 ---TIFLTSNKSQVLOFQNVRRVQIFRIMRLILKLARHSTGLQSLGFTLRSSYNEL 335
 QY 267 -ITAMYGFLVLISSFLVLYVEKDN-KPSTYADALWMGTTTLTIGYGDKTPLTWLG 324
 Db 336 GLILFLFAMGIMTSS-LVFFAEKDEDAKFTSTPASEFWMATITMTVGIGDIYPTLLG 394
 QY 325 RLISAGFALIGISFFALPAGILGSGFALKVOEHROKHEKRRNP-----AANL 373
 Db 395 KIYGGLCICIGAVLIALPIPIVNNFSEFYKEQKQKRAIKRREALERAKRNGSIYSML 454
 QY 374 IQCVMSY---AADEKSVSIATKPKPHKALHTCSPTNOKLSFKKEVRYMASPGGSITKR 429
 Db 455 KDAFARSMELIDVAVERAGESANIKSDVDNH-LSPSRKMKARKALSETSSNKSSENKYQ 513
 QY 430 QASVGRSPSTDTTAAEGRP--TKYK-SWGFNDTRRPPSRLLKSSOPKPYVDATALG 486
 Db 514 EYSGQKSHEDLN-TSSSSPOHLSAQKEMLYNETTKYQ-----THSHNP--DCOEOP 565
 QY 487 TDDVYDEKGCOCDSVEDLTPPLKTVIRA-----IRIMFHVAKRREKETLRPY 535
 Db 566 RPSAYEE---ETEMEVEVCPQEQALVAQTEVIVDMKSTSIDFTSCATFETTER-- 618
 QY 536 DVKDVIEQVSAGHDM 551
 Db 619 ---SPLPPPSASHLQW 631

RESULT 9

I56546
 Shaw type potassium channel - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Feb-2001
 C:Accession: I56546
 R:Goldman-Wohl, D.S.; Chan, E.; Baird, D.; Heintz, N.
 J. Neurosci. 14, 511-522, 1994
 A:Title: Kv3.3b: a novel Shaw type potassium channel expressed in terminally differen
 A:Reference number: I56546; MUID:94132879; PMID:8301351
 A:Accession: I56546
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-769 <RES>
 A:Cross-references: GB:S69381; NID:g545228; PIDN:AAC6067.1; PID:g545229
 C:Genetics:
 A:Gene: Kv3.3b
 C:Superfamily: potassium channel protein drkl

Query Match 5.3%; Score 251; DB 2; Length 769;
 Best Local Similarity 23.2%; Pred. No. 1.3e-08;

Matches 96; Conservative 65; Mismatches 162; Indels 90; Gaps 13;

QY 3 RHAGGEEGGAAGLWYSGAAAAAGGGRGSGMKDYESGRVYLLNSAARGDGLLLG 62
 Db 191 RQHRDAEALDSPDAPDSSANANANGAGADGLDD-EAGAG-----GGSLDAG 239
 QY 63 TRAAVL-----GGGGGGLRSGRKGQCARMSLGLKPLSTYSSQSCRNVKTRRQNYLYN 117
 Db 240 GELKRLCFQDAGAGAGLPGACGAGD-----TWRRRQPRVWA 278
 QY 118 VLERP---RGMAFIYAFVFLVFGCLLSV-----FSTIPEHTKLASS----- 158
 Db 279 LFEDPYSSAARVANAASLFFILISITFCELEHHEGTHISNKTYQASPIPGAPENIT 338
 QY 159 -----CLLIEFMIIVFGLFEIRIRMSAGCCCRMGQRLRPAKPCVDTIYL 210
 Db 339 NVEVETEPFLTYVEGVVWFTEFLMRV---TFC-----PKVEFLKSLNIIDCVAI 389
 QY 211 I-----ASTAVYSAKQGNIFATSAIRSEFLQILRMVMDRRGGTWKLLGSVVYAHKE 265
 Db 390 LPFYLEVGISGSKRAKAVL--GFLRVVAFVRLILFKILRHVGLRVLGHTLRASSTNE 447
 QY 266 -LITAMYGFLVLISSFLVLYVEKDNK-----FSTYADALWMGTTTLTIGYG 315
 Db 448 FLILIFIALGLVIFATMIYVARIADPPDILGNSHTYKKNLPIGFWMAVVTTLIGYG 507
 QY 316 DKTPITWLCRLSAGFALLGISFFALPAGILGSGFALKVOEHROKHEKRRN 368
 Db 508 DMVPTWGMVLVGLCALAGVLTAMPVPVIVNNFGMYSLAMAKOKLPKKN 560

RESULT 10

T34417
 delayed rectifier channel protein homolog exp-2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34417
 R:Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998
 A:Description: The sequence of C. elegans cosmid f12f3.

A:Reference number: Z21521

A:Accession: T34417

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-528 <FUL>

A:Cross-references: EMBL:U80022; PIDN:AAC25887.1; GSPDB:GN00023; CESP:F12F3.1

A:Experimental source: strain Bristol N2; clone F12F3

C:Genetics:
 A:Gene: exp-2; CESP:F12F3.1
 A:Map position: 5
 A:Introns: 42/2; 135/3; 173/3; 213/3; 271/3; 469/1

Query Match 5.3%; Score 248.5; DB 2; Length 528;

Best Local Similarity 23.5%; Pred. No. 1.1e-08;
Matches 72; Conservative 61; Mismatches 117; Indels 57; Gaps 8;

OY 110 RVQNYLYNLERP-----RGMAFYHAFFVFLVCGCLLSVSTIP----- 150
Db 226 KLRMRMTFLERPOSSMOAKAFELSTLEFAISVWG---LS-FGTIPDEQVTHLMPHNE 281
OY 151 -----EHTKLASSCLLLEFVAVVEGEEFIRISAGCCCRGQGR 195
Db 282 TVVLPNGTVVQVQVEQKRVHPAFVFERICIAFFVEYCLRPRA-----PRKL 332
OY 196 RFARKPCVYDIT-----VLASIAVSAKTGNIPTASLSRFLQILRMVMDR 247
Db 333 RFALKPLNLDLAIVPFYLELLTLGVDRLDLRMAFLVRLVRLVRIKIKGR 392
OY 248 RGTWKLKSGVVAHAKRLITAMVIGFLVLISSFLVLYVEKD-ANKESTYADALMWGT 306
Db 393 FSSGLQTFGMTLQNSQKQLQMMTVLTLGVVFFSTMIYFLEKDEGTPSTIPAAVWCI 452
OY 307 ITLTIGYDGTPLTLWLRSLSAGFALGISFPALPAGILSGFALKVOEHRKHPEKR 366
Db 453 VTMTTGVGDAVPATMTCKIITASAIMGVVLALPITIVDF-IKVADDEQAQOKN 511
OY 367 RNPAANL 373
Db 512 DQOSEQL 518

RESULT 11

B41359
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C:Accession: B41359
R:Butler, A.; Wei, A.; Baker, K.; Salkoff, L.
S:Science 243, 943-947, 1989
A:Title: A family of putative potassium channel genes in Drosophila.
A:Reference number: A41359; MUID:89146139; PMID:2493160
A:Accession: B41359
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
C:Cross-references: GB:M32659
C:Genetics:
A:Gene: FlyBase:Shab
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drkl

Query Match 5.3%; Score 248.5; DB 2; Length 924;
Best Local Similarity 26.2%; Pred. No. 2.5e-08;
Matches 98; Conservative 70; Mismatches 153; Indels 53; Gaps 15;

OY 107 KYRVOYLYNLERP-----RGMAFYHAFFVFLVCGCLLSVSTIP-----HTK 154
Db 413 KFSEYOKYLMELLEKPNTSFAARVIAVISILFVL-----STIALTLNLPOLQHDNGTP 468
OY 155 LASSCLLLEFVAVVEGEEFIRISAGCCCRGQGRARARPCVYDITVILA-S 213
Db 469 ODNPOLANEAACITWETFLYILIRSSS-----PDWKFFKGLNITIDLALPYF 519
OY 214 IAVSAKTGNIPTASLSRFLQILRMVMDRSGTWKLSGVVAHAKSKEL 266
Db 520 VSLFLETNKN--ATDQDQVRRVYGVFRIMRLVTLKLAHSGLSGSLFTLNKSKEL 577
OY 267 -ITANVIGFLVLISSFLVLYVEKD-ANKESTYADALMWGTITLTIGYDGTPLTWLG 324
Db 578 GLIMFLANGVLIFFS-LAYFAEKDEKDTKFSIPEAFWAGITMTVGIIDICPTALG 636
OY 325 RLISAGFALGISFPALPAGILSGFALKVOEHRKHPEKRNN---PANLQCYWRS 380
Db 637 KYIGVYCCICGVLYVALPPIIYNNRAEFKNOMRRKALKRREHSIVPSRGQCHLLPS 696
OY 381 YAADE---KSVSIATWPKPHLKALHTCSPTNOKLSFKERVMA SPR-GQSIKRSQASVQDR 436

Db 697 YQSERSPAKSMDLID-----YIVDTGKQTN--VVHPKGRQSTWIGKQTLIDVQSPGHN 749
OY 437 RSPSTDITAGESP 450
Db 750 LSQTDNGNSTGEEST 763

RESULT 12

T24238
hypothetical protein R186.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C:Accession: T24238
R:Barlow, K.
submitted to the EMBL Data Library, August 1996

A:Reference number: 219861
A:Accession: T24238
A:Molecule type: translated from GB/EMBL/DBJ
A>Status: preliminary;
A:Residues: 1-484 <WIL>
A:Cross-references: EMBL:Z76016; PIDN:CAB01442.1; GSPDB:GN00023; CESP:R186.5
A:Experimental source: clone R186
C:Genetics:
A:Gene: CESP:R186.5
A:Map position: 5
A:Introns: 30/2; 65/2; 85/3; 128/3; 235/3; 370/3; 409/3; 446/1
C:Superfamily: potassium channel protein drkl

Query Match 5.2%; Score 245; DB 2; Length 484;
Best Local Similarity 24.2%; Pred. No. 1.6e-08;
Matches 72; Conservative 59; Mismatches 117; Indels 50; Gaps 8;

OY 108 YRVOYLYNLERP-----RGMAFYHAFFVFLVCGCLLSVSTIP-----LSVFSTIP 151
Db 148 WQKTPRIWLRLEDFNSRSRQFIAISVFLITAIYVCLTHGRLPELAPFQNSR 207
OY 152 HTKLASS-----CLLLEFVAVVEGEEFIRISAGCCCRGQGR 193
Db 208 NHRSSSHIHQAQIMIDKANSRPHPTWIEFTICNWFTEIL-----ARFSSCP 258
OY 194 RLRFARKPCVYDITVILASIAVSAKTGNIPTASLSRFLQILRMVMDRSGTWK 253
Db 259 RFEYLRAPVNIID---IVATLTFYIDLSSMGFADDEFFSLIRIMRLEKTLHNSGK 315
OY 254 LLSGVVAHAKSKEL-ITANVIGFLVLISSFLVLYL--VERDANKESTYADALMWGTITLT 310
Db 316 ILMHTFRASAKELMLLVFPLVIGVVFASLVYAEVESNEDQFVSIFIGLMAIYVMT 375
OY 311 TIGYDGTPLTWLRSLSAGFALGISFPALPAGILSGFALKVDE-QHRKHPEKR 367
Db 376 TIGYDITPHYTLGRIGLSICALAGVLTALVPVIVSNFAFMYSHTOARSKMPKRR 433

RESULT 13

S17150
potassium channel protein - rat

C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Feb-2001
C:Accession: S17150
R:Lluneau, C.; Wiedmann, R.; Smith, J.S.; Williams, J.B.
FEBS Lett. 288, 163-167, 1991
A:Title: Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.
A:Reference number: S17150; MUID:91348257; PMID:1879548
A:Accession: S17150
A:Molecule type: DNA
A:Residues: 1-581 <LUN>
C:Superfamily: potassium channel protein drkl

Query Match 5.2%; Score 245; DB 2; Length 581;
Best Local Similarity 23.3%; Pred. No. 2.1e-08;
Matches 94; Conservative 79; Mismatches 138; Indels 92; Gaps 17;

QY 70 GGGGGLRESRRGKOGARMSL-----LCKPLSTYSSOSCRNNKYRRVONYLVNERP-- 122
 Db 176 GDDPDDEDLGGK---RLGIEDAAGLGGPDG-----KSGRWKRLQPRMMLPEDEYS 224
 QY 123 -RGMAFIYAFVFLVFG-----CL-----ILSVSTPEHKLKSSCLLI 162
 Db 225 SRAARFIAPASLFTLVSTTFTCLETHEADENIVKNKTEPVINGTSAVLQYEIETDPALTY 284
 QY 163 LEFVNIIVVEGLEFIIRIMSAGCCRRYRGWOGRLFAKRPFCVIDITIVY-----ASIAVY 217
 Db 285 VEGCVVWMTFEFLVIVFS-----PNKLEFINLNIIDFVALIPFLYELVGLSGL 335
 QY 218 SAKTGNIFATSLNSLRFLOILRMVMDRGGTGWLLGSVVAHSKE-LITAWYIGFLV 276
 Db 336 SSKAAKDVLT--GFLRVVRFRVIRILFKLTHFVGLVGHTRASTNEFLLIIFLALGV 393
 QY 277 LIFSFLVYLVK-----DANKPESTYADALMWGITITLTIGYGDTPLTWGLRL 326
 Db 394 LIFAT-MIYYAERVGAGQPDPSASEHTQFNIPDIGFWMAVVTMTTIGYDMYPTWISGML 452
 QY 327 LSAGFALLGISFPFALPAGIL---GSGFALTKVOEQ---HROKHF-----EKR 366
 Db 453 VGALCALAGVLIAMPVPIYVNNFGMYSLAMAKOKLPKRKKHIIPAPLASSPTFCKTE 512
 QY 367 RNPAANLIQ---CWRKSTIADEKSVSIATWKPPLKALHTCSPT 406
 Db 513 LMACNSTOSDYCIKCKENRLLEHNRSVAS---TLEPWESTSQF 552

RESULT 14

A42073
 potassium channel protein Kv3.3 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Feb-2001
 C:Accession: A42073; S22046
 R:Ghanshani, S.; Pak, M.; McHersson, J.D.; Strong, M.; Dethlefs, B.; Wasmuth, J.J.; Salik
 Genomics 12, 190-196, 1992
 A:Title: Genomic organization, nucleotide sequence, and cellular distribution of a Shaw
 A:Reference number: A42073; MUID:92155707; PMID:1740329
 A:Accession: A42073
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-679 <GNA>
 A:Cross-references: GB:X60796; NID:953759; PIDN:CAA43209.1; PID:9817994; GB:X60797
 C:Superfamily: potassium channel protein drkl

Query Match 5.1%; Score 243.5; DB 2; Length 679;
 Best Local Similarity 23.2%; Pred. No. 3.4e-08;
 Matches 96; Conservative 66; Mismatches 160; Indels 91; Gaps 14;
 QY 3 RHHAAGEBGAAGLWVKSAAAAAGGGLGSGMKDVESGRGVLLNSAARGDGLLLG 62
 Db 114 RQHRDAEALDSFEAPDSSANNANANAGAHADGLD-EGAG- -GGGLDGAG 162
 QY 63 TRATL-----GGGGGLRESRRGKOGARMSLIGKPLSTTSSOSCRNNKYRRVONYLVN 117
 Db 163 GELKRLCPDAGAGGAGDLPAGAA--GATW-----WRRQPRVMA 200
 QY 118 VLERP---RGWAFIYHAFVFLVFCCLILSV-----FTIPEHKLKSS----- 158
 Db 201 LFEDPYSSRARAYAFALPFLITISITTFCLTHEFHIISNTYQASIPGAPPENIT 260
 QY 159 -----CLILFEMVIVGLEFIIRIMSAGCCRRYRGWOGRLFAKRPFCVIDITIVL 210
 Db 261 NVEVETEFLLYVGVGVWMTFEFLMRV---FTC-----PDKVELKSLNIIDCVAI 311
 QY 211 I-----ASIAVYSAKTGGINIFATSLNSLRFLOILRMVMDRGGTGWLLGSVVAHSKE 265
 Db 312 LPTFLVGLSGLSSKAANDVL--GFLRVVRFRVIRILFKLTHFVGLVGHTRASTNE 369
 QY 266 -LITAWYIGFLVLIIFSFLVYLVKEDANKE-----FSTYADALMWGITITLTIGY 315
 Db 370 FLILITFLALGVLIIFATMIYYAERIGADPDOLIGSNHTYFKNIPGFMAVVTMTTIGY 429

QY 316 DKTPLTWLGRLISAGPALLGISFPFALPAGILGSGFALKVQEOHROKHEKRN 368
 Db 430 DMTPTKWSGMLVGLCALAGVLTAMPVPIYVNNFGMYSLAMAKOKLPKRKN 482

RESULT 15

T26983

hypothetical protein Y48A6B.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001

C:Accession: T26983

R:Gardner, A.

Submitted to the EMBL Data Library, June 1998

A:Reference number: Z20295

A:Accession: T26983

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-490 <WIL>

A:Cross-references: EMBL:AL023844; PIDN:CAA19530.1; GSPDB:GN00021; CESP:Y48A6B.6

A:Experimental source: clone Y48A6B

A:Gene: CESP:Y48A6B.6

A:Map position: 3

A:Insertions: 34/2; 94/1; 138/1; 175/3; 256/1; 282/1; 365/3; 410/2; 419/1; 429/1; 452/3

C:Superfamily: potassium channel protein drkl

Query Match

5.1%; Score 242.5; DB 2; Length 490;
 Best Local Similarity 27.1%; Pred. No. 2.4e-08;

Matches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

QY 104 RNKYRRVONYLVNVLERP---RGMAFIYAFVFLV-FGLIISVSTIPEHKLKSS 158
 Db 192 KTLRFEIRRCVWNITIEPPASSGKAQFAVCSVFLVISIGLVLSLPELQVATKORNN 251
 QY 159 -----CLILFEMVIVGLEFIIRIMSAGCCRRYRGWOGRL---FARKP 201
 Db 252 LTGEFTEMEPMPTLGIYEVCIWFMVEGKLKLV--ADRSKTFROLNITIDLLALIP 309
 QY 202 FCVIDITIVLIASIAVYSAKTGGINIFATSLNSLRFLOILRMVMDRGGTGWLLGSVYA 261
 Db 310 F-TIEMLLIFGISTEQLRLKGAFL--VRIILVLRVIRLKLGRYSSGLQMFCKTLKA 366
 QY 262 HSKELITAWYIGFLVLIIFSFLVYLVKED--ANKPESTYADALMWGITITLTIGYDGT 319
 Db 367 SFRQLGMAMVYVTVGVIFFESTLVYFLEKDEPASK-FHSIPAAKWCIVTMTTIGYGLTP 425
 QY 320 LTMWGLRLSAGFALLGISFPFALPAGILGSGFALKVQEOHR 359
 Db 426 VTVPGKLVATGAICVGLVLAFLPTITVDNF-MKVAETER 464

RESULT 16

A39402

potassium channel protein IIIA form 1, shaker-type - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Feb-2001

C:Accession: A39402

R:McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.

Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991

A:Reference number: A39402; MUID:91219512; PMID:2023956

A:Accession: A39402

A:Contents: cDNA

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-613 <MCC>

A:Cross-references: GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914

C:Superfamily: potassium channel protein drkl

Query Match

5.1%; Score 242; DB 2; Length 613;
 Best Local Similarity 24.1%; Pred. No. 3.6e-08;

Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY	70	GGGGGRLRSRRKQKQARMSL-----LCKPLSYSTSSQCRANVKRYVONLVNERP--	122
Db	176	GGDDPDEDLQK---RLGIEDAAGLGGPDG-----KSGRRKKLPQRMALREDPPS	224
QY	123	-RGMAFIHAFPELLVFG---CL-----ILVESTIPEHTKLASCLLI	162
Db	225	SRAAFINAFSLFELIVSTITPFCLETHPEAHINVKNKTEPVINGISAVLQYELIETDPLRY	284
QY	163	LEFVNIIVVFGLEFIIRIMSGCCCRKRGWQRLRFARKPCVDTIVLI-----ASIAVY	217
Db	285	VEGCVVWTFPEFLVIRIVES-----PNKLEFIKLNLIIDVAILPFLYELVGLSL	335
QY	218	SAKTQGNIFATSLKSLRFLQIILRMVMDRRGGTWMKLGSVYVAHSKE-LITAWYIGFLV	276
Db	336	SSKAAKDVL--GFLRVYRFEVRIILRIEKLTRHFVGLRVYGLHRLASTNEILLIIIFALGV	393
QY	277	LIFSSEIYLVLEK-----DANKEFSYADALMMGTLITLTIGYGDKNPLTWGLRL	326
Db	394	LIEAF-MIYARVRVGAOPNDPSASEHTQFNKPIGFWMAVYMTLTIGYGDMPQIWSGML	452
QY	327	LSAGFALLGISFPAIPLAGIL-----GSGFALKVQEO-----HROKH	362
Db	453	VGALCALAGVLTITAMPVPIYVNNFGMTYSLAMAQOKLPRKKRKH	496

RESULT 17

voltage-gated potassium channel protein Raw1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-2001
 C:Accession: S22703; A45292; S19099
 C:Retlig, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Rues
 EMBO J. 11, 2473-2486, 1992
 A:Title: Characterization of a shaw-related potassium channel family in rat brain.
 A:Reference number: S22702; MUID:92331599; PMID:1378392
 A:Accession: S22703
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-624 <RET>
 A:Cross-references: EMBL:X62839; NID:g57650; PIND:CAA44643.1; PID:g57651
 R:Rudy, B.; Kentros, C.; Weisler, M.; Fritulung, D.; Serodio, P.; Vega-Saenz de Miera, E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
 A:Title: Region-specific expression of a K⁺ channel gene in brain.
 A:Reference number: A45292; MUID:92262488; PMID:1374908
 A:Accession: A45292
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 594-624 <RND>
 A:Note: sequence extracted from NCBI backbone (NCBIN:1023300, NCBI:P.102305)
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
 F:230-246/Domain: transmembrane #status predicted <TM1>
 F:282-303/Domain: transmembrane #status predicted <TM2>
 F:315-335/Domain: transmembrane #status predicted <TM3>
 F:347-365/Domain: transmembrane #status predicted <TM4>
 F:382-401/Domain: transmembrane #status predicted <TM5>
 F:452-473/Domain: transmembrane #status predicted <TM6>

Query Match	5.1%	Score 242;	DB 2;	Length 624;
Best Local Similarity	24.1%	Pred. No. 3.7e+08;		
Matches 83;	Conservative 70;	Mismatches 117;	Indels 74;	Gaps 14;

[illegible]

```

Qy 218 SAKTQCNIFATSAIBRLRFQJLLRMVMDRGRGHWKLLGSVYVANSKE-LITAWYTGFLV 276
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 336 SSKAKDYL - GFLRVRRFVRLIKELTRFEVGLRVGLHTRASTNEILLIIFALGV 393
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 277 LIFESFLVYLVEK ----- DANKEFSYADALMWGTTLLTITGYDGTPLTWGLR 326
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 394 LIFAT-MITYAEVGAQPNPDSASEHTQFKIPIPGFWMAVYMTLLGYDMMIPIQWSGML 452
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 327 LSAGFALLGISFEFALPAGII-----GSGFALKVQED-----HROKH 362
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 453 VQALCALAGVLTITAMPEVPVIVNNFGMYSLAMAQKLEPRKKKH 496

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RESULT 18

potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: E90564
R:Chamblad, I.; Helling, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma F
A:Reference number: A99512; M01D:21267165; PMID:11353084
A:Accession: E90564
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <GUR>
A:Cross-references: GB:AL445566; PID:G14089835; PIDN:CAC13594.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MTPU_4210
A:Genetic code: SGC3

Query Match	5.1%;	Score 241.5;	DB 2;	Length 344
Best Local Similarity	26.3%;	Pred. No. 1.6e-08;		
Matches	81;	Conservative	69;	Mismatches 109;
				Indels 40

Best Local Similarity 26.3%; Pred. NO. 1.6e-08;
Matches 81; Conservative 69; Mismatches 109; Indels 49; Gaps 12.

QY 105 NAKYRRVQNTLVNL-----ERRGMAF--IYHAFVFLIVFGCILLVSTVPTHTK 154

Db 9 NQKYNIATKHNNVAINEKSEKDDQEVNLVDYLRKIWFIVLVLSFIILSPFLLLIDKFF 68

QY 155 LAS--SCLLTLEFVMVPEGLLEIRLWSAGCCCRVRGMOGRLEFARKPECVLDTIVLIA 212

Db 69 IASNSKEFLVELLTITFEVLADDEF--LTMTETVPYRKGK--KLISMTITPE--PTFGILIVS 123

```

QY      213 SIAY-----VSATOGNIF-----ATSALRSRLFLQILLRMVMDRREGT 2511
      |      : : : : :
Db      124 SFVPSITWLEAFIENKDINVSQNNKVKPTEISQVLSFLRSLFLRGRVTLMLQVEEP 1833

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QY      252  WKLGSVVVAHSEKELITAM-YIGFLVLAIFSSFLVLYE--KDNKESTSYADALMMGTI 307
      : | : : : : | : | : : : : | : : : : | : : : : |
Db      184  FKLVAEFNKKRIILSEVFIILILIF-SLIYSYETIGENANPNIKNYWAIYETTTI 242

```

QY 308 TLTTCGYDKPDLTWLGRLLNAGFALLGISFPALPACILGSGFALKVOEQ-----HKOK 361

QY	362	HEEKRNP	369
	:	! ! :	! !
Dh	303	NEEKRNP	310

RESULT 19

C;Species:

potassium channel protein Raw3 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 16-Sep-1992 #sequence.Revision 16-Sep-1992 #text.change 16-Feb-2001
C.Accession: S13919; S22702
R.Schroeder, K.H.; Ruppersberg, J.P.; Wunder, F.; Rettig, J.; Stocker, M.; Pongs, O.
FEBS Lett. 278, 211-216, 1991
A.Title: Cloning and functional expression of a TEA-sensitive A-type potassium channel
A.Reference number: S13919; MUID:91122287; PMID:1840526

A:Accession: S13919
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-625 <SCH>
 A:Cross-references: EMBL:X62841; NID:g57648; PIDN:CAA44645.1; PID:g57649
 R:Retlig, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Beckh, S.; Kues, E.M.B.O. J. 11, 2473-2486, 1992
 A:Title: Characterization of a shaw-related potassium channel family in rat brain.
 A:Reference number: S22702; MUID:92331599; PMID:1378392
 A:Accession: S22702
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-625 <RET>
 A:Cross-references: EMBL:X62841; NID:g57648; PIDN:CAA44645.1; PID:g57649
 C:Superfamily: potassium channel protein drk1
 C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
 F:228-246/Domain: transmembrane #status predicted <TM1>
 F:282-303/Domain: transmembrane #status predicted <TM2>
 F:315-335/Domain: transmembrane #status predicted <TM3>
 F:347-365/Domain: transmembrane #status predicted <TM4>
 F:382-401/Domain: transmembrane #status predicted <TM5>
 F:452-473/Domain: transmembrane #status predicted <TM6>
 F:257-266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 241.5; DB 2; Length 625;
 Best Local Similarity 21.9%; Pred. No. 4.1e-08;
 Matches 113; Conservative 75; Mismatches 194; Indels 133; Gaps 19;

OY 3 RHNAAGE-----GGAAGLWVSGAAAGAGGRLSGMKDVGSGRGLNSA 51
 DB 150 RQHDADAEALDIFSPDGGGAGGDEGDEDERELALRLGH-----EGSGP----- 199
 OY 52 AARDDGLLLCTRAATLGGGGGLRESRKGQARMSLLGKPLSYSSOSCRNRYRY 111
 DB 200 -----GAGSGG-----RGMPRMALFEDPYSSRA----- 226
 OY 112 ONLYLVNERPGMAFIYHAFVFLVFGCL-----ILSVSTIPEHKLAS----- 157
 DB 227 -----RYVAFSLFFILVSTTF-CLTEHAFNIDRNVEIHRVGNITSVRRREV 276
 OY 158 ---SCLILEFVMIVFGLFETIRIWSAGCCRYGMOGLRFPARKPCVITIVL--- 211
 DB 277 ETEPLIYIEGVCMWFFLEFLVR-----VCC-----PQLDFVKLNLNIDVAILPFY 327
 OY 212 --ASIANVSAKTQGNIFATSLRSIRFQIILMVRMDRGRGFWKLGVYVAHSE-LIT 268
 DB 328 LEVGLSGLSSKAARDVL--GFLRVRFVRLIRFKLTHFVGLRVGLHRLASTNEFL 385
 OY 269 AWYIGFVLIFSSFLVYLVK-----DANKEFSYADALMWGTTITLTIGGDKT 318
 DB 386 ITFLALGVLLFAT-MIYYAERIGARPSPPRGMDHTDFKNPIGFVMAVVTMTLGYDMY 444
 OY 319 PLTWGLRLSAGFALGISFPALPAGILSGFALVQ--EQRQKHREKRNPANLIQCV 377
 DB 445 PKTWSGLVGCALCALGLTAMPVPIVNNFGMYISLMAQKLPKRRKKHVRPPOLE 504
 OY 378 WRSYADDEKSVSTATWPKHKAHLTCSPFNOKLSKERVRMAAPRGQSTIKRSQASVDDR 437
 DB 505 SPLYCKSEER-----SPRSTYSYDTSPPAREEGVEYKRRADSKON-----GDAN 548
 OY 438 SPSTDTAEG-----SPTRVOKSWSPNDTRFR 465
 DB 549 AVLSDEBGAGLTOPLASAPTPPEERRALRRSGTRDR 583

RESULT 20
 A12384
 hypothetical protein all4633 (imported) - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: A12384
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: A12384
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <RUR>
 A:Cross-references: GB:BA000019; PIDN:BA076332.1; PID:g17133770; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all4633

Query Match 5.1%; Score 241; DB 2; Length 263;
 Best Local Similarity 27.1%; Pred. No. 1.2e-08;
 Matches 65; Conservative 55; Mismatches 94; Indels 26; Gaps 6;

OY 109 RRYQNYLVNERPGMAFIYHAFVFLVFGCLLSVFSSTIPEHKLASCLLLEFYMI 168
 DB 5 RQTEFYLVNDELTPGLKALNLTAVLVLSGIFVAQTALPDSIRLQ--LDQIDYIL 61
 OY 169 VYFGLFETIRIWSAGCCCRKRGQRLRFPARKPCVDTIVLISIAVSAKTQGNIFAT 228
 DB 62 VIFAEYVLRWLSA-----ENKLYTSEFYAIIIDLALIFEL-----GLVNI 104
 OY 229 SALRSLEFQILMVR-MDRRGFTWKLGSVYVAHSEKELTAWYIGFVLIFSSFLVYLV 287
 DB 105 SFIRILMRIRLILNIFIDK-----FLFGSISSEDDGIIFRILFTLFTIIVYSSLIQV 160
 OY 288 EKDANKE-ESTYADALMWGTTITLTIGYGKTPPLTWGLRLSAGFALGISFPALPACIL 346
 DB 161 EHVNAQVYSTFLDAEYFVSVMTWGFGDVTPESELGRILTLVMIITGVALIPQVGD 220

RESULT 21

S11049
 potassium channel protein - rat
 N:Alternate names: potassium channel RK3; shaker-related potassium channel RCK4
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
 C:Accession: S11049; E39113; S06710

R:Tseng-Crark, J.C.L.; Tseng, G.N.; Schwartz, A.; Tanouye, M.A.
 FEBS Lett. 268, 63-68, 1990
 A:Title: Molecular cloning and functional expression of a potassium channel cDNA iso1
 A:Reference number: S11049; MUID:90346174; PMID:2384173
 A:Accession: S11049
 A:Molecule type: mRNA

A:Residues: 1-654 <TSE>
 A:Cross-references: GB:M32867; NID:g205042; PIDN:AAA41469.1; PID:g205043
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan
 A:Reference number: A39113; MUID:91156654; PMID:1705709
 A:Accession: E39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA
 A:Residues: 1-41, 'R', '43-308', 'G', '310-654' <ROB>
 R:Stuehmer, M.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,

EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
 A:Reference number: S06708; MUID:90059914; PMID:2555158
 A:Accession: S06710
 A:Molecule type: mRNA

A:Residues: 1-41, 'A', '43-83', 'EEAT', '89-94', 'K', '95-308', 'G', '310-654' <STU>
 A:Cross-references: EMBL:X16002; NID:g57036; PIDN:CAA34133.1; PID:g57037
 C:Superfamily: potassium channel protein drk1

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:309-327/Domain: transmembrane #status predicted <TM1>
 F:372-393/Domain: transmembrane #status predicted <TM2>
 F:405-424/Domain: transmembrane #status predicted <TM3>
 F:425-462/Domain: transmembrane #status predicted <TM4>
 F:479-498/Domain: transmembrane #status predicted <TM5>
 F:514-523/Domain: transmembrane beta strand #status predicted <TM6>

F:524-532/Domain: transmembrane beta strand #status predicted <TM2>
 F:540-562/Domain: transmembrane #status predicted <TM6>
 F:553/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:600/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

Query Match 5.0%; Score 238; DB 2; Length 654;
 Best Local Similarity 21.5%; Pred. No. 7,46-08;
 Matches 74; Conservative 62; Mismatches 116; Indels 92; Gaps 10;

QY 135 LVFGCLILSVSTFPE-----HTKLASSC-----LTL 163
 Db 316 LVILISIVICFLELPFEDRDRLIMALSAGHSRLINDTSAPHLNENGHITFNDPFIV 375
 QY 164 EFMIIVFVGLFETIRIMSAGCCCRVGMQGLRFRARPCVITVLV---ASIAVVSXK 220
 Db 376 EYICVIFWSEFEVYRCFAC-----PSOALFFKINMNIIDIVSILPYFTLTDLAQ 426
 QY 221 TQC-----NIFATSLRSLRFLQILRMVMDRRGKTWKLGSVYVAHKKELITAWYIG 273
 Db 427 QQGGNGNQQQQAMSFALIRIRLVRFIRFKLSRNSKQLQILGHITLRASMRGLLIFEL 486
 QY 274 FLVLISSFLVLYVEKD-ANKKESTYADALMMGTTTLTIGYDKTPTLTWGLRLSAGRA 332
 Db 487 FIGVILFSSAVYFAEADPTTHFQSIDPAFWAVVTYVGYDMKPTIVGKIVGSLCA 546
 QY 333 LIGSFFALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCVMSYVADEKSVSIAT 392
 Db 547 IAGLITLALPVPVIVSNF---FYHRTENDEBQTLQTMNAVSC----- 587
 QY 393 WKPHLKALHTCPTNOKLSPKERVMA SPRGOSIKSROASVGR 436
 Db 588 --PVL-----PSNLKKFR-----SSTSSSLGDX 609

RESULT 22

A38101

potassium channel KCNA3 - human

N:Alternate names: potassium channel HLK3; potassium channel PCN3; shaker-related potass
 C:Species: Homo sapiens (man)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 01-Dec-2000

A:Accession: A38101; B38556; I52990
 R:Altali, B.; Romey, G.; Honore, E.; Schmid-Aliana, A.; Mattei, M.G.; Lesage, F.; Ricar

J. Biol. Chem. 267, 8650-8657, 1992
 A:Title: Cloning, functional expression, and regulation of two K(+) channels in human T

A:Reference number: A38101; MUID:92235098; PMID:1373731
 A:Accession: A38101

A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-523 <ATT>
 A:Cross-references: GB:M85217; NID:q186664; PIDN:AA59457.1; PID:q186665

R:Phillipson, L.H.; Hice, R.E.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Nelson, D.J.; St
 Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991

A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and
 A:Reference number: A38556; MUID:91095456; PMID:1986582

A:Accession: B38556
 A:Molecule type: DNA

A:Residues: 1-19, 'G', '21-36, 'V', '38-60, 'L', '62-90, 'V', '92-337, 'S', '339-418, 'S', '420-457, 'LS', '4
 R:Gal, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.

DNA Cell Biol. 11, 163-172, 1992
 A:Title: Characterization and functional expression of genomic DNA encoding the human 1y

A:Reference number: I52990; MUID:92189730; PMID:1547020
 A:Accession: I52990

A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA

A:Residues: 1-60, 'L', '62-523 <RES>
 A:Cross-references: GB:M38217; NID:q186670; PIDN:AA88073.1; PID:q186671

C:Genetics:
 A:Gene: GDB:KCNA3; HGK5

A:Cross-references: GDB:128079; OMIM:176263
 A:Map position: 1p21-1p13.3

C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; vola

Query Match 5.0%; Score 237; DB 2; Length 523;

Best Local Similarity 22.2%; Pred. No. 6,2e-08;
 Matches 68; Conservative 64; Mismatches 114; Indels 60; Gaps 8;

QY 104 RNKRYRVOYLYNVLERP-----KGMATYNAFVFLVGLLISVESTIPEH----- 152
 Db 157 RPLPRDFQFQVWLFEPYESSGPARIAIV---SVLVILISIVICFLELPFEDRD 212
 QY 153 -----TKLASSCLILFEMVIVFGLFETIRIMSAGCCCR 189
 Db 213 YPASTQDSPEAAGNSTSGSRAGASSPSDFVEVETICITWSEFLVRFAC----- 265
 QY 190 GMGRLRFARKPCVIDITVLI---ASIAVSAKTQGN---IFATSLRSLRFLQILRMV 243
 Db 266 --PSKATFSKINMLNDIVALLIPFTLIGTELARQNGNQQAMSLALRVIRLVRFIE 323
 QY 244 RMDRGGTWKLGSVVAHSEKEL-ITAWYIGFLVLISSFLVLYVEKDANKFSTYDAL 302
 Db 324 KLSRHSKGLQILQTLKASMRLELGLIFLFIQVILFSSAVYFAEADPTSGFSPDAF 383
 QY 303 WMGTITLTITGYGDKPTLWGLRLSAGFALGISFALPAGILGSGF-----ALKVOE 356
 Db 384 WMAVVTITVGYGDMHPVTIGKTVGSLCATAGVLTALPVPVIVSNFNYHRTBGE 443
 QY 357 QHROKH 362
 Db 444 QSQYMH 449

RESULT 23

A43531

potassium channel KV1.3 - rat

N:Alternate names: potassium channel KV3; potassium channel RCK3; potassium channel R
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 17-Nov-2000
 C:Accession: A43531; JH0168; S06708

R:Douglass, J.; Osborne, P.B.; Cai, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P
 J. Immunol. 144, 4841-4850, 1990

A:Title: Characterization and functional expression of a rat genomic DNA clone encodi
 A:Reference number: A43531; MUID:90278098; PMID:2351830

A:Accession: A43531
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-525 <DOU>

A:Cross-references: GB:M30312
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Polander, K.;

Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec

A:Reference number: JH0166; MUID:90297965; PMID:2361015
 A:Accession: JH0168

A:Molecule type: DNA
 A:Residues: 1-180, 'G', '182-525 <SMA>

A:Cross-references: GB:M31744; NID:9205104; PIDN:AAA41500.1; PID:9205105
 A:Experimental source: brain

A>Note: only a list of differences from sequence S06708 is given
 R:Stuehrmer, W.; Ruppertsberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,

EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels

A:Reference number: S06708; MUID:90059914; PMID:2555158
 A:Accession: S06708

A:Molecule type: mRNA
 A:Residues: 1-105, 'L', '107-180, 'G', '182-525 <STU>

A:Cross-references: EMBL:X16001; NID:957034; PIDN:CAA34132.1; PID:957035
 C:Superfamily: potassium channel protein drkl

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:185-203/Domain: transmembrane #status predicted <TM1>

F:245-266/Domain: transmembrane #status predicted <TM2>
 F:278-298/Domain: transmembrane #status predicted <TM3>

F:313-331/Domain: transmembrane #status predicted <TM4>
 F:348-367/Domain: transmembrane #status predicted <TM5>

F:383-392/Domain: transmembrane beta strand #status predicted <TM1>
 F:393-401/Domain: transmembrane beta strand #status predicted <TM2>

F:409-431/Domain: transmembrane #status predicted <TM6>
F:470/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match	5.0%;	Score 237;	DB 2;	Length 525;
Best Local Similarity	23.3%;	Pred. No. 6.2e-08;		
Matches 67;	Conservative 63;	Mismatches 104;	Indels 54;	Gaps 8

A:Accession: S01111
A:Molecule type: mRNA
A:Residues: 1-643 <SCH>
A>Note: The clone is designated as SHD1
R:Schwartz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 332, 740, 1988
A:Reference number: S01113
A:Contents: annotation; erratum
C:Genetics:
A:Gene: Shaker
A:Cross-references: FlyBase:FBgn0003380
C:Superfamily: potassium channel protein drk1
C:Keywords: alternative splicing; transmembrane protein

Query Match 4.9%; Score 234; DB 2; Length 643;
Best Local Similarity 22.4%; Pred. No. 1.3e-07;
Matches 87; Conservative 61; Mismatches 150; Indels 90; Gaps 11;

Dy 128 IYHAFVFL--VEGCL-----ILSFSTIPRETKL-----ASSCLLIIEFMIVF 171
| | | | | | | | | | | | | | : : : : :
Db 219 IISVVILLIIVIFCLETPREFKHYKVETNTNGKTIEDEVPIITDPFFLETICIME 278
| | | | | | | | | | | | | | : : : : :
172 GLEFIIRIMSAACCCRYRGQGRLEFRARKPCVVDITVL---ASIAVVA----- 219
| | | | | | | | | | | | | | : : : : :
279 TPVELV-----REFLAPCNKLNFCRDYMNVIDIATIIIFYTTLAVVAEEDPTLNLP 329
| | | | | | | | | | | | | | : : : : :
220 -----KTGNIFATSALRSILRFQLILRMVRMDRRGGTWKLGSVVYANSKEI-TAW 270
| | | | | | | | | | | | | | : : : : :
Db 330 KAPVSPODKSNQAMSLAIRIVRLVRFPLFKLSHSKGLOIGRTLKASMRLEGLLF 389
| | | | | | | | | | | | | | : : : : :
Oy 271 YIGFLVLTIRSSPLVLYLVENDANKEFSTYADALMGTITLTITGVGDKPPLTMGLSLSG 330
| | | | | | | | | | | | | | : : : : :
Db 330 FLFIGVLFESSAYFEAEAGSENSFPKSIPDAFMAAVVTMTTVGGDMRPVGWGKIVGS 449
| | | | | | | | | | | | | | : : : : :
Oy 331 FALLGISFEPALPGAGISGFALIKVOEQHRQKHFEKRNPANLLIOCVRSYADEKSVSI 390
| | | | | | | | | | | | | | : : : : :
Db 450 CAIAGVLTALTALPVPVYSNN----YFYHREDIQEMOSQNHH----- 490
| | | | | | | | | | | | | | : : : : :
Oy 391 ATWPKHLKALHTCSPTNQKLSPFERVRMASPRGOSIKSRQASVGDGRSDPTDIATEGSPT 450
| | | | | | | | | | | | | | : : : : :
Db 491 -TSCPVL-----PGTLGHMKKSSLSSESSDDMDLDDGVESTGP 528
| | | | | | | | | | | | | | : : : : :
Oy 451 KYOKSMSPNDRTFRPSLRKSSQPKPV 478
| | | | | | | | | | | | | | : : : : :
Db 529 LTF--THPGRSVAPPLGAQQQQQOPV 553
| | | | | | | | | | | | | | : : : : :

RESULT 27
A39922
potassium channel KCNA4 - human
N:Alternate names: potassium channel HK1; potassium channel PCN2; shaker-related potassiu
C:Species: Homo sapiens (man)
C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Nov-2000
C:Accession: A39922; S12630; I77465
R:Tankum, M.M.; Knöch, K.M.; Walbridge, J.A.; Kroemer, H.; Roden, D.M.; Glover, D.M.
FASEB J. 5, 331-337, 1991
A>Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs
A:Reference number: A39922; MUID:91160866; PMID:2001794
A:Accession: A39922
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-653 <TAM>
A:Cross-references: GB:M60450; NID:g308762; PIDN:AAA61275.1; PID:g308763
R:Phillips, L.H.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Steiner, D.F.
Nucleic Acids Res. 18, 7160, 1990
A>Title: Sequence of a human fetal skeletal muscle potassium channel cDNA related to RCN
A:Reference number: S12630; MUID:91088321; PMID:2263489
A:Accession: S12630
A:Molecule type: mRNA
A:Residues: 1-37,'R','39-41','R','43-83','EEEAAT','89-303','D','305-541','V','543-630','A','632-653'
A:Cross-references: EMBL:M55514; NID:g189659; PIDN:AAA60034.1; PID:g189660
R:Ramshawami, M.; Gautam, M.; Kamh, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990

A>Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: 157680
A:Accession: J77465
A>Status: A:preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-653 <RES>
C:Genetics:
A:Gene: GDB:KCNM4
A:Cross-references: GDB:126730; OMIM:176266
A:Map position: 11p14-11p14
C:Superfamily: potassium channel protein drk1
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; v

Query Match 4.9%; Score 234; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 1.4e-07;
Matches 70; Conservative 55; Mismatches 109; Indels 62; Gaps 9;

DQ 152 HKKLASSCLLLEFWMIVGFEITRIRWAGCCCRFRGMGRIFARFKPCVIDITYLI 211
|| : : || : | | | : | : | : | : | : | : | : | : | : | :
DQ 364 HT-FINDPEFTVETVICWFSEFFVRCEFC-----PSQLFFKNINIIDIVSL 413
| : : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 212 ---ASIAVVASAKTQG-----NIPATSAKLSLFELILRMVNRMDRGTKLLGSVYA 261
: : : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 414 PFYITLTGLDLAQGGSGNGQQAMSPAILRIILVRFELKSRHSKGLOIIGHTLRA 473
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 262 HSKELITAVYIGFLVIFSSFLYLVEKD-ANKFSTYADALMWGTITLTGYGDKPPL 320
: | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 474 SMRELLDILFFELFGIVLFSSAVYFADEPTTHQSIPDAFMVAVMVTMYGVYDMKPI 533
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 321 TWLGRLISGFALGISFPFLPGITIGSGFALKVOEHRKHFEKRPPAANLIOCVMRS 380
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 534 TVGGKTVGSLCALAGVLTLPVPVIYSNN---YFHRELNEEQOTOLTQNAVSC---- 586
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 381 YADEXSVSIATWKPHLKALHTCSPTNQKLSFKERVRMASPRGOSIKRQASVDGR 436
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DQ 587 -----PVL-----PSNLKKFR-----SSTSSLGDK 608
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 28
JH0193
potassium channel shaker form epsilon - fruit fly (Drosophila melanogaster)
N.Alternate names: potassium channel protein A
C.Species: Drosophila melanogaster
C.Date: 31-Dec-1991 #sequence-revision 31-Dec-1991 #text-change 01-Dec-2000
C.Accession: JH0193; S00508; S01110; S00479; S00482; S02822; S01674
R.Kamb, A.; Tseung-Crank, J.; Tanouye, M.A.
Neuron 1, 421-430, 1988
A>Title: Multiple products of the Drosophila Shaker gene may contribute to potassium
A:Reference number: JH0193; MUID:90166523; PMID:3272175
A:Accession: JH0193
A:Molecule type: mRNA
A:Residues: 1-656 <RAM>
A>Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in the putative G
R.Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1988
A>Title: Multiple potassium-channel components are produced by alternative splicing a
A:Reference number: S00508; MUID:88122563; PMID:2448635
A:Accession: S00508
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-512,514-564,'Q','565-583,'HV',586-656 <SCH>
A:Cross-references: GB:X06742; NID:g288441; PIDN:CAA29917.1; PID:g288442
A:Accession: S01110
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'MOMT',57,'VAG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',5
, 'OL',577-579,'LO',582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LKS', 'T
R.Pongs, O.; Kecskemeti, N.; Mueller, R.; Krahn-Jenigens, I.; Baumann, A.; Kiltz, H.H
EMBO J. 7, 1087-1096, 1988
A>Title: Shaker encodes a family of putative potassium channel proteins in the nervous
A:Reference number: S00479; MUID:88296413; PMID:2456921
A:Accession: S00479

Db 75 TWFTADYLLRLGA-----RRPLRYALSPFGLVDLLTLPSTLLPFGTOYLL- 124

QY 227 AHSALSLRFLQLRWVRMDRGCTWKLGSVVAHSEKELITANYIGL--VLIFSSPLV 284

Db 125 ---VVRALRLRVRFKIARYSDOALISEALO-A-SREKLIFFISVLSMAYFGT--LL 179

QY 285 YLVEKANKNEFSYADLMMGTITLTITIGGDKPLTWLGLSLAGFALLGISFPALPAG 344

Db 180 YME-GESEFTIPISTIYAVVITVIGIDISPKIGLGFATLMLSGAIIAYPTG 238

QY 345 ILGSGFALKVQEQHR 359

Db 239 IYTVVGLQ-QAQEAR 252

RESULT 31

B39113

Potassium channel KV1.1 - rat

N:Alternate names: potassium channel A; potassium channel RK1

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Aug-1991 #sequence,revision 30-Aug-1991 #text_change 17-Nov-2000

C:Accession: B39113; A41353; S01161

R:Roberts, S.L.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel

A:Reference number: A39113; MUID:91156694; PMID:1705709

A:Accession: B39113

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-495 <ROB>

R:Christie, M.J.; Adelman, J.P.; Douglass, J.; North, R.A.

Science 244, 221-224, 1989

A:Title: Expression of a cloned rat brain potassium channel in Xenopus oocytes.

A:Reference number: A41353; MUID:89203264; PMID:2539643

A:Accession: A41353

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-495 <CHR>

A:Cross-references: GB:M26161; NID:g206490; PIDN:AAA1982.1; PID:g206491

R:Baumann, A.; Grube, A.; Ackermann, A.; Pongs, O.

EMBO J. 7, 2457-2463, 1988

A:Title: Structure of the voltage-dependent potassium channel is highly conserved from D

A:Reference number: S01161; MUID:89052659; PMID:3191911

A:Accession: S01161

A:Molecule type: mRNA

A:Residues: 1-495 <BAU>

A:Cross-references: EMBL:X12589; NID:g55957; PIDN:CAA31102.1; PID:g55958

C:Superfamily: potassium channel protein drkl

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane bet

F:361-379/Domain: transmembrane beta strand #status predicted <TMB1>

F:371-379/Domain: transmembrane beta strand #status predicted

F:207/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 4.9%; Score 230; DB 2; Length 495;

Best Local Similarity 19.6%; Pred. No. 1.7e-07;

Matches 75; Conservative 80; Mismatches 142; Indels 86; Gaps 10;

QY 104 RNKRYRYQNTLYNLEPR--GMAFIYHAFVLLVFGCLISVSTIRE----- 151

Db 142 RPLPEKEQROVWMLFEYPSGSPARVIAIVSMVLISIVIFCLETTELKDKDPGTG 201

QY 152 -----HTKLAASCLLIEFVMIVVFGLEFIIRIMSAGCCCRYGWQGRLEFPARK 200

Db 202 IHRIDNTVITYTSNFTDPFFLETCIIMFSFELVRFAC-----PSKIDPEKN 252

QY 201 PFCVIDITVL---ASIAVSAKTOGN-----IFATSALRSRLFLQILRMVRMDRGGTW 252

Db 253 IMNFIDYAIIPYFTLIGETAEGNKGQATSLAIRVIRLVAVFRILKSRHSGKL 312

QY 253 KLUGSVVAHSEKEL--ITMAYIGFLVLISSFLYLVKEKANKFSTYADALMMGTITLT 311

Db 313 QILGOTLKASMKELGILTFIFIGVILFSSAVYFAAEAEASHSSIPDAFMAVAVSM 372

QY 312 IGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFALKVQEQHRQHFEKRRNPAA 371

Db 373 VCGMDYPTIGKIKVSLCAINGVLTALPVPYVSNEN---YFHRRETEGEQ----- 424

QY 372 NLIQCVSRSTYADEKSVSTATWPKHKAHTCSP-----TNOKLSFKRRVMMAS 420

Db 425 -----ROLHVSSPNLASDLSRRSSSTISSEYMETEE 459

QY 421 PRGQSIKS--RQASVGRSRSPSTD 442

Db 460 DMNNSTAHYRQANIRGTGCTATD 482

RESULT 32

A46020

Potassium channel KCNC1 - human

N:Alternate names: potassium channel NGK2-KV4; Shaw-related potassium channel KV3.1

C:Species: Homo sapiens (hmn)

C:Date: 21-Sep-1993 #sequence,revision 19-May-1994 #text_change 08-Dec-2000

C:Accession: A46020; A45072

R:Ried, T.; Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.

Genomics 15, 405-411, 1993

A:Title: Localization of a highly conserved human potassium channel gene (NGK2-KV4; K

A:Reference number: A46020; MUID:93194190; PMID:8449507

A:Accession: A46020

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-511 <RLE>

A:Cross-references: GB:S56770; NID:g298602; PIDN:AB25764.1; PID:g298603

A:Note: sequence extracted from NCBI backbone (NCBIN:127271, NCBIPI:127272)

R:Grissmer, S.; Chanshanli, S.; DeChlefs, B.; McPherson, J.D.; Wasmuth, J.J.; Gutman, J.

J. Biol. Chem. 267, 20971-20979, 1992

A:Title: The Shaw-related potassium channel gene, KV3.1, on human chromosome 11, enco

A:Reference number: A45072; MUID:93016011; PMID:1400413

A:Accession: A45072

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 244-475 <GR1>

A:Cross-references: GB:M96747; NID:g186672; PIDN:AAA59458.1; PID:g186673

A:Experimental source: Louckes lymphoma cells

A:Note: sequence extracted from NCBI backbone (NCBIR:116151)

C:Genetics:

A:Gene: GDB:KCNC1

A:Cross-references: GDB:128082; OMIM:176258

A:Map position: 11p15.1-11p15.1

C:Superfamily: potassium channel protein drkl

C:Keywords: alternative splicing; glycoprotein; potassium channel; transmembrane prot

Query Match 4.9%; Score 230; DB 2; Length 511;

Best Local Similarity 21.8%; Pred. No. 1.7e-07;

Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

QY 3 RHRAEGEGGAGLWVSGAAAAAGGRLSGMKVDSEGRKRVLLNSAAAGDGLILLG 62

Db 110 RQHRDAEE-----ALDSFGAPLDSAD-----ADAQPG----- 140

QY 63 TRANTLGGGGGLRESRRGKGARMSLLGKPLSTYSOSCRNNKYRYRYQNTLYNLEPR 122

Db 141 -----DSGGEDELEMT---KRLALSDSDGRGGGWRRQPRIMALFEDP 163

QY 123 RGMAFI-YHAFVLLVFGCLISV-----ESTIPEHTKL----- 155

Db 184 YSSRYARVAVASLFF--LIVSTTFLETHERENPIYKKEILEVRNGTOVRYREAE 240

QY 156 ASSCLLIEFVMIVVFGLEFIIRIMSAGCCCRYRMQGRIRARPKFCVIDITVL----- 211

Db 241 TEAFLYIEGVGVWTFEFLMRV---IFC-----PNKVERIKNSLTIIDVALIPYL 291

QY 212 -ASIAVSAKTOGNIFATSRLRFLQILRMVRMDRGCTWKLGSVVAHSEKEL--LITA 269

Db 292 EVGLSGSSKRAKAVL--GFLRYRVFVRIIRFKLRHVGVRVGLHTRASTNEFLLI 349

QY 270 WYIGFLVLIFFSSFLYLVKE-----DANKFSTYADALMMGTITLTITIGDKTP 319

Db 350 IFLLALGVLLFAF-MIYAEERIGAGPNDPSASETHFKNIPIGFWMAVVTTLTGDMYP 408
 320 LTMGLRLSAGFALLGISFFALPAGILSGFALKVQ-EQHRQKHEKRRNPANLIGCW 378
 Db 409 QTMGMLVLCALAGVLTAMPVPIVYNNFGMYSLAMAKOLPKKKKHIPRPOLGS 468
 379 RSYADEKSVSIATWPKHKLHTCSPTNOKLSFKERVRMASPGOSI 426
 Db 469 PNCK-----SVNSPHSTQSDTCPLAQEELLEIRAKRKLPGMSI 511

RESULT 33

S07095

potassium channel protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Dec-2000

C:Accession: S07095

R:Tokoyama, S.; Imoto, K.; Kawamura, T.; Higashida, H.; Iwabe, N.; Miyata, T.; Numa, S.

FEBS Lett. 259, 37-42, 1989

A:Title: Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells. Primary str

A:Reference number: S07095; MUID:90092535; PMID:2599109

A:Accession: S07095

A:Molecule type: mRNA

A:Residues: 1511 <YOK>

A:Cross-references: EMBL:Y07521; NID:953997; PIDN:CAA68814.1; PID:953998

C:Superfamily: potassium channel protein drk1

C:Keywords: alternative splicing; membrane protein

Query Match 4.9%; Score 230; DB 2; Length 511;

Best Local Similarity 21.8%; Pred. No. 1.7e-07;

Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

QY 3 RHAGGEGGAGLWVSGAAAGGRLSGMKDVESGGRVLLNSAARDGLLLG 62
 Db 110 RGRDAE-----ALDSFGAPLNSAD-----ADAGPG----- 140
 QY 63 TRATLGGGGGGLRESRRGKQAGNMSLGLKPLSYSSQSCRNVYRVVNYLYLERP 122
 Db 141 -----DSCDGEDELEMT---KRLALSDSPDGRGCFWRWQPRIMALFEDP 183
 123 RGMATF-YHAFVFLVFGCLLSV-----FSTPEHKKL----- 155
 184 YSRKRYAVAFASLFF---LIVSTITTCLFHERHNPVYNNKTEINNRNGTGVRYRAE 240
 QY 156 ASSCLLLEFVMTVFGLEFLIRIMSAGCCCRKMGQRLRFARKPCVITVLT---- 211
 Db 241 TEAFLEYIEGVYVWFEEFLMRV---VFC-----PKVERIKNSLNIIDVAILPFL 291
 QY 212 -ASINAVSAKTOGNIFATLSRLFLQIILAMVRMDRGGTWKLGSVYVANSKE-LITA 269
 Db 292 EVGLSGLSKAAKQVL--GFLRVRFVRLIRIFKLRHFGVGLRVLGHTLRASTNEFLDI 349
 QY 270 WYIGFVLIFSSFLVYLVK-----DANKFSTYADALMGTTITLTIGYDKRP 319
 Db 350 IFLLALGVLLFAF-MIYAEERIGAGPNDPSASETHFKNIPIGFWMAVVTTLTGDMYP 408
 QY 320 LTMGLRLSAGFALLGISFFALPAGILSGFALKVQ-EQHRQKHEKRRNPANLIGCW 378
 Db 409 QTMGMLVLCALAGVLTAMPVPIVYNNFGMYSLAMAKOLPKKKKHIPRPOLGS 468
 QY 379 RSYADEKSVSIATWPKHKLHTCSPTNOKLSFKERVRMASPGOSI 426
 Db 469 PNCK-----SVNSPHSTQSDTCPLAQEELLEIRAKRKLPGMSI 511

RESULT 34

I57680

potassium channel KCNA1 - human

N:Alternate names: potassium channel protein HKC-1

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001

C:Accession: I57680; A60173

R:Ramshaw, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
 Mol. Cell. Neurosci. 1, 214-223, 1990

A:Title: Human potassium channel genes: molecular cloning and functional expression.

A:Reference number: I57680

A:Accession: I57680

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1495 <RAM>

A:Cross-references: GB:L02750; NID:9186662; PIDN:AAA36139.1; PID:9186663

R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Brammar, W.J.

Biochem. Soc. Trans. 18, 891, 1990

A:Title: Cloning and characterization of a cDNA encoding a human brain potassium chan

A:Reference number: A60173; MUID:91192386; PMID:2128063

A:Accession: A60173

A:Molecule type: mRNA

A:Residues: 263-264,266-314, 'R' <PRE>

C:Gene: GDB:KCNA1; RBK1; HUK1; MBK1; AEMK; KVL.1

A:Cross-references: GDB:127903; OMIM:176260

A:Map position: 12p13-12p13

C:Superfamily: potassium channel protein drk1

Query Match 4.8%; Score 229.5; DB 2; Length 495;

Best Local Similarity 19.9%; Pred. No. 1.8e-07;

Matches 73; Conservative 82; Mismatches 142; Indels 69; Gaps 9;

QY 104 RNVRKRRQNYLYNLER--GMATYNAFVFLVFGCLLSVSTIPE----- 151
 Db 142 RPLPERKQYQVWLFEYESSGPARYVAVSVVILISIVICLFLPELKDDEFTGT 201
 152 -----HTKLASCLLLEFVMTVFGLEFLIRIMSAGCCCRKMGQRLRFARK 200
 QY 202 VHRIDNTVIVYNSLFTDFFIETLCITMFSELYVRFAC-----PSKTDFKN 252
 Db 201 PCVVIDTVLT---ASINAVSAKTOGN---TATSALSLRFLQIILAMVRMDRGGTW 252
 QY 253 IMNFIDVAILIIFYFTLGEIEAEQENQGEQATSLALIVIRLVRFKLSRHSKGL 312
 Db 313 QILGOTLAKSRLELLIFLFTIGVLESAYFAEAESEHSSTIPDAFWMAVSMTP 372
 QY 312 IGYDKPTLTMGLRLSAGFALLGISFFALPAGILSGFALKVQEQHRQKHEKRRNPAA 371
 Db 373 VGYGDMVPTIGKIVGICALAGVLTAMPVPIVYNNR---YFHREGEQ-----A 425
 QY 372 NLIOCVMSYAAD-----EKVSATWPKPHKALHTCSPTNOKL 410
 Db 426 OLHVSSPMLASDSDLSSRSTSMKSEYMEITEEDMNNISIAHYROVINRTANCTTANQC 485
 QY 411 SFKERV 416
 Db 486 VNKSRL 491

RESULT 35

A39372

potassium channel protein Shal1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999

C:Accession: A39372

R:Park, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salikoff, L.

Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991

A:Title: mshal, a subfamily of A-type K(+) channel cloned from mammalian brain.

A:Reference number: A39372; MUID:91239573; PMID:2034678

A:Accession: A39372

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-651 <PAK>

A:Cross-references: GB:M64226; NID:9199812; PIDN:AAA39745.1; PID:9199813

Query Match 4.8%; Score 228; DB 2; Length 651;

Best Local Similarity 21.1%; Pred. No. 3.4e-07;

Matches 102; Conservative 76; Mismatches 172; Indels 134; Gaps 20;

QY 115 LVNVLRRPR-----GMATIAFAVFLVFGCLISVFSTI-----PEHKLASSC----- 159
 Db 172 LMRAPENPHSTALVAYVYVGFPIAV--SVIANVETITPCGRPRMPSKQSCDREPT 229
 QY 160 -LLILEFVMIIVFGLFEIIRIWSAGCCCRYGMOGRPFCKVIDITVLIASIVAS 218
 Db 230 AFECMDACVLITFGEILLRLEFA-----PSRCFLRSVMSLIDVAILP--YYIG 278
 QY 219 AKTQGNIFATSAISSLRFLQILRMVRMDRGTKLLGSVYVASHKELITAMYGFL--- 275
 Db 279 LEPKNDVDSGAEFTVLRVFRFRIFKFSRHSGRLIIGYTLKSCASEL-----GFLIFS 332
 QY 276 ----VLIFSSFLVLYVEKDANKESYADALMMGTITLTIGYDGTPLTWGRLLSAGF 331
 Db 333 LTMALIFATVMEFAEGSTSTNFTSLPAAFWYITVMTLGYGDMVSTIAGKILFGSIC 392
 QY 332 ALIGISFPALPAGILGSGFALKVOEHRQKHFEKRR-----TCSPTNQLSKF 413
 Db 393 SLGSLVIALPVPYIVSNFS---RIYHONQADRRKRAQKYLARILAKSGTTNAFLQY 449
 QY 368 -----NPAANLIQCVMSYADEKSVSIATWPKPLKALH-----TCSPTNQLSKF 413
 Db 450 KONGLEDSSGSDGOMLCV--RSRAFEQO-----HHHLHCLEKTCHEFTDELAFPS 500
 QY 414 ERRMASPRQSTIKRSQASVDRRSPDTIDAE--SPFKYOKSMFNDRTRRPSLRKS 472
 Db 501 EAL-----GAVSLGRTSRSTVSQPGPSLFSGCC--SRVNRRAIRLNM 546
 QY 473 SQPK-----PYIDADTALG-----TDVYDEKGCQCD-----VSEVDLTP 507
 Db 547 STASVSRGSMQELDTLAGLRSPAPQRTSSLNARPHDSLIDNCDSRDPVAILISIP--TP 604
 QY 508 PLKT 511
 Db 605 PANT 608

RESULT 36
 J00271
 voltage-sensitive potassium channel protein [validated] - rat
 N:Alternate names: rat sha/1
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
 C:Accession: J00271; A39113
 R:Balduin, T.D.; Tsaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.
 A:Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K⁺ channel
 A:Reference number: J00271; MUID:92000693; PMID:1840649
 A:Accession: J00271
 A:Molecule type: mRNA
 A:Residues: 1-630 <BAL>
 A:Cross-references: GB:S64320; NID:g236196; PIDN:AAB19939.1; PID:g236197
 A:Experimental source: hippocampus
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
 A:Reference number: A39113; MUID:91156694; PMID:1705709
 A:Accession: A39113
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>
 A:Cross-references: GB:M59980; NID:g203467; PIDN:AAA0929.1; PID:g203468
 C:Function:
 A:Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [valid]
 C:Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel
 F:3/8/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #sta
 F:54,280,489,606/Binding site: phosphate (Thr) (covalent) (by protein kinase II) #sta
 F:70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
 F:101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta
 F:113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase
 F:592/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match
 Best Local Similarity 4.8%; Score 227.5; DB 2; Length 630;
 Matches 84; Conservative 70; Mismatches 144; Indels 77; Gaps 13;

QY 102 CRRNRYRRVQN-----YYNVLRRPGNAFIYH-----AEVFLVFG 139
 Db 133 CYEEYKDRRENAERLDDADDTNNTGESALPTMARORVWRAPENPHTSMALVYVYTG 192
 QY 140 CIL-LSVFSTIPEHTKLASS-----CLLIEFVMIIVFGLFEIIRWSAG 183
 Db 193 FETAVSVIANVAVFVPCGSSPHIKELPCGERAVAFECUPTACMIFVTEYLKLA-A 251
 QY 184 CCCRYGMOGRLEFARKPFVIDITVLI-A-SIAVASAKTQGNIFATSAISSLRFLQILRM 242
 Db 252 -----PSRYFVRVSVMSIIDVALLPYIGLVMDNED---VSGAFVLRVFRVRI 300
 QY 243 VRMDRGTKWLLGSVYVASHKELITAMYGFL-----VLIFSSFLVLYVEKDANKF 295
 Db 301 FKFSRHSQGLRIIGYTLKSCASEL-----GFLFSILMALIIFATVMEFAEKSSASKF 354
 QY 296 STYADALMMGTITLTIGYDGTPLTWGRLLSAGFALIGISFPALPAGILGSGFALKVO 355
 Db 355 TSIPAAFWYITVMTLGYGDMVPKTLAGKILFGSICSLGVLVIALPVPYIVSNFS---R 411
 QY 356 EHRQKHFEKRR--NPAANLIQCVMSYADEKSVSIATWPKPLKALHTCSPTNQLSKF 414
 Db 412 IYHONQADRRKRAQKYLARILAKSGTTNAFLQY 462
 QY 415 RVMASPRQSTIKSR 429
 Db 463 EPAFVSKSGSSFEQO 477

RESULT 37
 A39395
 delayed rectifier potassium channel Kv4, neuronal - rat
 N:Alternate names: potassium channel protein Raw2
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 08-Dec-2000
 C:Accession: A39395; S22704; S19100
 R:Luneau, C.J.; Williams, J.B.; Marshall, J.; Levitan, E.S.; Oliva, C.; Smith, J.S.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 3933-3936, 1991
 A:Title: Alternative splicing contributes to K(+) channel diversity in the mammalian
 A:Reference number: A39395; MUID:91219486; PMID:2023941
 A:Accession: A39395
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-585 <LUN>
 A:Cross-references: GB:M68880; GB:M37845; NID:g205106; PIDN:AAA41501.1; PID:g205107
 R:Retig, J.; Wunder, F.; Stocker, M.; Lichtinghagen, R.; Mastlaue, F.; Beckh, S.; Ku
 EMBO J. 11, 2473-2486, 1992
 A:Title: Characterization of a shaw-related potassium channel family in rat brain.
 A:Reference number: S22702; MUID:92331599; PMID:1378392
 A:Accession: S22704
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-585 <RET>
 A:Cross-references: EMBL:X62840; NID:g57652; PIDN:CAA44644.1; PID:g57653
 C:Superfamily: potassium channel; protein drk1
 C:Keywords: alternative splicing; glycoprotein; ion channel; leucine zipper; transmem
 F:191-209/Domain: transmembrane #status predicted <TM1>
 F:245-266/Domain: transmembrane #status predicted <TM2>
 F:278-298/Domain: transmembrane #status predicted <TM3>
 F:310-328/Domain: transmembrane #status predicted <TM4>
 F:345-364/Domain: transmembrane #status predicted <TM5>
 F:415-456/Domain: transmembrane #status predicted <TM6>

Query Match
 Best Local Similarity 4.8%; Score 227; DB 2; Length 585;
 Matches 92; Conservative 72; Mismatches 138; Indels 112; Gaps 17;

QY 3 RHNAEGEGGAAGLWVSGAAAAAGGRLSGMKRVDSGKRGVLLNSAANGDGLLLG 62


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Db 110 ROHRAE-----ALDSFGAPLDNSAD-----ADADGPG-----140
QY 63 TRAAITLGGGGGLRESRRKOGARMSLGLKPLSTSSQSCRNRYRQVLYNVLERP 122
Db 141 -----DSGDEDELEMT-----KRLASDSPDGRPGGFWRMQPRIMALFDDP 183
QY 123 RGMAFI-YHAFVLLVFGCLLSV-----FSTIPERTKL-----155
Db 184 YSSRYARVAFASLFP-----ILVSIITFCTETHERFNIVKTELENRNGQVRYRAE 240
QY 156 ASSCLLIEFVIVVGFETIRMSAGCCCRKRGWGLRFAPKPCVIDITVLI-----211
Db 241 TEAFITLYEGVGVWTFEFLMKV-----VFC-----PNKVEFINSLNIIDFVILPEYL 291
QY 212 -ASIAVSAKTGNIATFATLSRLFLQILIRVMDRGGTWKLLGSVVAHSKE-LITA 269
Db 292 EVGLISGLSKAKADVL--GFLRVYRVRILIRIKLRHFGRLVGLTLRASTNEFLLI 349
QY 270 WYIGFLVLIFFSEFLVLYEK-----DANKFSTYADALMGTITLTITIGYDKTP 319
Db 350 IFLAGVLIFAT-MIYVARIQAQPNPDSAEHTHEKNIPIGFWMAVAVTMTLTIGYDKTP 408
QY 320 LTWIGRLSAGALLGISFPALPAGIL-----GSGFALKVQDQ-----HROKHFEK 365
Db 409 QTWGSMVLGALCALAGVLTITAMPVPIVNNFGMYISLAMAKOKLPPKKKKHPIR 462

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RESULT 38

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T23991
hypothetical protein R07M4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C:Accession: T23991; T24278
R:Coltage, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19827
A:Accession: T23991
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-558 <MI>
A:Cross-references: EMBL:Z67756; PIDN:CAA91765.1; GSPDB:GN00028; CESP:R07M4.1
A:Experimental source: clone R07M4
R:Lennard, N.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19868
A:Accession: T24278
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-558 <MI>
A:Cross-references: EMBL:Z68010; PIDN:CAA92011.1; GSPDB:GN00028; CESP:R07M4.1
A:Experimental source: clone T01C1
C:Genetics:
A:Gene: CESP:R07M4.1
A:Map position: X
A:Locations: 32/1; 65/2; 91/3; 138/2; 177/3; 242/2; 439/3; 470/3; 507/1; 528/1
C:Superfamily: potassium channel protein drkl

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Query Match. 4.8%; Score 226.5; DB 2; Length 558;
Best Local Similarity 21.6%; Pred. No. 3.4e-07;
Matches 83; Conservative 67; Mismatches 166; Indels 69; Gaps 11;

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```

QY 104 RNKRYRQVNYLYNVLERP--GMAFIYHAFVLLVFGCLLSVFSSTI-----PEHTKLASS 158
Db 179 KRIFWMLKLPQMSLFDLP-----YSSQAKLINGSIVLFIPTISFSCCLKTHQSRRLP 232
QY 159 CLILIEVVM-----IVFGL-LEFIRIV-SAGCCCRYGWQGLRFPARK 200
Db 233 VILGQNTMPGVQVPSIERVSTPLPTFGQIEMCNWTFELILIRFVCSKIRFFKS 292
QY 201 PFCVIDITVLI-----SIAVSAKTGNIATFATLSRLFLQILIRVMDRGGTWKL 254
Db 293 PLNMIDVATLSTFYADAMKAVVEDEPK-----DVEFLSMIRILFRKLKLTQHHGLOI 346

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QY 255 LGSVVAHSKELLIPAWYIGFLVLIFFSEFLVLYEK-----DANKFSTYADALMGTITLT 311
Db 347 LIHTFRASAKELLIVFLILIGIVFALVYAAEKMEANPNQOFISPLGMAWICTMTT 406
QY 312 IGYGDKPTPLTWLGRILSAGFALLGISFPALPAGILGSGFALKVQDQHRKHFEKRRN---368
Db 407 VGXGDMTPHTSFGRLVGSLSAVMGVLTITLPPVIVSNFAMFYSHNQARDKLPKRRRVL 466
QY 369 PAANLIQCVKRSVAADKSVSIATW-----KPIKALHTCSPTNQLSEKERVAM 418
Db 467 PVEQILQARRHAAVLEPPSASQGGIGGQAIRRMPIIIDQNCDEEHNHKKHRE-----522
QY 419 ASPRGQIKRSQASVGRSPSTDI 443
Db 523 -----KENSEDEGTINSSITGV 539

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RESULT 39

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A40090
potassium channel KVL1 protein - mouse
N:Alternate names: potassium channel A; potassium channel MK1
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Nov-2000
C:Accession: A40090; S06378; I60746
R:Chandry, K.C.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanshani, S.; Tempel,
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regio
A:Reference number: A40090; MUID:9016196; PMID:2305265
A:Accession: A40090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHA>
A:Cross-references: GB:M30439; NID:q199702; PIDN:AAA39711.1; PID:q199703
R:Tempel, B.L.; Jan, Y.N.; Jan, L.Y.
Nature 332, 837-839, 1988
A:Title: Cloning of a probable potassium channel gene from mouse brain.
A:Reference number: S06378; MUID:88189348; PMID:2451788
A:Accession: S06378
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-495 <TEM>
A:Cross-references: GB:Y00305; GB:M36456; NID:q53605; PIDN:CAA68408.1; PID:q53606
A:Note: It is uncertain whether Met-1 or Met-4 is the initiator
C:Genetics:
A:Gene: MK1
C:Superfamily: potassium channel protein drkl
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
E:361-370/Domain: transmembrane beta strand #status predicted <TM1>
E:371-379/Domain: transmembrane beta strand #status predicted <TM2>
E:207/Binding site: carbonylate (Asn) (covalent) #status predicted

```

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Query Match 4.8%; Score 226; DB 2; Length 495;
Best Local Similarity 21.1%; Pred. No. 3.1e-07;
Matches 66; Conservative 74; Mismatches 125; Indels 48; Gaps 8;

```

```

QY 104 RNKRYRQVNYLYNVLERP--GMAFIYHAFVLLVFGCLLSVFSSTI-----151
Db 142 RLPEKEIYQVWMLFEYESSGPARYIAVSVVILISVIFCLEPLPELKDQDFTGT 201
QY 152 -----HTKLASSCLLIEFVIVVGFETIRMSAGCCCRYGWQGLRFPARK 200
Db 202 IHRIDNTVITYISNIFTDFEIVETLCIWFSELVVRFAC-----PSKTDFFKN 252
QY 201 PFCVIDITVLI-----SIAVSAKTGQGN-----IFATLSRLFLQILIRVMDRGGTW 252
Db 253 IMNFIDVIAIIPYFTLIGTEIAEQEONQGEQATSLAILVIRIVRFRIFKLSRHSKGL 312
QY 253 KLIGSVVAHSKEL-ITAYIGFLVLIFFSEFLVLYEKDANKKESTYADALMGTITLT 311
Db 313 OILGOTLASAMELGLIIFLPIGVILFSSAVFAAEFESEHSSTIPDAFWMAVVSFTT 372
QY 312 IGYGDKPTPLTWLGRILSAGFALLGISFPALPAGILGSGFALKVQDQHRKHFEKRRPAA 371

```


Db 373 VGGDMFVITGKIVSLCAIAGVLTALPVIVSNFN---YRHETBEDEQ----A 425
 Oy 372 NLQCVWRSYAAD 384
 Db 426 QLLHVSFNPILASD 438

RESULT 40

JH0166
 potassium voltage-gated channel - rat
 N:Alternate names: potassium channel KV1; potassium channel RK4; shaker-related potassium
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 17-Nov-2000
 C:Accession: JH0166; D39113; 155392
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunt
 Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed recti
 A:Reference number: JH0166; MUID:90297965; PMID:2361015
 A:Accession: JH0166
 A:Molecule type: mRNA
 A:Residues: 1-602 <SMA>
 A:Cross-references: GB:M27158; NID:9205100; PID:AAA41498.1; PID:9205101
 A:Experimental source: Brain
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channel
 A:Reference number: A39113; MUID:91156694; PMID:1705709
 A:Accession: D39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-552, 'S', 554-602 <ROB>
 R:Morl, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
 J. Biol. Chem. 268, 26482-26493, 1993
 A:Title: The transcription of a mammalian voltage-gated potassium channel is regulated b
 A:Reference number: 155392; MUID:94075338; PMID:8253777
 A:Accession: 155392
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-15 <RES>
 A:Cross-references: GB:L23434; NID:9443766; PID:AAA42337.1; PID:9443767
 A:Experimental source: Sprague-Dawley
 C:Genetics: KVL.5
 A:Gene: KVL.5
 C:Superfamily: potassium channel protein drkl
 C:Keywords: glycoprotein, phosphoprotein, potassium channel, transmembrane protein, volt
 F:242-260/Domain: transmembrane #status predicted <TM1>
 F:346-356/Domain: transmembrane #status predicted <TM2>
 F:347-368/Domain: transmembrane #status predicted <TM3>
 F:387-408/Domain: transmembrane #status predicted <TM4>
 F:423-444/Domain: transmembrane #status predicted <TM5>
 F:464-505/Domain: transmembrane #status predicted <TM6>
 F:1044,116,181,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:81,535,546,569/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.7%; Score 223.5; DB 2; Length 602;
 Best Local Similarity 24.9%; Pred. No. 6, 1e-07;
 Matches 68; Conservative 49; Mismatches 111; Indels 45; Gaps 8;

Oy 162 ILFPMIVFGLFIRIRWSAGCCCRKRGWGRARPKPCVITIVL---IASIAVVS 218
 Db 317 IVEVTVIMFTEFLVRFAC-----PSKAEFSRNTMNTIDVAIFPFIITOTEL 367
 Oy 219 AKTO-----GNIFATSLRLPLOTILRMVRMDRGRTWKLGSVVAHSKELTAW 270
 Db 368 AEQDGGGGGQNGQAMSLAILKIVIRLVRFIKLSRHSKGLQILGKTLDASNREGLLI 427
 Oy 271 YIGFLVLIFSSFLVYLVEKDN-KKESTYADALMWGITITLTIGYGDPLTWLGRLLSA 329
 Db 428 PFLFVIGVILFSSAVFAEADNHGSHRSIPDAFMMVAVMTITVGYGDMRPIVCGKIVGS 487
 Oy 330 GFALGIGISFALPAGLISGF-----ALKVOEQRHQRKFEKRRRNPANLIIQ 375

Db 488 LCAIAGVLTALPVIVSNFNFYRHETDEEQALK-EEQNGRRESGIDTGQORVVS 546
 Oy 376 CVWRSYAAD-----EKSVSIATW-----KPHIKA 399
 Db 547 CSKASFCKTGSGLESDSIRRGSCPLKCHKA 579

RESULT 41

A35312
 potassium channel protein Shal2 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 08-Dec-2000
 C:Accession: A35312; S12747
 R:Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salkoff, L.
 Science 248, 599-603, 1990
 A:Title: K⁺ current diversity is produced by an extended gene family conserved in Dro
 A:Reference number: A35312; MUID:90239553; PMID:2335511
 A:Accession: A35312
 A:Molecule type: mRNA
 A:Residues: 1-490 <WEI>
 A:Cross-references: GB:M32660; NID:9158456; PID:9158457
 R:Butler, A.; Wei, A.; Salkoff, L.
 Nucleic Acids Res. 18, 2173-2174, 1990
 A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.
 A:Reference number: S12746; MUID:90245668; PMID:2336395
 A:Accession: S12747
 A:Molecule type: mRNA
 A:Residues: 1-490 <BUT>
 A:Cross-references: EMBL:M32660; NID:9158456; PID:9158457
 C:Genetics: shal2
 A:Gene: shal2
 A:Cross-references: FlyBase:FBgn0005564
 C:Superfamily: potassium channel protein drkl
 C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane prote

Query Match 4.7%; Score 222.5; DB 2; Length 490;
 Best Local Similarity 23.4%; Pred. No. 5, 2e-07;
 Matches 78; Conservative 65; Mismatches 136; Indels 55; Gaps 13;

Oy 89 LIGKPLSYTSSQSRNRYRQNYLYNVLRPR-----GNAFIYHAFVLLFGCLIS 144
 Db 148 LMDKLSBNGDONQQLTNMQO---KMRARENPTTSALVFYVTGFIIV--SVMAN 202
 Oy 145 VFSTIP-----BHTKLASSCLLLEFVMIVGELFIRIRWSAGCCCRNG 190
 Db 203 VVEIVPCGRHRRAGTLPCCGERKIVFC---LDPAQWIFPAEYLLRFLAA----- 251
 Oy 191 WQGRLEFARKPCVITIVLTAIAVVA3AKTQGNIFATSLASLRLPQLIRVMDRGG 250
 Db 252 -PDCKEFKRSWMSIDVAIMP--YYIGLITDNDVSGAFVTLRVFRVFRIFKFSRHSQ 308
 Oy 251 TWKLGSVVAHSKRELTAWYIGFLV-----LIFSSFLVLEKDN-KKESTYADAL 302
 Db 309 GLRILGTLKSCASL-----GLVFSIAAMIIIFATVMT-AENNVGNTFTSIPAPF 361
 Oy 303 WMGITITLTIGYGDPLTWLGRLLSAGFALLGISFALPACILGSGFA-LKVQEQHRK 361
 Db 362 WYTIWMTTLTGCGDMVPEPIAGKIVGVCISLGVALVLPVIVSNFESRIYHQNRADK 421
 Oy 362 HFEKRRNPANLIIQCVWRSYAA--DEKSVSIATW 393
 Db 422 RKAQRKARLARIRAKASSGAFAVSKKAAEARW 455

RESULT 42

C72692
 Probable potassium channel APE0955 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: C72692
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
 DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyperthermophilic Crenarchaeon, *Aeropyrum*
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: C72692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KAM>
A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAH79939.1; PID:d1043725; PID:g5104188;
A:Experimental source: strain K1
A:Genetics:
A:Gene: APE0955

Query Match	4.7%	Score 221.5	DB 2	Length 295
Best Local Similarity	26.1%	Pred. No. 2.8e-07		
Matches	65	Conservative 52	Mismatches 97	Indels 35
			Gaps	9
<hr/>				
QY	110	RVQNTLVNLERPGRNAFIYHAFVFLVFCGLISVFSTIDPTHTKLASS---	CILILER	165
Db	27	RRRN-IGDME-----HPLVELGSYAALLSVIYVVEYTMQSGEYLVRLRYLDV		76
<hr/>				
QY	166	VMIVVGLFEFIIRISAGCCCFRGMQGRLEAFARKPCVIDITPIVLASIVASAKTQNI		225
Db	77	ILVITLMADYARARVYSGDPAGI-----YAKTLEYEALVPAGLIATL---	EGHL	123
<hr/>				
QY	226	FATSLARSLRFQILRMVRMDRGGTWKLLGSVVYASHSKELITAWI---	GFLVLIFFSF	282
Db	124	AGLGEFRVRLRFLRILILISRGS--KFLSAINDADK--IRFHYLGCAYMLVLYGAF		179
<hr/>				
QY	283	LVYLVE-KDANKFEFVADALIMWGTTITLTIGVGDKNPLWTGLRLLSGFALGISEFNL		341
Db	180	ALVIYEYDDPNSIKSVFDALIMWAVYATITVIGIDVVPATPIGKVIIGIAVMTLGISALT		239
<hr/>				
QY	342	PAGILGSGF	350	
Db	240	LIGTVSNMF	248	

RESULT 43
S51212
BAK5 protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 17-Nov-2000
C:Accession: S51212
R:Garcia-Guzman, M.; Sale, F.; Criado, M.; Sala, S.
FEBS Lett. 354, 173-176, 1994
A:Title: A delayed rectifier potassium channel cloned from bovine adrenal medulla functionally expressed in *Xenopus* oocytes
A:Reference number: S51212; MUID:95046337; PMID:7957920
A:Accession: S51212
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-597 <GAR>
A:Superfamily: potassium channel protein drk1

[illegible]

RESULT 44
S19552
potassium channel protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-2001
C:Accession: S19552
R:Lee, J.
submitted to the EMBL Data Library, January 1992
A:Reference number: S19552
A:Accession: S19552
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <LEE>
A:Cross-References: EMBL:211585; NID:g29935; PIDN:CA67671.1; PID:g29936
C:Superfamily: potassium channel protein drk1

[illegible]

```

RESULT 45
T27759
hypothetical protein ZK1321.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C:Accession: T27759
R:Gardner, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: Z20415
A:Accession: T27759
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <MIL>
A:Cross-references: EMBL:Z48584; PIDN:CAA88477.1; GSPDB:GN00020; CESP:ZK1321.2
A:Experimental source: clone ZK1321
C:Genetics:
A:Gene: CESP:ZK1321.2
A:Map position: 2
A:Intons: 21/2; 61/2; 89/2; 120/2; 153/3; 211/2; 264/1; 300/2; 331/2; 391/3; 398/2;
A:Superfamily: potassium channel protein diki

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	Query Match	4.6%	Score 215.5;	DB 2;	Length 460;
	Best Local Similarity	22.2%;	Pred. No. 1.e-06;		
	Matches 64; Conservative	67;	Mismatches 114;	Indels 43;	Gaps 7;
QY	110 RVQNYLYVNLERP-----RGNAFIYAHEFLVFGCLILTSVFSPRIPEH--TKLASSCGL 161	:	:	:	:
DG	180 KTORIWELMEPPDSSLARSARIIAIFSLAVIALSIISCWEIVPDIIEKPIINSAITELL 239	:	:	:	:
QY	162 -----ILFEVMIVFGLLEPTIRISWAGCCCRYGWGQRLLRFARRPCVIDTTV 209	:	:	:	:
DG	240 DEMDEKHYSPEFWIELMCIWFTEILLERISCP-----KVTPATSVLTNIIDFVA 290	:	:	:	:
QY	210 L---IASIAVVASAKTGNGIFAATSLSLRPLQLRLRMVRMDRGCTWKLLGSVVYAHSKEL 266	:	:	:	:
DG	291 IAPFFVNFEFDSTKSNSMSFAVLNVLRLRRVFRFKLRHSVGLDLGGTFTRSSVOEF 350	:	:	:	:


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QY 152 ---HTKLASSCLLIEFVMIYVGLFEIIRIWSAGCCCRYRGMOGRLEFARKPCVIDTI 208
DB 204 VFKYNIFDPFVETLITIMFSFELVAFPA--CSKDEFFNNIMF-----IDIV 254
QY 209 VLI---ASIAVSAKTQG-----NIPATSAIRSLRFLQILRMVMDRGTGWLKLSVYV 260
DB 255 AIIPEFILTGMABEQEPQKQATSLALRLVLRVFRIFRFLSHRSKQLQILGOTLK 314
QY 261 AHSKRL-ITAWIGLVLVLFSSFLVVLVEKDANKERSTYADALMWGITTLTIGYDKTP 319
DB 315 ASMRGLGLTFELFGLVILLFSSAVYFAEAEDESHFISIDAFWMAVAVSMTTVGDMYP 374
QY 320 LTMWGLRSLAGFALLGISFPAIAGILSGFALKVOEQHROKHKEKRRNPANILQCYWR 379
DB 375 VTIGKIVGSLCANGVLTALPVPYIVSNFN---YFHHTEEGEO----- 418
QY 380 SYADEKSVSIATWPKPHKALHTCSP---TNOKLSFKERYRMASPRGOSIKS----- 428
DB 419 -----ADLLHVSSPNLASNSDLSSRSSAMSKSEYMEIEDLNNSIDN 461
QY 429 -ROASV 433
DB 462 FREANI 467

RESULT 49
A:Accession: A49507
A:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Nov-2000
C:Accession: A49507; B49507
J:Altali, B.; Lesage, F.; Ziliani, P.; Guillemaire, E.; Honore, E.; Waldmann, R.; Hugnot,
R. Biol. Chem. 268, 24283-24289, 1993
A:Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 delayed rectifier K(+)
A:Reference number: A49507; MUID:94043264; PMID:8226976
A:Accession: A49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-602 <AT2>
A:Cross-references: GB:L22218; NID:9435603; PIDN:AAA9365.1; PID:9435604
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 201-602 <AT2>
A:Cross-references: GB:L22218
C:Superfamily: potassium channel protein drkl
C:Keywords: alternative splicing

Query Match 4.5%; Score 214.5; DB 2; Length 602;
Best Local Similarity 24.1%; Pred. No. 2.4e-06;
Matches 58; Conservative 53; Mismatches 105; Indels 25; Gaps 6;

QY 139 GCLILVSFTI-PHTKLASSCLLIEFVMIYVGLFEIIRIWSAGCCCRYRGMOGRLEF 197
DB 293 GSGVLSGTYAPRLPRLADPEFIVETTCVIMFTFELLVREFAC-----PSKAEF 343
QY 198 ARRPFCVIDTIVL---IASIAVSAKTQ-----GNIFATSAIRSLRFLQILRMVMD 246
DB 344 SRNIMNIIIDYAIAPYFILTCTELAEQPGGGGQNGQAMSLALRLVLRVFRIFRFLKLS 403
QY 247 RRGGMWLLSVVAHSKELITAWIGLVLVLFSSFLVVLVEKD-ANKERSTYADALMWG 305
DB 404 RHSKGLQILGTTQASMRGLGLTFELFGLVILLFSSAVYFAEADNQSOLSSIPDAFWMA 463
QY 306 TITLTIGYDKTPPLTMWGLRSLAGFALLGISFPAIAGILSGFALKVOEQHROKHFEK 365
DB 464 VVMTITVYGDMRPTTYGKIVGSLCANGVLTALPVPYIVSNFN---YFHHTEEDHEE 520
QY 366 R 366
DB 521 Q 521

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RESULT 50
JC4787
shaw protein - California spiny lobster
C:Species: Panulirus interruptus (California spiny lobster)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 08-Dec-2000
C:Accession: JC4787
R:Baro, D.J.; Cole, C.L.; Harris-Warrick, R.M.
Gene 170, 267-270, 1996
A:Title: The lobster shaw gene: Cloning, sequence analysis and comparison to fly shaw
A:Reference number: JC4787; MUID:96235147; PMID:8666257
A:Accession: JC4787
A:Molecule type: mRNA
A:Residues: 1-489 <BAR>
A:Cross-references: GB:L48691; NID:g1100226; PID:g1100227
C:Comment: This protein is a voltage-dependent potassium (K+) channel protein.
C:Genetics:
A:Gene: shaw
C:Superfamily: potassium channel protein drkl
C:Keywords: membrane protein; phosphoprotein; transmembrane protein
F:171-190/Domain: transmembrane #status predicted <TM1>
F:126-248/Domain: transmembrane #status predicted <TM2>
F:260-280/Domain: transmembrane #status predicted <TM3>
F:291-311/Domain: transmembrane #status predicted <TM4>
F:324-342/Domain: transmembrane #status predicted <TM5>
F:387-410/Domain: transmembrane #status predicted <TM6>
F:18-190/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II)
F:19,41,48,86,140,163,228/Binding site: phosphate (Tyr) (covalent) #status predicted
F:122,66,316,475/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #statu
F:126,157,281,320/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #sta
F:320,483/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred

Query Match 4.5%; Score 214; DB 2; Length 489;
Best Local Similarity 23.3%; Pred. No. 1.9e-06;
Matches 61; Conservative 52; Mismatches 113; Indels 36; Gaps 6;

QY 111 VONYLVNLEPRPGMAFYHAFFELVFGCLILVSFTIPEHTKLASSCLLIEFVMIYV 170
DB 199 IGNITVQNTMENTAW-----TLDKKAINNAHAFYIEVCYTW 236
QY 171 FGLFEIIRIWSAGCCCRYRGMOGRLEFARKPCVIDTIVLIA-SIAVSAKTQGNIFATS 229
DB 237 FFEIILIRLIAS-----PNKFMELKASVNMIDFATLSFYVDILQKFAHLENAD 287
QY 230 ALRSLRFLQILRMVRMDRGTGWLKLSGVVAHSKEL-ITAWIGLVLVLFSSFLVYL- 286
DB 288 ILEFSIIRIKMLFKLTRHSSGKILQITRASAKELTLVFFVLGIVIFASLVYAEER 347
QY 287 VEKDANKERSTYADALMWGITTLTIGYDKTPPLTMWGLRSLAGFALLGISFPAIAGIL 346
DB 348 IOANPHNDNSIPLGLMNLVMTITVGYGDMARPTTYGMEVGALCALAGVLTALPVPVI 407
QY 347 GSGFALKVOE-QHROKHFEKRR 367
DB 408 VSNFMYYSHTQARAKLPKRR 429

```

Search completed: June 14, 2003, 17:45:11
 Job time : 59 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:27 ; Search time 26 Seconds
(without alignments)
1472.410 Million cell updates/sec

Title: US-09-825-147-2

Sequence: 1 MPRHHAGGEEGGAAGLWKS.....SICKAGESTALSLPHVKLK 923

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4527.5	95.7	897	1	Q9n822 homo sapien
2	4227.5	89.3	878	1	C105_HUMAN
3	1991	48.1	695	1	C104_HUMAN
4	1805.5	32.1	852	1	C102_RAT
5	1784	37.7	872	1	C102_HUMAN
6	1756	37.1	759	1	C102_MOUSE
7	1620.5	34.2	873	1	C103_HUMAN
8	1590.5	33.6	866	1	C103_BOVIN
9	1589.5	33.6	866	1	C103_BOVIN
10	1102	23.3	676	1	C101_HUMAN
11	1101	23.3	669	1	C101_RAT
12	1100.5	23.3	604	1	C101_MOUSE
13	1083.5	22.9	660	1	C101_SOUAC
14	899.5	19.0	377	1	C101_XENLA
15	647	13.7	276	1	C104_MOUSE
16	591.5	12.5	172	1	C101_PELCA
17	538.5	11.4	169	1	C101_CAVPO
18	486.5	9.4	155	1	C101_RABIT
19	446.5	9.4	168	1	C104_RAT
20	409.5	8.7	123	1	C101_PIG
21	291.5	6.2	854	1	C101_HUMAN
22	289	6.1	853	1	C101_HUMAN
23	282	6.0	806	1	C101_HUMAN
24	276.5	5.8	806	1	C101_HUMAN
25	272	5.7	806	1	C101_HUMAN
26	251	5.3	769	1	C101_HUMAN
27	250.5	5.3	582	1	C101_HUMAN
28	248	5.2	985	1	C101_HUMAN
29	247	5.2	757	1	C101_HUMAN
30	244	5.2	889	1	C101_HUMAN
31	242	5.1	638	1	C101_HUMAN
32	241.5	5.1	625	1	C101_HUMAN
33	240.5	5.1	654	1	C101_HUMAN
34	240.5	5.1	655	1	C101_HUMAN
35	237	5.0	523	1	C101_HUMAN
36	237	5.0	525	1	C101_HUMAN
37	235.5	5.0	660	1	C101_HUMAN
38	234	4.9	654	1	C101_HUMAN
39	233	4.9	653	1	C101_HUMAN
40	233	4.9	656	1	C101_HUMAN
41	232	4.9	528	1	C101_HUMAN
42	230	4.9	405	1	C101_HUMAN
43	230	4.9	511	1	C101_HUMAN
44	230	4.9	511	1	C101_HUMAN
45	229.5	4.8	495	1	C101_HUMAN
46	229.5	4.8	495	1	C101_HUMAN
47	226	4.8	601	1	C101_HUMAN
48	225.5	4.8	602	1	C101_HUMAN
49	223.5	4.7	602	1	C101_HUMAN
50	222.5	4.7	602	1	C101_HUMAN
51	214.5	4.5	598	1	C101_HUMAN
52	213	4.5	499	1	C101_HUMAN
53	212.5	4.5	499	1	C101_HUMAN
54	212.5	4.5	499	1	C101_HUMAN
55	212	4.5	498	1	C101_HUMAN
56	211.5	4.5	613	1	C101_HUMAN
57	210	4.4	530	1	C101_HUMAN
58	207.5	4.4	499	1	C101_HUMAN
59	199	4.2	529	1	C101_HUMAN
60	192.5	4.1	579	1	C101_HUMAN
61	192.5	4.1	580	1	C101_HUMAN
62	188.5	4.0	574	1	C101_HUMAN
63	180	3.8	209	1	C101_HUMAN
64	178.5	3.8	536	1	C101_HUMAN
65	176.5	3.7	580	1	C101_HUMAN
66	174	3.7	561	1	C101_HUMAN
67	168	3.5	160	1	C101_HUMAN
68	163.5	3.5	724	1	C101_HUMAN
69	163.5	3.5	736	1	C101_HUMAN
70	159.5	3.4	732	1	C101_HUMAN
71	153.5	3.2	731	1	C101_HUMAN
72	142.5	3.0	425	1	C101_HUMAN
73	142.5	3.0	425	1	C101_HUMAN
74	142	3.0	2161	1	C101_HUMAN
75	142	3.0	2212	1	C101_HUMAN
76	141	3.0	2516	1	C101_HUMAN
77	140.5	3.0	2223	1	C101_HUMAN
78	137.5	2.9	2327	1	C101_HUMAN
79	137.5	2.9	2373	1	C101_HUMAN
80	137	2.9	1966	1	C101_HUMAN
81	137	2.9	2164	1	C101_HUMAN
82	136.5	2.9	2272	1	C101_HUMAN
83	135	2.9	1610	1	C101_HUMAN
84	133	2.8	1835	1	C101_HUMAN
85	132.5	2.8	2336	1	C101_HUMAN
86	132.5	2.8	2378	1	C101_HUMAN
87	131.5	2.8	1547	1	C101_HUMAN
88	130	2.7	1156	1	C101_HUMAN
89	129.5	2.7	783	1	C101_HUMAN
90	129.5	2.7	783	1	C101_HUMAN
91	129	2.7	528	1	C101_HUMAN
92	129	2.7	2688	1	C101_HUMAN
93	128.5	2.7	705	1	C101_HUMAN
94	128.5	2.7	1939	1	C101_HUMAN
95	128	2.7	411	1	C101_HUMAN
96	127.5	2.7	668	1	C101_HUMAN
97	127.5	2.7	2190	1	C101_HUMAN
98	127.5	2.7	2259	1	C101_HUMAN
99	127	2.7	793	1	C101_HUMAN
100	127	2.7	1308	1	C101_HUMAN
101	127	2.7	2365	1	C101_HUMAN
102	126.5	2.7	2505	1	C101_HUMAN
103	126.5	2.7	1897	1	C101_HUMAN
104	125.5	2.7	1687	1	C101_HUMAN
105	125.5	2.7	1873	1	C101_HUMAN
106	125.5	2.7	1873	1	C101_HUMAN
107	125.5	2.7	1873	1	C101_HUMAN
108	125.5	2.7	1873	1	C101_HUMAN
109	125.5	2.7	1873	1	C101_HUMAN
110	125.5	2.7	1873	1	C101_HUMAN
111	125.5	2.7	1873	1	C101_HUMAN
112	125.5	2.7	1873	1	C101_HUMAN
113	125.5	2.7	1873	1	C101_HUMAN
114	125.5	2.7	1873	1	C101_HUMAN
115	125.5	2.7	1873	1	C101_HUMAN
116	125.5	2.7	1873	1	C101_HUMAN
117	125.5	2.7	1873	1	C101_HUMAN
118	125.5	2.7	1873	1	C101_HUMAN
119	125.5	2.7	1873	1	C101_HUMAN
120	125.5	2.7	1873	1	C101_HUMAN
121	125.5	2.7	1873	1	C101_HUMAN
122	125.5	2.7	1873	1	C101_HUMAN
123	125.5	2.7	1873	1	C101_HUMAN
124	125.5	2.7	1873	1	C101_HUMAN
125	125.5	2.7	1873	1	C101_HUMAN
126	125.5	2.7	1873	1	C101_HUMAN
127	125.5	2.7	1873	1	C101_HUMAN
128	125.5	2.7	1873	1	C101_HUMAN
129	125.5	2.7	1873	1	C101_HUMAN
130	125.5	2.7	1873	1	C101_HUMAN
131	125.5	2.7	1873	1	C101_HUMAN
132	125.5	2.7	1873	1	C101_HUMAN
133	125.5	2.7	1873	1	C101_HUMAN
134	125.5	2.7	1873	1	C101_HUMAN
135	125.5	2.7	1873	1	C101_HUMAN
136	125.5	2.7	1873	1	C101_HUMAN
137	125.5	2.7	1873	1	C101_HUMAN
138	125.5	2.7	1873	1	C101_HUMAN
139	125.5	2.7	1873	1	C101_HUMAN
140	125.5	2.7	1873	1	C101_HUMAN
141	125.5	2.7	1873	1	C101_HUMAN
142	125.5	2.7	1873	1	C101_HUMAN
143	125.5	2.7	1873	1	C101_HUMAN
144	125.5	2.7	1873	1	C101_HUMAN
145	125.5	2.7	1873	1	C101_HUMAN
146	125.5	2.7	1873	1	C101_HUMAN
147	125.5	2.7	1873	1	C101_HUMAN
148	125.5	2.7	1873	1	C101_HUMAN
149	125.5	2.7	1873	1	C101_HUMAN
150	125.5	2.7	1873	1	C101_HUMAN

107	125	2.6	985	1	NAHL_YEAST	099271	saccharomyc
108	125	2.6	2222	1	CCAE_RAT	007652	rattus norv
109	125	2.6	2339	1	CCAB_HUMAN	000975	homo sapien
110	124.5	2.6	1311	1	FMK2_HUMAN	P31810	homo sapien
111	124.5	2.6	1852	1	CCAS_CYPCA	P22316	cyprius ca
112	124	2.6	1375	1	BNR1_YEAST	P40450	saccharomyc
113	124	2.6	1518	1	KMR1_YEAST	P34244	saccharomyc
114	123.5	2.6	1272	1	FMK2_MOUSE	051112	mus musculu
115	123.5	2.6	1972	1	P531_HUMAN	012888	homo sapien
116	123.5	2.6	2339	1	CCAB_RABIT	005152	oryctolagus
117	123	2.6	707	1	Y39C_YEAST	P47166	saccharomyc
118	123	2.6	2169	1	CCAC_RAT	P20002	rattus norv
119	122	2.6	722	1	MEP1_TOBAC	09m714	nicotiana t
120	122	2.6	2359	1	CCAA_RAT	09eg60	rattus norv
121	122	2.6	2424	1	CCAA_RABIT	P27884	oryctolagus
122	122	2.6	2468	1	YADP_HUMAN	P46821	homo sapien
123	121.5	2.6	343	1	MYD7_METUA	058732	methanococc
124	121.5	2.6	1939	1	MYH1_HUMAN	P12882	homo sapien
125	121.5	2.6	3562	1	PGCV_CHICK	090953	gallus gall
126	121	2.6	417	1	KCH_ECOLI	P31059	escherichia
127	121	2.6	1961	1	MYH9_RAT	062812	rattus norv
128	120.5	2.5	427	1	KCN4_HUMAN	015554	homo sapien
129	120.5	2.5	552	1	HMEN_DROME	P02836	dirosophila
130	120.5	2.5	1039	1	MSL1_DROME	P50353	dirosophila
131	120.5	2.5	1253	1	SHK2_HUMAN	Q9UPX8	homo sapien
132	120.5	2.5	1324	1	CUT3_SCHPO	P41004	schizosacch
133	120.5	2.5	1971	1	MC3A_MOUSE	Q9WU99	mus musculu
134	120.5	2.5	4377	1	ANK3_HUMAN	012955	homo sapien
135	120	2.5	1087	1	AKA9_RABIT	Q28658	oryctolagus
136	120	2.5	1828	1	MAP2_MOUSE	P20357	mus musculu
137	119.5	2.5	921	1	TD2D_DROME	P47825	dirosophila
138	119.5	2.5	1159	1	HERG_HUMAN	Q12809	homo sapien
139	119.5	2.5	2492	1	TALA_DICDI	P54633	dictyostell
140	118.5	2.5	538	1	C1WA_HUMAN	P57789	homo sapien
141	118.5	2.5	1140	1	YM96_YEAST	004693	saccharomyc
142	118.5	2.5	1618	1	NEST_HUMAN	P46861	homo sapien
143	118.5	2.5	2139	1	CCAC_MOUSE	003165	mus musculu
144	118.5	2.5	3969	1	HRX_HUMAN	Q03164	homo sapien
145	117.5	2.5	1159	1	N12A_SCHPO	009904	schizosacch
146	117.5	2.5	1873	1	CCAS_RABIT	P07293	oryctolagus
147	117.5	2.5	2845	1	APC_MOUSE	061315	mus musculu
148	116.5	2.5	980	1	BOB1_YEAST	P38041	saccharomyc
149	116.5	2.5	997	1	BIR1_SCHPO	014064	schizosacch
150	116.5	2.5	1861	1	MAP2_RAT	P15146	rattus norv

ALIGNMENTS

RESULT 1
 CIO5_HUMAN STANDARD; PRT: 897 AA.
 AC 09NRG2; 09NRN0; 09NYA6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 5.
 GN KCNO5.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20357367; PubMed=10787416;
 RA Lerche C., Scherer C.R., Seebach G., Derst C., Wei A.D., Busch A.E.,
 RA Steinmeyer K.;
 RT "Molecular cloning and functional expression of KCNO5, a potassium
 channel subunit that may contribute to neuronal M-current
 diversity";
 RL J. Biol. Chem. 275:22395-22400(2000).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Brain;
 RX MEDLINE=20379054; PubMed=10816588;
 RA Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C.,
 RA Jentsch T.J.;
 RT "KCNO5, a novel potassium channel broadly expressed in brain, mediates
 M-type currents";
 RL J. Biol. Chem. 275:24089-24095(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kanamura C., Blevett B., Hechenberger M., Engels H., Steinlein O.K.;
 RT "The new voltage gated potassium channel KCNO5 and early infantile
 convulsions";
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain, and Retina;
 RA Kniazeva M., Han M.;
 RT "A new gene of the voltage-gated potassium channel KCNO family, KCNO5,
 is a candidate gene for retinal disorders";
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
 RX MEDLINE=21095345; PubMed=11159685;
 RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
 RT "Characterization of KCNO5/Q3 potassium channels expressed in
 mammalian cells";
 RL Br. J. Pharmacol. 132:381-384(2001).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 CC EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
 CC WHICH CONTRIBUTES TO M-TYPE CURRENT, A SLOWLY ACTIVATING AND
 CC DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
 CC DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS.
 CC MAY CONTRIBUTE, WITH OTHER POTASSIUM CHANNELS, TO THE MOLECULAR
 CC DIVERSITY OF AN HETEROGENEOUS POPULATION OF M-CHANNELS, VARYING IN
 CC KINETIC AND PHARMACOLOGICAL PROPERTIES, WHICH UNDERLY THIS
 CC THERAPEUTICALLY IMPORTANT CURRENT. INSENSITIVE TO
 CC TETRAETHYLAMMONIUM, BUT INHIBITED BY BARIUM, LINDAPIDINE AND
 CC XE991. ACTIVATED BY NIFEDIPINE ACID AND THE ANTI-CONVULSANT
 CC RETIGABINE. MUSCARINIC SUPPRESSORS KCNO5 CURRENT IN XENOPUS OOCYTES
 CC IN WHICH CLOVED KCNO5 CHANNELS WERE COEXPRESSED WITH M(1)
 CC MUSCARINIC RECEPTORS.
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ISOFORM 1 (SHOWN HERE), 2 AND 3;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN AND SKELETAL
 CC MUSCLE. IN BRAIN, EXPRESSED IN CEREBRAL CORTEX, OCCIPITAL POLE,
 CC FRONTAL LOBE AND TEMPORAL LOBE. LOWER LEVELS IN HIPPOCAMPUS AND
 CC PUTAMEN. LOW TO UNDETECTABLE LEVELS IN MEDULLA, CEREBELLUM AND
 CC THALAMUS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC
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 CC
 CC EMBL: AF249278; AAF91335.1; ALT_TNIT.
 CC EMBL: AF202677; AAF69797.1; -
 CC EMBL: AF272506; CAC88112.1; -
 CC EMBL: AJ272507; CAC88112.1; JOINED.
 CC EMBL: AJ272508; CAC88112.1; JOINED.
 CC EMBL: AJ272509; CAC88112.1; JOINED.
 CC EMBL: AJ272510; CAC88112.1; JOINED.
 CC EMBL: AJ272511; CAC88112.1; JOINED.

DR EMBL: AJ272512: CAC88112.1; JOINED.
 DR EMBL: AJ272513: CAC88112.1; JOINED.
 DR EMBL: AJ272514: CAC88112.1; JOINED.
 DR EMBL: AJ272515: CAC88112.1; JOINED.
 DR EMBL: AJ272516: CAC88112.1; JOINED.
 DR EMBL: AJ272517: CAC88112.1; JOINED.
 DR EMBL: AJ272518: CAC88112.1; JOINED.
 DR EMBL: AJ272519: CAC88112.1; JOINED.
 DR EMBL: AF263835: AAF73446.1; -.
 DR HSSP: Q54397: 1BL8.
 DR GeneW: HGNC:6299: KCNQ5.
 DR InterPro: IPR001622: K+channel_pore.
 DR InterPro: IPR003946: K+channel.
 DR InterPro: IPR003091: K_channel.
 DR InterPro: IPR000636: M+channel_nlg.
 DR Pfam: PF00520: Ion_trans. 1.
 DR Pfam: PF03520: KCNQ1_channel. 1.
 DR PRINTS: PR00169: KCHANNEL.
 DR KIM: Ion channel; Transmembrane; Ion transport; Voltage-gated channel;
 Multigene family; Alternative splicing.
 FT TRANSMEM 91 111 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 122 142 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 166 186 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 195 217 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 232 252 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 264 284 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 291 311 SEGMENT S6 (POTENTIAL).
 FT VARSPDIC 372 381 KKEGEASSS -> N (IN ISOFORM 2).
 FT VARSPDIC 372 381 KKEGEASSS -> NKFCSNKOKLEFRMYTSRKQS (IN
 ISOFORM 3).
 FT VARSPDIC 372 381 KP -> SR (IN REF. 1).
 FT CONFLICT 57 58 Y -> H (IN REF. 4).
 FT CONFLICT 692 692 A -> V (IN REF. 4).
 FT CONFLICT 764 764 T -> P (IN REF. 4).
 FT CONFLICT 822 822 S -> R (IN REF. 4).
 FT CONFLICT 874 874 R -> Q (IN REF. 4).
 SQ SEQUENCE 897 AA; 99024 MM; 0FD7C731C1DBD11 CRC64;

Query Match 95.7%; Score 4527.5; DB 1; Length 897;
 Best Local Similarity 98.9%; Pred. No. 6.4e-255;
 Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 36 MKDVESGGRVLLNSAARGDGLLLGTRATLGGGGGLRSRRKQAGARMSLLGKPPS 95
 DB 1 MKDVESGGRVLLNSAARGDGLLLGTRATLGGGGGLRSRRKQAGARMSLLGKPPS 60
 QY 96 YTSQSCRNVKRYRVONYLVLERPRGMAFIYHAFVFLVFGCLLSVFSTIPETKL 155
 DB 61 YTSQSCRNVKRYRVONYLVLERPRGMAFIYHAFVFLVFGCLLSVFSTIPETKL 120
 QY 156 ASSCLLIEFMYVFGLEFIIRIWSAGCCCRGMQGLRARRKFCVIDITVLASTA 215
 DB 121 ASSCLLIEFMYVFGLEFIIRIWSAGCCCRGMQGLRARRKFCVIDITVLASTA 180
 QY 216 VSAKTGGINATFATSLRSLRFQLIRMYMDRGGTWKLLGSVVAHSHKELITAWYIGFL 275
 DB 181 VSAKTGGINATFATSLRSLRFQLIRMYMDRGGTWKLLGSVVAHSHKELITAWYIGFL 240
 QY 276 VLISSFLVYVEKDKNEFSTYADALMWGTTTLTIGYGDTPPLTWLGLLSAGFALLG 335
 DB 241 VLISSFLVYVEKDKNEFSTYADALMWGTTTLTIGYGDTPPLTWLGLLSAGFALLG 300
 QY 336 ISFELPAGLIGSGFALVQEOHROKHFEKRRNPANLLQCVWRSYAADEKSVSIATWPK 395
 DB 301 ISFELPAGLIGSGFALVQEOHROKHFEKRRNPANLLQCVWRSYAADEKSVSIATWPK 360
 QY 396 HLKALHTCSPT-----NOKLSFERVNRMASPRGOSIKRSQASVGRDRSPSTDTAAE 446
 DB 361 HLKALHTCSPT-----NOKLSFERVNRMASPRGOSIKRSQASVGRDRSPSTDTAAE 420
 QY 447 GSPFVYQKSWSNDRTRRPSRLKSSQKPYVDADTALGTDVYDEKGGCCVSVVDLT 506
 DB 421 GSPFVYQKSWSNDRTRRPSRLKSSQKPYVDADTALGTDVYDEKGGCCVSVVDLT 480

QY 507 PPLKTVIRAIRIMKHFVAKRKKEETLRPYDVKDVIEOYSAGHLMCRISLQTRVDQIL 566
 DB 481 PPLKTVIRAIRIMKHFVAKRKKEETLRPYDVKDVIEOYSAGHLMCRISLQTRVDQIL 540
 QY 567 GKQILTSDKSRKRIKTAHEHTTDLMLGRVVEKVOVQSIKSLDCLDIYQOVLKRS 626
 DB 541 GKQILTSDKSRKRIKTAHEHTTDLMLGRVVEKVOVQSIKSLDCLDIYQOVLKRS 600
 QY 627 ASALALASFOIPPEEEOISDYOSPVDSKLSAQAQNSGLSRSTANISRGLOFILLPN 686
 DB 601 ASALALASFOIPPEEEOISDYOSPVDSKLSAQAQNSGLSRSTANISRGLOFILLPN 660
 QY 687 EFSAQEFYALSPMHGSOATQVPISSQSGVAATNTIANTOINPKRAAPTLLQIPPLP 746
 DB 661 EFSAQEFYALSPMHGSOATQVPISSQSGVAATNTIANTOINPKRAAPTLLQIPPLP 720
 QY 747 AIKHLRPETLHPNPAQLOESIDVYTCVLAASKENVOAQNLRKDSMRKSPDMGSETL 806
 DB 721 AIKHLRPETLHPNPAQLOESIDVYTCVLAASKENVOAQNLRKDSMRKSPDMGSETL 780
 QY 807 LSYCPWPKDGLKSLVQNLIRSTEEINQLSGSESSGSGSODFPYKWRKSLFTDEE 866
 DB 781 LSYCPWPKDGLKSLVQNLIRSTEEINQLSGSESSGSGSODFPYKWRKSLFTDEE 840
 QY 867 VGEPEETETFDAPAPARAEAFASDSLRTGRSSSOSICKAGSTALSLPHVKLK 923
 DB 841 VGEPEETETFDAPAPARAEAFASDSLRTGRSSSOSICKAGSTALSLPHVKLK 897

RESULT 2
 C105_MOUSE
 ID C105_MOUSE STANDARD; PRT: 878 AA.
 AC Q9JRK45;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 5 (Fragment).
 GN KCNQ5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RA Knazeva M., Han M.,
 RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
 RT Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 RL -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 CC EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
 CC WHICH CONTRIBUTES TO M-TYPE CURRENT. A SLOWLY ACTIVATING AND
 CC DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
 CC DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS.
 CC MAY CONTRIBUTE, WITH OTHER POTASSIUM CHANNELS, TO THE MOLECULAR
 CC DIVERSITY OF AN HETEROGENEOUS POPULATION OF M-CHANNELS, VARYING IN
 CC KINETIC AND PHARMACOLOGICAL PROPERTIES, WHICH UNDERLY THIS
 CC PHYSIOLOGICALLY IMPORTANT CURRENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ3 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -----
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DR EMBL; AF263836; AAF73447.1; -

DR HSSP; Q54397; 1BL8.

DR MGD; MGI:1924937; Kcnq5

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR003946; KCNQ1_channel.

DR InterPro: IPR003091; K_channel.

DR Pfam; PF00520; M+channel_nlg.

DR Pfam; PF03520; Ion_trans. 1.

DR PRINTS; PR00169; KCCHANNEL.

KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Multigene family.

FT TRANSMEM 72 92 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 103 123 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 147 167 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 176 198 SEGMENT S4 (POTENTIAL).

FT TRANSMEM 213 233 SEGMENT S5 (POTENTIAL).

FT DOMAIN 245 265 SEGMENT H5 (PORE-FORMING) (POTENTIAL).

FT TRANSMEM 272 292 SEGMENT S6 (POTENTIAL).

SEQUENCE 878 AA; 97029 MW; 35779FC7D630F55 CRC64;

Query Match Best Local Similarity 89.3%; Score 4227.5; DB 1; Length 878;

Matches 827; Conservative 14; Mismatches 27; Indels 9; Gaps 1;

55 GDCILLGTRATGGGGGGLRESRRGKOGAMSLGKPLSTSSQSCRNVYRRVQNY 114

1 GDGILLGTRAAALGGGGGGLRESRRGKOGAMSLGKPLSTSSQSCRNVYRRVQNY 60

115 LYNLEPRGMALYHAFVFLVFGCLLSYESTIPEHTKLASSCLILEFVIVFEGLE 174

61 LYNVLEPRGMALYHAFVFLVFGCLLSYESTIPEHTKLASSCLILEFVIVFEGLE 120

175 FLIRIMAGCCCRGRRGOGRRFARKPRCVITLYLISIAVYSAKTOGNIFATSLRSL 234

121 FLIRIMAGCCCRGRRGOGRRFARKPRCVITLYLISIAVYSAKTOGNIFATSLRSL 180

235 RFLQILRMVMDRRGRTGKTLGSLVYVAHSEKITAMYGELVLFSSFFVYVERKANKE 294

181 RFLQILRMVMDRRGRTGKTLGSLVYVAHSEKITAMYGELVLFSSFFVYVERKANKE 240

295 FSTYADALMWGTTLTITIGYGDKPTPLWGLRSLSGFALLGISFPALPAGILSGFALYV 354

241 FSTYADALMWGTTLTITIGYGDKPTPLWGLRSLSGFALLGISFPALPAGILSGFALYV 300

355 QEOHROKHFEKRRNPANLIQCVKRSYAADKSVSIATWPKHLKALHTCSPT----- 406

301 QEOHROKHFEKRRNPANLIQCVKRSYAADKSVSIATWPKHLKALHTCSPTKKDEGAS 360

407 -NOKLSFEKRVNMA SPRGOSIKSROASVGDPRSPTDTAAGSPKRYOKSWGFNDRTPR 465

361 SSOKLSFEKRVNMA SPRGOSIKSROASVGDPRSPTDTAAGSPKRYOKSWGFNDRTPR 420

466 PSRLRLKSSQPKPYIDADTALGTDVYDEKGCOCVSVEDLTPRLKTVIRAIRIMKEHVAK 525

421 PSRLRLKSSQPKPYIDADTALGTDVYDEKGCOCVSVEDLTPRLKTVIRAIRIMKEHVAK 480

526 RRFKETLRPYDVADVEYOYSAGHLDMLCRISLQTRVDOLIGKQOMTSDDKSREKITAHEH 585

481 RRFKETLRPYDVADVEYOYSAGHLDMLCRISLQTRVDOLIGKQOMTSDDKSREKITAHEH 540

586 EPTDLSMLGRVYKVKVQVIESKIDCLDIYQOVLARKGSASALALASFOIPRECEQOT 645

541 EPTDLSMLGRVYKVKVQVIESKIDCLDIYQOVLARKGSASALALASFOIPRECEQOT 600

646 SDYSPVDSKDLGSGNONGSCLSRSSANISRGLOFLTPNEFSAOFTFALSPTMHSQAT 705

601 SDYSPVDSKDLGSGNONGSCLSRSSANISRGLOFLTPNEFSAOFTFALSPTMHSQAT 660

QY 706 QVPISODGSAVAATNTIANQINTAPKPAFTTLQIPRLPAIKHLRPRELHPRLDAGLO 765

DB 661 QVPMSONDSSSVATNTNINANOISAPKPAFTTLQIPPLSAIHLSPRLSPMTGLQ 720

QY 766 ESISDVTTCLVASKENVOVAQSNLTKDRSNKRSFDMGGETLLSYCPMPKDLGKSLSYON 825

DB 721 ESISDVTTCLVASKENVOVAQSNLTKDRSNKRSFDMGGETLLSYCPMPKDLGKSLSYON 780

QY 826 LIRSTPEELNIQOLSGSSSGSGSGSODFPKPKRESKLTFTDEVGEEFTETDFDAAPQPAR 885

DB 781 LIRSTPEELNIQOLSGSSSGSGSGSODFPKPKRESKLTFTDEVGEEFTETDFDCTPPVAG 840

QY 886 EAAFAASDSLRTGSRSSQSGICKAGESTDALSLPHVKL 922

DB 841 EAAFAASDSLRTGSRSSQSGICKAGESTDALSLPHVKL 877

RESULT 3

C104_HUMAN

ID C104_HUMAN STANDARD; PRT; 695 AA.

AC P56696; O96025;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Voltage-gated potassium channel protein KCOT-like 4.

GN KCNQ4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_Taxid=9606;

RA El Amraoui A., Marlin S., Petit C., Jentsch T.J.;

RT "KCNQ4, a novel potassium channel expressed in sensory outer hair cells, is mutated in dominant deafness.";

RL Cell 96:437-446(1999).

[2]

RP INHIBITION BY M1 MUSCARINIC RECEPTORS.

RX MEDLINE=20176300; PubMed=10713961;

RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J., Brown D.A.;

RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells via M1 muscarinic acetylcholine receptors.";

RL J. Physiol. (Lond) 522:349-355(2000).

[3]

RP PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.

RX MEDLINE=21143874; PubMed=11245603;

RA Soegaard R., Ljungstrom T., Pedersen K.A., Olesen S.-P., Jensen B.S.;

RT "KCNQ4 channels expressed in mammalian cells: functional characteristics and pharmacology.";

RL Am. J. Physiol. 280:C859-C866(2001).

[4]

RP VARIANTS DFNA2 SER-276; CVS-285 AND SER-321.

RX MEDLINE=99299248; PubMed=10369879;

RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattman I., Van Velzen D., Meyers J., Ensink R.J., Verstrecken M., Declau F., Marres H., Kastury K., Bhasin S., McGill W.T., Smith R.J.H., Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D., Van Camp G.;

RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant deafness in four DFNA2 families.";

RL Hum. Mol. Genet. 8:1321-1328(1999).

[5]

RP VARIANT DFNA2 SER-281.

RX MEDLINE=20040027; PubMed=10571947;

RA Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;

RT "Novel mutation in the KCNQ4 gene in a large kindred with dominant progressive hearing loss.";

RL Hum. Mutat. 14:493-501(1999).

[6]

RP VARIANT DENA2 HIS-274
 RX MEDLINE-2038752; PubMed-10925378;
 RA Van Hauwe P., Coucke P.J., Enslin R.J., Huygen P., Cremers C.W.R.J.,
 RA Van Hauwe P., Coucke P.J., Enslin R.J., Huygen P., Cremers C.W.R.J.,
 RT "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal
 RT dominant hearing loss, cluster in the channel pore region.";
 RL Am. J. Med. Genet. 93:184-187(2000)
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 CC EXCITABILITY. MAY UNDERLIE A POTASSIUM CURRENT INVOLVED IN
 CC REGULATING THE EXCITABILITY OF SENSORY CELLS OF THE COCHLEA. KCNQ4
 CC CHANNELS ARE BLOCKED BY LINOPIRIDIN, XE991 AND BEPRIDIL, WHEREAS
 CC CLOXOREMORINE-H STRONGLY SUPPRESS KCNQ4 CURRENT IN CHO CELLS IN
 CC WHICH CLONED KCNQ4 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINIC
 CC RECEPTORS.
 CC -1- SUBUNIT: MAY FORM HETEROMULTIMERS WITH KCNQ3.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SITUATED AT THE
 CC BASAL MEMBRANE OF COCHLEAR OUTER HAIR CELLS (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
 CC SENSORY HAIR CELLS OF THE COCHLEA. SLIGHTLY EXPRESSED IN HEART,
 CC BRAIN AND SKELETAL MUSCLE.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF NONSYNDROMIC
 CC SENSORINEURAL DEAFNESS TYPE 2 (DFNA2), AN AUTOSOMAL DOMINANT FORM
 CC OF PROGRESSIVE HEARING LOSS.
 CC -1- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT BY
 CC EXPRESSING IN XENOPUS OOCYTES KCNQ4 MUTANTS EITHER INDIVIDUALLY
 CC (HOMOMULTIMERS) OR IN COMBINATION WITH WILD-TYPE KCNQ4 (MUT/WT
 CC HOMOMULTIMERS) IN A RATIO OF 1:1. TO MIMIC THE SITUATION IN A
 CC HETEROZYGOTIC DFNA2 PATIENT.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -1- DATABASE: NAME-Hereditary hearing loss homepage;
 CC NOTE-Genes page:
 CC WWW-<http://www.uia.ac.be/dnablab/hhh/hhgenes.html>.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL: AF105202; AAD14680.1; -
 DR EMBL: AF105216; AAD14681.1; -
 DR EMBL: AF105203; AAD14681.1; JOINED.
 DR EMBL: AF105204; AAD14681.1; JOINED.
 DR EMBL: AF105205; AAD14681.1; JOINED.
 DR EMBL: AF105206; AAD14681.1; JOINED.
 DR EMBL: AF105207; AAD14681.1; JOINED.
 DR EMBL: AF105208; AAD14681.1; JOINED.
 DR EMBL: AF105209; AAD14681.1; JOINED.
 DR EMBL: AF105210; AAD14681.1; JOINED.
 DR EMBL: AF105211; AAD14681.1; JOINED.
 DR EMBL: AF105212; AAD14681.1; JOINED.
 DR EMBL: AF105213; AAD14681.1; JOINED.
 DR EMBL: AF105214; AAD14681.1; JOINED.
 DR EMBL: AF105215; AAD14681.1; JOINED.
 DR HSSP: O54397; 1BL8.
 DR GeneW: HGNC:6298; KCNQ4.
 DR MIM: 603537; -
 DR MIM: 600101; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF03520; KCNQ1_channel; 1.

DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel: Transmembrane: Ion transport; Voltage-gated channel;
 KW Multigene family: Disease mutation: Deafness: Alternative splicing.
 FT TRANSMEM 98 118 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 132 152 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 173 193 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 202 224 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 238 258 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 271 292 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 297 317 SEGMENT S6 (POTENTIAL).
 FT VARSPLIC 378 431 MISSING (IN ISOFORM 2).
 FT VARIANT 274 274 L -> H (IN DENA2).
 FT VARIANT 276 276 W -> S (IN DENA2).
 FT VARIANT 281 281 L -> S (IN DENA2).
 FT VARIANT 285 285 L -> S (IN DENA2).
 FT VARIANT 285 285 /FTID=VAR_010937.
 FT VARIANT 285 285 /FTID=VAR_008727.
 FT VARIANT 285 285 G -> S (IN DENA2).
 FT VARIANT 321 321 /FTID=VAR_001547.
 FT VARIANT 321 321 G -> S (IN DENA2).
 FT MUTAGEN 285 285 /FTID=VAR_008728.
 FT 285 G->S: NO CURRENT (HOMOMULTIMERS); 90% WT
 FT CURRENT REDUCTION (MU/WT HOMOMULTIMERS).
 SQ SEQUENCE 695 AA; 77091 MW; A58737BD845E1A3A CRC64;
 Query Match 42.1%; Score 1991; DB 1; Length 695;
 Best Local Similarity 57.8%; Pred. No. 4.1e-108;
 Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;
 25 AAAGGRLGSGMDESGRVLNLSAARGLLGLTTRATLTGGGGGGLRESNRKGG 84
 2 AEAPRRRLGGLPPGDAFRAELVALTAVQSRG-----EAGGGSPR----- 43
 85 ARMSLLGKPL-----SYSSGSCRNNKRYRQNTLYNLEPRGNAFTYH 130
 44 -RLGLGSLPLPGCAPLDPGSGSGSAGCGRSSAHRKRYRQNTLYNLEPRGNAFTYH 102
 131 AFPEFLVFGCLLSVFSTPEHTLASGCLLLEFVMVLVGLFTIRFMSAGCCRYRG 190
 103 VFPEFLVFGCLLSVFSTPEHTLASGCLLLEFVMVLVGLFTIRFMSAGCCRYRG 162
 191 MGRRLRRARRPFCYDITVLVLAIVSAKTQGNIFATLSALSLRFLQILRMVRMDRGG 250
 163 MGRFRARRPFCYDITVLVLAIVSAKTQGNIFATLSALSLRFLQILRMVRMDRGG 222
 251 TWKLLGSVVYAAHAKSELITAMTIGFLVLIFFSFLVLYVERKDANKERSTYADALMGTYLT 310
 223 TWKLLGSVVYAAHAKSELITAMTIGFLVLIFFSFLVLYVERKDANKERSTYADALMGTYLT 282
 311 TIGYGDTPPLTWLGRLLSAGFALLGISFPFALGSGFALKYOEORHOKHFERRRNPA 370
 283 TIGYGDTPPLTWLGRLLSAGFALLGISFPFALGSGFALKYOEORHOKHFERRRNPA 342
 371 ANLTQCYWRSYAAD-EKSVSIATW----- 393
 343 ANLTQCYWRSYAAD-EKSVSIATW----- 402
 394 -----KHLKALHT-----CSPTNOKISFEFERRMSAPROGISTSRQ--ASVGR 436
 403 PVPDAPSRYPPVATCHRRPGSTSFPGSSRRGIRDRIMSSQRRTGSGKQOLAPPIYMP 462
 437 RSPNDITAEQ-SPTKYQKSMNSFNDRTRFRPSLRKSSQKPEVIDADTALGTDVYDEKG 495
 463 TSPSEQGEATSPKYQKSMNSFNDRTRFRPSLRKSSQKPEVIDADTALGTDVYDEKG 516
 496 CQCVSVEDLTPLPKTVIRAIRIMKFFHAKKRFKELTRYDYKVDYEOYSAGHIDMLCRL 555
 517 YQCELTVDIDIMPAVKTVIRISIRILKFLVAKRKFELTRYDYKVDYEOYSAGHIDMLCRL 576
 556 KSIQTRVDQILGKGITSDKRSRE---KTAHETTTDLISMLGRVYKVKOVQSIKSLD 612

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Db 577 KSLQTRVQIVRG--PGRRKAREKCDKGPDAEYVDEISMGMGRVYVEKQVSIENKLD 634
QY 613 CLUDYQOVLKRSASALALSPQIPFCEORTSDOSPDSDSLSSAQNQSGLSRST 672
Db 635 LLGAYVSCILRGSTGA--SLGAVQVLEFPDITSDHSPVDHEDISVSAQTLISRSVS 691
QY 673 ANI 675
Db 692 TMM 694

RESULT 4
C102_RAT STANDARD: PRT: 852 AA.
AC 088943;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 2.
GN KCNQ2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RN Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA MEDLINE=20493350; PubMed=11038262;
RN Jow F., Wang K.-W.;
RT "Cloning and functional expression of rKCNQ2 K(+) channel from rat
brain.";
RL Brain Res. Mol. Brain Res. 80:269-278(2000).
[3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Sympathetic ganglion;
RA MEDLINE=21154288; PubMed=11230508;
RN Pan Z., Selyanko A.A., Hadley J.K., Brown D.A., Dixon J.E.,
McKinnon D.;
RT "Alternative splicing of KCNQ2 potassium channel transcripts
contributes to the functional diversity of M-currents.";
RL J. Physiol. (Lond) 531:347-358(2001).
[4]
RP TISSUE SPECIFICITY.
RA MEDLINE=99055398; PubMed=9836639;
RN Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
the M-channel.";
RL Science 282:1890-1893(1998).
-1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING
THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE
RESPONSIVENESS TO SYNAPTIC INPUTS. KCNQ2 CURRENT IS BLOCKED BY
BARIUM AND TETRAETHYLAMMONIUM WHEREAS 4-AMINOPIPERIDINE AND
CHARYBDOXIN HAVE NO EFFECT ON KCNQ2 CURRENT. TYROSINE KINASE
INHIBITORS GENSTEIN OR HERBIMYCIN A MARKEDLY DOWN-REGULATE KCNQ2
CURRENT. MUSCARINIC AGONIST OXOTREMORINE-M SUPPRESSED KCNQ2/KCNQ3
CURRENT IN CHO CELLS IN WHICH CLONED KCNQ2/KCNQ3 CHANNELS WERE
COEXPRESSED WITH HUMAN M1 MUSCARINIC RECEPTORS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS: 9 isoforms; A (shown here), splice isoforms
G, H and I; are produced by alternative splicing, splice isoforms
fell into three classes, those that contain an in frame exon 16

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CC (Isoforms A-I) those that contain an out-of-frame exon 16 due to
CC an alternative splice junction in exon 14 and those that terminate
CC prematurely to exon 16. Only the forms containing an in frame exon
CC 16 are able to form functional channels. A similar splice pattern
CC is also produced for splice variants that contain an out-of-frame
CC exon 16. A wide variety of different truncated isoforms were
CC isolated for splice variants that terminate prematurely to exon
CC 16.
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SYMPATHETIC GANGLIA. IN
CC BRAIN, EXPRESSED IN CORTEX, HIPPOCAMPUS, AND CEREBELLUM. IN
CC SYMPATHETIC GANGLIA, EXPRESSED AT LOWER LEVELS IN CELIAC GANGLIA
CC AND SUPERIOR MESENTERIC GANGLIA THAN IN SUPERIOR CERVICAL GANGLIA.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1- MISCELLANEOUS: WHEN CO-EXPRESSED WITH KCNQ3 SUBUNIT IN CHO CELLS
CC OR XENOPUS OOCYTES, ISOFORM B WAS FOUND TO HAVE SIGNIFICANTLY
CC DIFFERENT DEACTIVATION-ACTIVATION KINETICS. THE KINETICS WAS 2.5
CC TIMES MORE SLOWLY THAN THE KINETICS OF OTHER ISOFORMS. THE
CC PRESENCE OF EXON 15A IN ISOFORM B ACCOUNTS FOR THE SLOW
CC DEACTIVATION-ACTIVATION KINETICS. ALTERNATIVE SPLICING OF THE
CC KCNQ2 GENE MAY CONTRIBUTE TO THE VARIATION IN M-CURRENT KINETICS
CC SEEN IN VIVO.
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
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DR EMBL: AF087453; AAC36722.1;
DR HSSP: 054397; 1BL8.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF005020; Ion_trans_1.
DR Pfam: PF03520; KCNQ1_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Multigene family; Phosphorylation; Alternative splicing.
FT TRANSMM 92 112 SEGMENT S1 (POTENTIAL).
FT TRANSMM 123 143 SEGMENT S2 (POTENTIAL).
FT TRANSMM 167 187 SEGMENT S3 (POTENTIAL).
FT TRANSMM 198 221 SEGMENT S4 (POTENTIAL).
FT TRANSMM 232 252 SEGMENT S5 (POTENTIAL).
FT DOMAIN 265 285 SEGMENT H5 (POTENTIAL).
FT TRANSMM 292 312 SEGMENT H6 (POTENTIAL).
FT MOD_RES 52 52 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT VARSPPLIC 373 382 MISSING (IN ISOFORM C, ISOFORM F AND
FT ISOFORM H).
FT VARSPPLIC 416 416 S -> SKRRPGCGLCGRRGHS (IN ISOFORM D,
FT ISOFORM E, ISOFORM F AND ISOFORM H).
FT VARSPPLIC 417 428 MISSING (IN ISOFORM B).
FT VARSPPLIC 491 491 MISSING (IN ISOFORM D, ISOFORM F AND
FT ISOFORM I).
FT VARSPPLIC 571 571 R -> RIDMIVGPPPTSRHKYTPKGPAPRSPQYSP
FT R (IN ISOFORM B AND ISOFORM G).
SQ SEQUENCE 852 AA; 93949 MW; 8255FE625AF259A CRC64;

Query Match 38.1%; Score 1805.5; DB 1; Length 852;
Best Local Similarity 47.8%; Pred. No. 3e-97;
Matches 418; Conservative 100; Mismatches 209; Indels 147; Gaps: 23;

QY 21 GAAAGGAGGGLGSGMKVSGRGVYLNSAARGDGLLGTGRAATLGGGGGLESRR 80
Db 9 GYVPGTSGEKKLVGFVGLDPCA-----PSTRGALILASGEAPK---RGSVLSKPR 59
QY 81 GKQGARSLGKPLPSTYSQSCRRVVKYRVONYLYNVERGMAFYTHAFVLLVFGC 140
Db 60 GGACA-----GKP-----PKRNATYKRLQNLNLYNVERGMAFYTHAFVLLVFC 106

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QY 141 LITVSTIEPHKIKASSCLLIEFVMIYVEGLEFIRMSAGCCCRGMGRRLRFARK 200
 DB 107 LTVSVSTIEKREKSSGALYILEITVTVFVGVFVRIMAGCCCRGRMRGRKLFARK 166
 QY 201 PFCVIDITVLIASIAVAVSAKTOGNIFATSLARLFLIOILMVRMDRGRGTWKLGSVYV 260
 DB 167 PFCVIDIMVLASIAVLAAGSOGVAFATSLARLFLIOILMVRMDRGRGTWKLGSVYV 226
 QY 261 AHSKELITANYIGFVLVIESSFLVYLVKDKANKEFSITYADALMGTITLTITIGYDQPL 320
 DB 227 AHSKELITANYIGFVLVIESSFLVYLVKDKANKEFSITYADALMGTITLTITIGYDQPL 286
 QY 321 TWIGRLISAGFALIGSFALIPAGILSGFALKVOEORHOFKERRRPAANLIGCVMS 380
 DB 287 TWIGRLISAGFALIGSFALIPAGILSGFALKVOEORHOFKERRRPAANLIGCVMS 346
 QY 381 YAADEKSVSI-ATWK-----PHLKALHTC----- 403
 DB 347 YATNLSTDLHSTWQYERTVTPMISQOTOTYGASRLIPPLNQLMRLNLSKSGLTFR 406
 QY 404 -----SPTNOLISFEKERVMASSPRGOSIKSQAASVD--RRSPTDITAGSFTKYOK 454
 DB 407 KEPQPEPSP-SOKVSLKDRV-FSSPRGVAAKKGSPQAQTVRRSPSADQSLDSDSPKYPK 464
 QY 455 SMSFNDTRRPRSLRLKSSQPKVITADTALGTDDVDYDEKGGCCVSVEDLTPPLKTIVR 514
 DB 465 SMSFNDTRRPRSLRLKSSQPKVITADTALGTDDVDYDEKGGCCVSVEDLTPPLKTIVR 524
 QY 515 AIRMKFHVAKRKKEKTLRPYDVADVIEQYSGHLMCLRLKSLQTRVQDLIGKQITSD 574
 DB 525 AVCMRRLVLSKRRKESRLRPDVADVIEQYSGHLMCLRLKSLQTRVQDLIGKQITSD 584
 QY 575 KKSREKTTAEHTTDDLSMLGRVYKVEKOVOSIESKLDCLDIYQVLRKGSASALALAS 634
 DB 585 -KQTKRPAETLEPDESMGRKLVKVEKOVLSMEKKLDLFIYSITYQ--RMG----- 632
 QY 635 FOJPFPC-----EQTSQSPYVSKDLSGSAONSQC-----LSRSTANISRLQFT 682
 DB 633 --IPPAETEAIFYGAKKEPPAPYHSPEDSRD---HADHGCLIKIKYRSTSS----- 678
 QY 683 LTPNEFSQOTFYALSPTHSQATQVPIQSODGSAVAANTJANQINTAPKPAAPTLQIP 742
 DB 679 -----TGQRKYAAPVPM--PPAECPPSTSS-----WQOSHQRHGTSPVGHGSLVRIP 723
 QY 743 PPLPAIKHLPRPELHNPALQESISDYTCIVASKENVOYAQSNLTR--DRSMKSPD 800
 DB 724 PP-----PAH-ERLSLAYSGGNRASTEFRLLEGTPACRPSAALRDS-- 764
 QY 801 MGETLLVCPMPKDLGKSLSYONLIRSTEELN 834
 DB 765 ---DTSISIPSVDHLELRSFSGPSISQSKENLN 795
 RESULT 5
 CIO2_HUMAN STANDARD: PRT: 872 AA.
 AC 043526: 099454: 043796: 095845: 075580: Q96559;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein KOT-1like 2 (Neuroblastoma-
 specific potassium channel protein).
 GN KCNQ2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE=Neuroblastoma;
 RA MEDLINE=97191543; PubMed=9039501;
 RA Yokoyama M., Nishi Y., Yoshii J., Okubo K., Matsubara K.;

RT "Identification and cloning of neuroblastoma-specific and nerve
 RT tissue-specific genes through compiled expression profiles.";
 RL DNA Res. 3:311-320(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS BPNC1 C-284 AND T-306.
 RC TISSUE=Brain, fetal brain, and Temporal cortex;
 RX MEDLINE=98085864; PubMed=9425895;
 RA Singh N.A., Charlier C., Stauffer D., Dupont B.R., Leach R.J.,
 RA Melis R., Ronen G.M., Bjerre I., Quatlebaum T., Murphy J.V.,
 RA Meharg M.L., Gagnon D., Rosales T.O., Peiffer A., Anderson V.E.,
 RA Leppert M.;
 RT "A novel potassium channel gene, KCNQ2, is mutated in an inherited
 RT epilepsy of newborns.";
 RL Nat. Genet. 18:25-29(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=fetal brain;
 RX MEDLINE=98092527; PubMed=9430594;
 RA Biervert C., Schroeder B.C., Kubisch C., Berkovic S.F., Propping P.,
 RA Jentsch T.J., Steinlein O.K.;
 RT "A potassium channel mutation in neonatal human epilepsy.";
 RL Science 279:403-406(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC MEDLINE=99053398; PubMed=9836339;
 RX Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
 RA Dixon J.E., McKinnon D.;
 RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
 RT the M-channel.";
 RL Science 282:1890-1893(1998).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 5).
 RX MEDLINE=99043242; PubMed=9827540;
 RA Tinel N., Jauritzen I., Chouabe C., Lazdunski M., Borsotto M.;
 RT "The KCNQ2 potassium channel: splice variants, functional and
 RT developmental expression. Brain localization and comparison with
 RT KCNQ3.";
 RL FEBS Lett. 438:171-176(1998).
 RN [6]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC TISSUE=Brain, and fetal brain;
 RX MEDLINE=98344027; PubMed=9677560;
 RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
 RA Neubauer M.G., Blamir M.A.;
 RT "Functional expression of two KvLOT1-related potassium channels
 RT responsible for an inherited idiopathic epilepsy.";
 RL J. Biol. Chem. 273:19419-19423(1998).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=21114072; PubMed=11160379;
 RA Smith J.S., Iannotti C.A., Dargis P.G., Christian E.P., Aiyar J.;
 RT "Differential expression of KCNQ2 splice variants: implications to M
 RT current function during neuronal development.";
 RL J. Neurosci. 21:1096-1103(2001).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE=Eye;
 RA Strausberg R.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP MOTAGENESIS OF SER-52; GLY-279 AND TYR-284.
 RX MEDLINE=99087323; PubMed=9872318;
 RA Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
 RT "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
 RT channels causes epilepsy.";
 RL Nature 396:687-690(1998).
 RN [10]
 RP INVOLVEMENT IN M-LIKE CURRENT.
 RX MEDLINE=99410758; PubMed=10479678;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
 RA Buckley N.J., London B., Brown D.A.;
 RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to

RT the M-like current in a mammalian neuronal cell.";
 RL J. Neurosci. 19:7742-7756(1999).
 RN [11]
 RP ASSOCIATION WITH KCNE2.
 RX MEDLINE=20487128; PubMed=11034315;
 RA Tinel N., Dichter S., Lauritzen I., Barhanin J., Lazdunski M.,
 RT Borsoello M.;
 RN "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
 subunit.";
 RL FEBS Lett. 480:137-141(2000).
 RN [12]
 RP SURFACE EXPRESSION OF HETEROMERS.
 RX MEDLINE=20250883; PubMed=10788442;
 RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
 RT "Surface expression and single channel properties of KCNQ2/KCNQ3,
 J. Biol. Chem. 275:13343-13348(2000).
 RN [13]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20150152; PubMed=10684873;
 RA Shapiro M.S., Roche J.P., Kafan E.J., Cruzblanca H., Mackie K.,
 RT Hill B.;
 RN "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+) channels that underlie the neuronal M current.";
 RL J. Neurosci. 20:1710-1721(2000).
 RN [14]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE=20178300; PubMed=10713961;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
 RT Brown D.A.;
 RN "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells via M1 muscarinic acetylcholine receptors.";
 RL J. Physiol. (Lond) 522:349-355(2000).
 RN [15]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20368587; PubMed=10908292;
 RA Main M.J., Cayan J.E., Dupre J.R., Cox B., Clare J.J., Burbridge S.A.;
 RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant retigabine.";
 RL Mol. Pharmacol. 58:253-262(2000).
 RN [16]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20411474; PubMed=10953053;
 RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
 RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3 potassium channels.";
 RL Mol. Pharmacol. 58:591-600(2000).
 RN [17]
 RP ACTIVATION BY RETIGABINE.
 RX MEDLINE=20180045; PubMed=10713399;
 RA Rundfeldt C., Netzer R.;
 RT "The novel anticonvulsant retigabine activates M-currents in Chinese hamster ovary-cells transfected with human KCNQ2/3 subunits.";
 RL Neurosci. Lett. 282:73-76(2000).
 RN [18]
 RP TISSUE DISTRIBUTION, AND BIOCHEMICAL CHARACTERIZATION.
 RX MEDLINE=20234795; PubMed=10781098;
 RA Cooper E.C., Aldade K.D., Abosch A., Barbaro N.M., Berger M.S.,
 RT Peacock W.S., Jan Y.N., Jan L.Y.;
 RN "Colocalization and coassembly of two human brain M-type potassium channel subunits that are mutated in epilepsy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4914-4919(2000).
 RN [19]
 RP VARIANT THR-780.
 RX MEDLINE=99254826; PubMed=10323247;
 RA Bievart C., Steinlein O.K.;
 RT "Structural and mutational analysis of KCNQ2, the major gene locus for benign familial neonatal convulsions.";
 RL Hum. Genet. 104:234-240(1999).
 RN [20]
 RP VARIANT BFNC1 TRP-214.
 RX MEDLINE=21037661; PubMed=11175290;
 RA Miraglia del Giudice E., Coppola G., Scuccimarra G., Cirillo G.,

RA Bellini G., Pascotto A.;
 RT "Benign familial neonatal convulsions (BFNC) resulting from mutation of the KCNQ2 voltage sensor.";
 RL Eur. J. Hum. Genet. 8:994-997(2000).
 RN [21]
 RP FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING THE NATIVE M-CURRENT. A SLOWLY ACTIVATING AND DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE RESPONSIVENESS TO SYNAPTIC INPUTS. KCNQ2/KCNQ3 CURRENT IS BLOCKED BY LINOPIRINE AND XE991, AND ACTIVATED BY THE ANTICONVULSANT RETIGABINE. MUSCARINIC AGONIST OXOBORONINE-M STRONGLY SUPPRESSES KCNQ2/KCNQ3 CURRENT IN CELLS IN WHICH CLODED KCNQ2/KCNQ3 CHANNELS WERE COEXPRESSED WITH M1 MUSCARINIC RECEPTORS.
 CC SUBUNIT: HETEROMULTIMER WITH KCNQ3. MAY ASSOCIATE WITH KCNE2.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS: 1 (SHOWN HERE), 2, 3, 4, 5 AND 6/HNSPC; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN ADULT AND FETAL BRAIN. HIGHLY EXPRESSED IN AREAS CONTAINING NEURONAL CELL BODIES, LOW IN SPINAL CHORD AND CORPUS CALLOSUM. ISOFORM 2 IS PREFERENTIALLY EXPRESSED IN DIFFERENTIATED NEURONS, WHEREAS ISOFORM 6 IS PROMINENT IN FETAL BRAIN, UNDIFFERENTIATED NEUROBLASTOMA CELLS, AND BRAIN TUMORS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- PTM: IN XENOPUS OOCYTES KCNQ2/KCNQ3 HETEROMERIC CURRENT CAN BE INCREASED BY INTRACELLULAR CYCLIC AMP, AN EFFECT THAT DEPENDS ON PHOSPHORYLATION OF SER-52 IN THE AMINO TERMINUS REGION.
 CC -1- DISEASE: DEFECTS IN KCNQ2 ARE THE CAUSE OF BENIGN FAMILIAL NEONATAL CONVULSIONS TYPE 1 (BFNC1); ALSO KNOWN AS EPILEPSY BENIGN NEONATAL TYPE 1 (EBN1); BFNC1 IS AN AUTOSOMAL DOMINANT FORM OF EPILEPSY IN THE NEWBORN THAT CLEARS SPONTANEOUSLY AFTER A FEW WEEKS AND IS FOLLOWED BY NORMAL PSYCHOMOTOR DEVELOPMENT.
 CC -1- MISCELLANEOUS: INCLUSION OF ISOFORM 6 IN HETEROMULTIMERS RESULTS IN ATTENUATION OF POTASSIUM CURRENT. PROMINENT EXPRESSION OF

Query Match 37.7% Score 1784; DB 1; Length 872;
 Best local similarity 46.8%; Pred. NO. 5.4e-96;
 Matches 411; Conservative 92; Mismatches 196; Indels 180; Gaps 25;

21 GAAAAAGGRLGSGNKGVRGRLVLSNAAAGDGLLGTAAATLGGGGGLRESRR 80
 9 GYVPEPSGKKLVGVGVDPGA-----PDSIRDGLALLAGSAPK---RGSILSKPRA 59
 81 GKQGRMSLLGKPLSTSSQSCRNVKRRVNYLVNLERPGMAFIYHAFVFLVFGC 140
 60 GGAGA-----GKP-----PKRNAFYKRLQNFVLERPRGMAFIYHAYVFLVESC 106
 141 LILSVFTPEHTKLASSCLLLEFPMIVGEGLEFIIRMSAGCCCGYRGMGRLRARK 200
 107 LVLVSFTIKEYKESGALYILEVTIVFGEYEVYRMAACCCCHYRGMGRGLKARK 166
 201 PFCVVDITVLASIVASAKTOGNFATSAIRSLRELQILRMVMDRGRGTWKLIGSVVY 260
 167 PFCVIDIWLASIVASIVLAAGSGNVFATSAIRSLRELQILRMVMDRGRGTWKLIGSVVY 226
 261 AHSKELTAWYIGFLVLFSSFLVLYVERDKANKESTYADALMWGTTTLTIGYGDTP 320
 227 AHSKELTAWYIGFLVLFSSFLVLYVERDKANKESTYADALMWGTTTLTIGYGDTP 286
 321 TWLGRILSAGFALGILSFPALPAGILSGFALKVQSOHQKHEKRRNPANLITQCVWS 380
 287 TWNGRLAATITLIGVSFFALPAGILSGFALKVQSOHQKHEKRRNPANLITQCVWS 346
 381 YAAD-----EKSVSIATWK-----PHKALHT-----402
 347 YATNLSRTDLSTWQYERTVIVPMVSSQOTQYTGASRLPLPLQDLRLNLKSKSGIAFR 406
 403 -----CSP--TNOKLSFEKVENRNASPGQSTKSKQASVGD--RR 437
 407 KDPPPEPSKSGSPCRGPLCGCCPGRSQKSVLSIKDRV--FSSPRGVAAKGSGPOAQTVRR 465

QY	438	SPSNDITTEGSEPTKOKMSFNDIRFRSLRSLSSOPRYADIALATGDYUDEKGC	497
Dd	466	SPSADOSIEDPSKYPKMSFECDRSRAKAFIKGAASQNSE-EASLFGEDLVDDKSCP	524
QY	498	CDVASEDDLTPPLKITIVAIRIIMKFHVAKRKRETELAPRVUDKVIEGYSGNHLMLCRKS	557
Dd	525	CEVFATEDLTGLTKISAVISARCVAMRFVLSKRKFRESLEPRVDUMDVIIEGYSAGHLDMLSRKS	584
QY	558	LQTRVDOLLGGQOITSDDKSKREKTIAENHTTDDLSMGRVVUYEKVOVSIESKLDCILD	617
Dd	585	LQSRVDQTVGRRPATTD-KDRFKGRAEALPEDPBSMWIGKEVLGYEKVULSMERKLDELVTNI	643
QY	618	YOQVLYRKSSAALALASFQIPPEC-----EGTSOYQSVPVSDKDLSGSANSGCLS	668
Dd	644	YMO-----IPPLETBATYGAKERPARPYRHSHEDSRE---HYDRNGCIV	687
QY	669	RSTSANISRGLQFIILTPNEFSAQOTFYVALSPTHMSQAOTVPISOS-----DGSAAVAAT	720
Dd	688	KIVSSSSSTG-----QKNFSAP--AAPR-----VQORPRTSWQPNHRQGNGHSRV	733
QY	721	NTIANQITARKRAPFTLIQT-----PP-----PLPAT	748
Dd	734	GDHGSLVLRIPPAHERSLSAVGGNRASMEFLROEDTCRCRPREGNLRDSDTSLSPSV	793
QY	749	KHLRPERTLHPNPAGLOESIDVTTCVLAASKENUVAOAS	787
Dd	794	DH-----ELERSFGCF--SISO-----SKETDLALNS	819

```

RESULT 6
C102_MOUSE
ID C102_MOUSE STANDARD: PRT: 759 AA.
AC Q9Z351: Q9Z350; Q9Z349; Q9Z348; Q9Z347; Q9Z346; Q9Z345; Q9Z344;
AC Q9Z343; Q9QW9; Q9Z342;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 2.
GN KCNQ2 OR KQT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 TO 11).
RC TISSUE=Brain;
RX MEDLINE=98330948; PubMed=9666519;
RA Nakamura M., Watanabe H., Kubo Y., Yokoyama M., Matsumoto T.,
RA Sasaki H., Nishi Y.;
RT "KQT2, a new putative potassium channel family produced by alternative
RT splicing. Isolation, genomic structure, and alternative splicing of
RT the putative potassium channels."
RL Recept. Channels 5:255-271(1998).
RN [2]
RP ROLE IN NEURAL HYPEREXCITABILITY.
RX MEDLINE=20312851; PubMed=10854243;
RA Watanabe H., Nagata E., Kosakal A., Nakamura M., Yokoyama M.,
RA Tanaka K., Sasaki H.;
RT "Disruption of the epilepsy KCNQ2 gene results in neural
RT hyperexcitability."
RL J. Neurochem. 75:28-33(2000).
CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNQ3 TO FORM A POTASSIUM CHANNEL
CC WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING
CC THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
CC POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
CC THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THEIR
CC RESPONSIVENESS TO SYNAPTIC INPUTS.
CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ3.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 11 ISOFORMS, ISOFORM 1/KQT2.1 (SHOWN HERE),
CC 2/KQT2.2, 3/KQT2.3, 4/KQT2.4, 5/KQT2.5, 6/KQT2.6, 7/KQT2.7,

```

[illegible]

[illegible]

15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-gated potassium channel protein KQT-like 3.
KCNO3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-310 AND GLY-318.
TISSUE=Brain;
MEDLINE=99087323; PubMed=9872318;
Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
"Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
channels causes epilepsy.";
Nature 396:687-690(1998).
[2]
SEQUENCE OF 48-872 FROM N.A., AND VARIANT EBN2 VAL-310.
TISSUE=Brain;
MEDLINE=98085869; PubMed=9425900;
Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J.,
Leppert M.;
"A pore mutation in a novel KQT-like potassium channel gene in an
idiopathic epilepsy family";
Nat. Genet. 18:53-55(1998).
[3]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
TISSUE=Brain, and Fetal brain;
MEDLINE=98344027; PubMed=9677360;
Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Ramakrishnan P.,
Neubauer M.G., Blannar M.A.;
"Functional expression of two KVLQT1-related potassium channels
responsible for an inherited idiopathic epilepsy.";
J. Biol. Chem. 273:19419-19423(1998).
[4]
INVOLVEMENT IN M-LIKE CURRENT.
MEDLINE=99410758; PubMed=10479678;
Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
Buckley N.J., London B., Brown D.A.;
"Two types of K(+) channel subunit, Evg1 and KCNQ2/3, contribute to
the M-like current in a mammalian neuronal cell";
J. Neurosci. 19:7742-7756(1999).
[5]
ASSOCIATION WITH KCNE2.
MEDLINE=20487128; PubMed=11034315;
Tinel N., Dicotot S., Lauritzen I., Barhain J., Lazdunski M.,
Borsotto M.;
"M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
subunit.";
FEBS Lett. 480:137-141(2000).
[6]
SURFACE EXPRESSION OF HETEROMERS.
MEDLINE=20250883; PubMed=10788442;
Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
"Surface expression and single channel properties of KCNQ2/KCNQ3,
M-type K+ channels involved in epilepsy.";
J. Biol. Chem. 275:13343-13348(2000).
[7]
INHIBITION BY M1 MUSCARINIC RECEPTORS.
MEDLINE=20150152; PubMed=10684873;
Shapiro M.S., Roche J.P., Kafan E.J., Cruzblanca H., Mackie K.,
Hille B.;
"Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+)
channels that underlie the neuronal M current";
J. Neurosci. 20:1710-1721(2000).
[8]
INHIBITION BY M1 MUSCARINIC RECEPTORS.
MEDLINE=20178300; PubMed=10711361;
Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
Brown D.A.;
"Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
via m1 muscarinic acetylcholine receptors.";

RL J. Physiol. (Lond) 522:349-355(2000).
 RN [9]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20368587; PubMed-10908292;
 RA Main M.J., Cryan J.E., Dupere J.R., Cox B., Clare J.J., Burdidge S.A.;
 RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
 retigabine.";
 RL Mol. Pharmacol. 58:253-262(2000).
 RN [10]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20411474; PubMed-10953053;
 RA Wickenham A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
 RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/3
 potassium channels.";
 RL Mol. Pharmacol. 58:591-600(2000).
 RN [11]
 RP ACTIVATION BY RETICABINE.
 RX MEDLINE-20180045; PubMed-10713399;
 RA Rundfeldt C., Netzer R.;
 RT "The novel anticonvulsant retigabine activates M-currents in Chinese
 hamster ovary-cells transfected with human KCNQ2/3 subunits.";
 RL Neurosci. Lett. 282:73-76(2000).
 RN [12]
 RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
 RX MEDLINE-21095345; PubMed-1159685;
 RA Wickenham A.D., Zou A., Wagoner P.K., Jegla T.;
 RT "Characterization of KCNQ5/Q3 potassium channels expressed in
 mammalian cells.";
 RL Br. J. Pharmacol. 132:381-384(2001).
 RN [13]
 RP VARIANT BFNC2 ARG-309.
 RX MEDLINE-20309392; PubMed-10852552;
 RA Hirose S., Zentgraf F., Akiyoshi H., Fukuma G., Iwata H., Inoue T.,
 RA Kaneo S., Mitsudomi M., Muranaka H., Kurokawa T., Hanai T., Wada K.,
 RA Yonekura M., Tsubota M.;
 RT "A novel mutation of KCNQ3 (C.925T->C) in a Japanese family with
 benign familial neonatal convulsions.";
 RL Ann. Neurol. 47:822-826(2000).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
 EXCITABILITY. ASSOCIATES WITH KCNQ2 OR KCNQ5 TO FORM A POTASSIUM
 CHANNEL WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL
 CHANNELLYING THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND
 DEACTIVATING POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN
 DETERMINING THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS
 WELL AS THE RESPONSIVENESS TO SYNAPTIC INPUTS.
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNQ2 OR KCNQ5. MAY ASSOCIATE WITH
 KCNQ2.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ3 ARE THE CAUSE OF BENIGN FAMILIAL
 NEONATAL CONVULSIONS TYPE 2 (BFNC2); ALSO KNOWN AS EPILEPSY,
 BENIGN NEONATAL TYPE 2 (BEN2); BFNC2 IS AN AUTOSOMAL DOMINANT FORM
 CC OF EPILEPSY IN THE NEWBORN THAT CLEARS SPONTANEOUSLY AFTER A FEW
 CC WEEKS AND IS FOLLOWED BY NORMAL PSYCHOMOTOR DEVELOPMENT.
 CC -1- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT IN XENOPUS
 CC OOCYTES BY CO-EXPRESSION OF EITHER KCNQ3(MOT) AND KCNQ2 AT THE
 CC RATIO OF 1:1, OR OF KCNQ3(MOT), KCNQ3(WT) AND KCNQ2 AT THE RATIO
 CC OF 1:1/2, TO MIMIC THE SITUATION IN A HETEROZYGOUS PATIENT WITH
 CC BFNC2 DISEASE.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KOT
 CC SUBFAMILY.
 CC -----
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DR EMBL: AF071491; AAC96101.1; -
 DR EMBL: AF071478; AAC96101.1; JOINED.
 DR EMBL: AF071479; AAC96101.1; JOINED.
 DR EMBL: AF071480; AAC96101.1; JOINED.
 DR EMBL: AF071481; AAC96101.1; JOINED.
 DR EMBL: AF071482; AAC96101.1; JOINED.
 DR EMBL: AF071483; AAC96101.1; JOINED.
 DR EMBL: AF071484; AAC96101.1; JOINED.
 DR EMBL: AF071485; AAC96101.1; JOINED.
 DR EMBL: AF071486; AAC96101.1; JOINED.
 DR EMBL: AF071487; AAC96101.1; JOINED.
 DR EMBL: AF071488; AAC96101.1; JOINED.
 DR EMBL: AF071489; AAC96101.1; JOINED.
 DR EMBL: AF071490; AAC96101.1; JOINED.
 DR EMBL: AF071491; AAC96101.1; JOINED.
 DR HSP: Q54397; 1BL8.
 DR Genew: HGNC:6297; KCNQ3.
 DR MIM: 602232; -.
 DR MIM: 121201; -.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR006536; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF03520; KCNQ1_channel; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 122 142 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 153 173 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 197 217 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 226 247 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 262 282 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 304 324 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 331 351 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 13 24 POLY-GLY.
 FT VARIANT 309 309 W -> R (IN BFNC2).
 FT VARIANT 310 310 G -> V (IN BFNC2).
 FT VARIANT 310 310 G -> V (IN BFNC2).
 FT MUTAGEN 310 310 G->V: ABOUT 50% REDUCTION OF WT
 HETEROERIC CURRENT; RATIO OF 1:1, OR
 20%; RATIO OF 1:1:2.
 FT MUTAGEN 318 318 G->S: >50% REDUCTION OF WT HETEROERIC
 CURRENT; RATIO OF 1:1 AND 1:1:2.
 FT SEQUENCE 872 AA; 96742 MM; BB79C69EBE51A84 CRC64;
 Query Match 34.2%; Score 1620.5; DB 1; Length 872;
 Best Local Similarity 42.2%; Pred. No. 1.6e-86;
 Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;
 Oy 7 GGEDEAGAGLVMSGAAAAAGGGRGSSGKMDVSSGR-----VILNSAAGDGLL 60
 Db 14 GGDGDDGGG-----GGANPDAGGAAAAAGDERVVGAPGVDEYVTLALGAGADKDTLL 68
 Oy 61 LGRRAATLGGGGGGLRESRKGQAGARMSLIGK-PLSTSSQSCRNNKYRRVQNTLVNL 119
 Db 69 L-----EGGDRDEQRRTPQS--IGLAKTPELSRPV--RNNAKRYRIQTLIVYAL 115
 Oy 120 ERPRGMAFIYHAFVLLVFCGLLISVSTPEHTKLASSCLLLEFWMIVVGFETIRI 179
 Db 116 ERPRGMAFIYHAFVLLVFCGLLISVSTPEHTKLASSCLLLEFWMIVVGFETIRI 175
 Oy 180 WSAAGCCCRVYMGGRGLRFARKEPVIDITVILASIVASAKTQGNIFATSLRFLQI 239
 Db 176 WAAAGCCCRVYMGGRGLRFARKEPVIDITVILASIVASAKTQGNIFATSLRFLQI 234
 Oy 240 LRAVMDRDRGCTKMLGSSVYVAHSEKELIFAMVIGFLVIFSSFLVYVYKDA----- 291
 Db 235 LRAVMDRDRGCTKMLGSSVYVAHSEKELIFAMVIGFLVIFSSFLVYVYKDA----- 294
 Oy 292 --NKESTVADALMWGTTITLTIGYGKPTLWLGRLISAGFALLGISFFALPAGILGSG 349
 Db 292 --NKESTVADALMWGTTITLTIGYGKPTLWLGRLISAGFALLGISFFALPAGILGSG 349

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Db 295 EMKEEFYADALWMLTTLATIGYGDTPKWTWEGRLIATFSLIGVSPFALPAGILGSG 354
QY 350 FALKVOEHOHROKHEKRRNPANLIQCVRYAADADEKSYS-IATWK-----PHLKAL 400
Cc 355 LALKVOEHOHROKHEKRRNPANLIQCVRYAADADEKSYS-IATWK-----PHLKAL 400
Db 401 HTCSPTNOKLSFKERVRNAPRGOSIKSQAQSVGDRSPSTDTAGSPPTKVOKSWSFND 460
QY 415 QLEMASSOKLGLDRVRLSNRPGSNMTK-----GKLFPLNDVAIESPSEKPKVGLNN 468
Cc 461 RTTRRPLRLK-----SSQKPRVADADALGTDDVYDEKGCOCDDVSEDLTPPLKTVIR 514
Cc 469 KERRTAPRMKAVYFWOSSE-----DAGTG---DPMAEORGYGNDPPIEDMIPDKNAIR 520
QY 515 AIRIMKFRVAKRKEKTELPYDVKYEQYSAGHLDMLCRISLOTFRVDOILGKQOTSD 574
Cc 521 AVRLQPLRYKKKKKRETLRPYDVKYEQYSAGHLDMLCRISLOTFRVDOILGKQOTSD 580
QY 575 KKR-----EKITAEHETT--DDLMLGRVYKVEKOVOSIESKLDCLL 615
Cc 581 KHKKSQKSAFTFPSQOSPRNEPYVAPRSTSEIEDQSMGKFKVVERQVODMGKLDLFLV 640
QY 616 DYOQVLR-----KGSALALASQIPEPEOJSDVSPVSKLGSQAN 663
Cc 641 DMHQMERLOVQVTEYPTKGTSS-----PAEKEDKNYS-DLKTILCNYS 689
QY 664 SGLSRSTANISGLQFILPNEFSQOTFYALSPTMHQATQVPIQSQSGSAVANTNTI 723
Cc 690 TGPPEPYSFH-----QVITDKVSPYGFPAHDP-----VNLPRGGSSGQVQNT--- 733
QY 724 ANQINTPKRAPPTLQIPPLPAIKHLPRPTLHPNAGLOESIDVTTCVASKENVO 783
Cc 734 -----PSSATTYVERPYLPLTLTLDSDRVSC-HSQADLOGPYSD-----RIS 775
QY 784 VAOSNLTKDRSMRKSPDMGCELTLSVCPMPVPRDKLSVONLIRSTEELNQLSGSESS 843
Cc 776 PRQ-----RSTIRSDPTPLSL-----MSVNH-----EELNPSGSGSIS 810
QY 844 GSRGSDPYF---KMRSKLFTDEVEGPEETEDTF 877
Cc 811 QDRDVFYFGNGSSMMREKRYLAE--GEMTDVDPDF 845
Db 811 QDRDVFYFGNGSSMMREKRYLAE--GEMTDVDPDF 845

RESULT 8
C1Q3_RAT STANDARD; PRT: 873 AA.
AC 088944; Q92240;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN Voltage-gated potassium channel protein KQT-like 3.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA MEDLINE=905398; PubMed=983639;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
the M-channel.";
RL Science 282:1890-1893(1998).
CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNQ2 TO FORM A POTASSIUM CHANNEL.
CC WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING

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Cc THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
Cc POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
Cc THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE
Cc RESPONSIVENESS TO SYNAPTIC INPUTS.
Cc -1- SUBUNIT: HETEROMULTIMER WITH KCNQ2.
Cc -1- SUBCELLULAR LOCATION: Integral membrane protein.
Cc -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; MAY BE
Cc PRODUCED BY ALTERNATIVE SPLICING.
Cc -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SYMPATHETIC GANGLIA. IN
Cc BRAIN, EXPRESSED IN CORTEX, HIPPOCAMPUS AND AT MUCH LOWER LEVELS
Cc IN CEREBELLUM. IN SYMPATHETIC GANGLIA, EXPRESSED AT APPROXIMATELY
Cc EQUAL LEVELS IN BOTH SUPERIOR CERVICAL GANGLIA AND PREVERTEBRAL
Cc GANGLIA.
Cc -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
Cc CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
Cc EVERY THIRD POSITION (BY SIMILARITY).
Cc -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
Cc SUBFAMILY.
Cc -----
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Cc or send an email to license@isb-sib.ch).
Cc -----
Cc EMBL: AF087454; AAC36723.2; -
Cc EMBL: AF091247; AAC79846.1; -
Cc HSSP: Q54397; 1BL8.
Cc InterPro: IPR001622; K+channel_pore.
Cc InterPro: IPR003946; KCNQ1_channel.
Cc InterPro: IPR00636; M+channel_nlg.
Cc Pfam: PF00520; ion_trans_1.
Cc DR Pfam: PF03520; KCNQ1_channel; 1.
Cc KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Cc Multigene family; Alternative splicing.
Cc FT TRANSMEM 123 143 SEGMENT S1 (POTENTIAL).
Cc FT TRANSMEM 154 174 SEGMENT S2 (POTENTIAL).
Cc FT TRANSMEM 198 218 SEGMENT S3 (POTENTIAL).
Cc FT TRANSMEM 227 248 SEGMENT S4 (POTENTIAL).
Cc FT DOMAIN 263 283 SEGMENT S5 (POTENTIAL).
Cc FT TRANSMEM 305 325 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
Cc FT DOMAIN 332 352 SEGMENT S6 (POTENTIAL).
Cc FT POLY-GLY.
Cc FT VARSPLIC 1 83 MGLARRAGAGAGGGGGGGGGAANPAGGSAVAGDEE
Cc FT KAVGLAPGEVQYTLALGTADKDTLLTGCGREGEQRT
Cc FT P-> MALEPPLQPPPPPPRTPPSAFASSRSSSGEGAPSG
Cc FT GADGAQGS (IN ISOFORM 2).
Cc FT H-> R (IN REF. 2).
Cc SQ SEQUENCE 873 AA; 96897 MW; D77AF8808051E15 CRC64;

Query Match 33.6%; Score 1590.5; DB 1; Length 873;
Best Local Similarity 41.7%; Pred. No. 8; 7e-85;
Matches 389; Conservative 108; Mismatches 273; Indels 163; Gaps 27;

QY 7 GGEAGAGLWVKSAAAAAGG-----RLSGMKDYSGRGVLLNSAAAGDG 57
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 15 GGGGGGGG-----GGANPAGGDSVADDERKAVLAGDVQ---VTALGTGADKG 66
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 58 LLLLTTRATLGGGGGGLRESRRKQAGARSLGK-PLSTYSQSCRNVKRYRVQVLY 116
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 67 TLLT-----EGGREGGQRRTPQG--IGLAKTPLSRPV---RNAKYRRIQLIY 113
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 117 NVLEPRGMATLYAHFVFLVVGCLILSVSTIIPETKTLASSCLLLEFMYVGELETF 176
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 114 DALERPRGMATLYAHFVFLVVGCLILAVLTTFKEKETVSGDWLLLEFPAIFGEFA 173
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 177 IRIASAGCCRYRGQGLRFARPCVCVITVLINIAVSAKTOGNIPATSLRLRF 236
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 174 LRIAAAGCCRYRGQGLRFARPCVCMIDIVLINIAVSAKTOGNVLAISLRF 232
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 237 LQILRMVMDRRGGTWWLLGSLVVAHSEKELITAWYIGLVLIFFSFLVLYVERDA----- 291
Cc 11 111 111 111 111 111 111 111 111 111 111 111 111 111

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Db 233 LQILRLRMRRGGTWWLLGSAICAHSKELLTANTIGTLTLLSSFLVYLVKDVPEMDA 292
Qy 292 -----NKEFSTYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGIL 346
Db 293 QGEEMKEEFETYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGIL 352
Qy 347 GSGFALKVVOQHROKHFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PIL 397
Db 353 GSGGALKVVOQHROKHFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PIL 412
Qy 398 KALHTCSPTNOKLSFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PIL 457
Db 413 RKQGLKAAAGOKGLIDRLVRLSNRPGSNWK-----GKLFPLNDALIEESPKEKPVG 466
Qy 458 FNDTRFRPSLRK-----SSQKRYVDADTALGTIDVYDEKGCOCVSVDDLPLPKT 511
Db 467 LNNKERRTAFAKMAFYWQSSSE-----DAGTG---DPMETDRGYGNDPLIEDMPTLKA 518
Qy 512 VITAIRILMKFHVAKRKFEETLRPYDQVITBOYSAGHIDMLCRISLQTRVDQILGKQI 571
Db 519 AIRAVRILQFLRYKKRKFEETLRPYDQVITBOYSAGHIDMLSRITYLQTRIMIFPGFP 578
Qy 572 TSDKSSREK-----ITAEHTTDLTSLMGRVYKKEKOVQSIKSKLD 612
Db 579 STPKHKKSQKSAFTYPSQSPRNEPYVARATSETEQSMGKFKVRYQVHDMGKLD 638
Qy 613 CLLDIYQOVLKRGKASALALASFOIPECEQTSIDQSVV---SKDLSGSAONSCLSR 669
Db 639 FLVYMHMHQMER-----LQVHVEYYPFKGASSPABEKKEDNYSDLKTIICNV 688
Qy 670 STSANISGLOFILLTP-NEFSAQFYALSPTHMSQATOVPISSQSSAQAATNTIANQIN 728
Db 689 SESPPRPDPYTFHOVPIDRVGPGYGFANDP-----VKLRGGSSSKQAQNLSS--- 737
Qy 729 TAPKPAATTLQIPEPLPAIKHLPRETLHPNAGLQESISDVTTCLVASKENVOYAQSN 788
Db 738 -----SGSTVABRPVLPLTLTLDSCSYH-----SQFLQGPYSD 773
Qy 789 LTKRSMARKSFDMGGETILSCVPMVFKDLGKSLVONLIRSEBELNIQSLGSSSSSRGS 848
Db 774 HISPR-QHRSITRSDTPLSL-----MSVNH-----EELERSPSGFSISODRDD 816
Qy 849 QDFYR-----KWRSEKLFITDEVEGPEDETDF 877
Db 817 YVFGPSGSSGSMWRKRYIAE---GETDIDTDF 846

RESULT 9
C103_BOVIN STANDARD: PRT: 866 AA.
AC P58126;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 3.
GN KCNO3
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. ASSOCIATES WITH KCNO2 TO FORM A POTASSIUM CHANNEL
CC WITH ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING
CC THE NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING
CC POTASSIUM CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING
CC THE SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS AS WELL AS THE
CC RESPONSIVENESS TO SYNAPTIC INPUTS (BY SIMILARITY).

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CC -!- SUBUNIT: HETEROMULTIMER WITH KCNO2 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE325548; AKL1221.1; -
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNO1_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR000636; M_channel_nlg.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF03520; KCNO1_channel; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Multigene family.
FT TRANSEM 122 142 SEGMENT S1 (POTENTIAL).
FT TRANSEM 153 173 SEGMENT S2 (POTENTIAL).
FT TRANSEM 197 217 SEGMENT S3 (POTENTIAL).
FT TRANSEM 226 247 SEGMENT S4 (POTENTIAL).
FT TRANSEM 262 282 SEGMENT S5 (POTENTIAL).
FT DOMAIN 304 324 SEGMENT H5 (POTENTIAL).
FT TRANSEM 331 351 SEGMENT S6 (POTENTIAL).
FT DOMAIN 13 24 POLY-GLY.
SQ SEQUENCE 866 AA; 9564 MW; 4399616107A0424 CRC64;

Query Match 33.6%; Score 1589.5; DB 1; Length 866;
Best Local Similarity 41.1%; Pred. No. 9,9e-85;
Matches 394; Conservative 104; Mismatches 272; Indels 189; Gaps 30;

7 GGEBCGAAGLVKSGAAGGAGGRLGSGMDVEGGRK-----VLNSAARGGLL 60
14 GGGGGGGGG-----GGAANPAGGDAAGADEERKGLAPGVEQYTLALGADKDTLL 68
Qy 14 LGTRATITGGGGGGLRESRGKQAGRMISLKG-PLSYTSSGCRNRVRYRYONYLYNL 119
Db 61 L-----EGGDEGQRRTPOG---IGLAKTPTLSRPK---RNNAKTRRIQTLIYDAL 115
Qy 69 L-----EGGDEGQRRTPOG---IGLAKTPTLSRPK---RNNAKTRRIQTLIYDAL 115
Db 120 ERPRGMAFIYHAFVLVFGCLISVSFTIPEHFKLASSCLLLEFVMIVFGLEFIIRI 179
Db 116 ERPRGMALYHALVLYLVGLILAVLTFFREYVSGDWLLELTFALFEGAEFALRI 175
Qy 180 WSAGCCCRKMGQGLRTRARKRFVYIDITVILASTAVYSAKQGNFAISALRSLEIQI 239
Db 176 WAAGCCCRKMGQGLRTRARKRFVYIDITVILASTAVYSAKQGNFAISALRSLEIQI 234
Qy 240 LRMVMDRGGTWWLLGSAICAHSKELLTANTIGTLTLLSSFLVYLVKDVPEMDA----- 291
Db 235 LRMVMDRGGTWWLLGSAICAHSKELLTANTIGTLTLLSSFLVYLVKDVPEMDA 294
Qy 292 --NKEFSTYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGILSG 349
Db 295 EMKEEFETYADALMGGTITLTIGYDXTPLTWLGRLLSAGFALLGISFPALPAGILSG 354
Qy 350 FALKVQEOHROKHFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PILKAL 400
Db 355 LALKVQEOHROKHFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PILKAL 414
Qy 401 HTCSPTNOKLSFEKRRNPANLIQCWRSYAADEKSVS-IATWK-----PILKAL 460
Db 415 QLDPAASOKLGLIDRLVRLSNRPGSNWK-----GKLFPLNDALIEESPKEKPVGSNN 468

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QY 461 RTFRPSRLK-----SSQPKVIDADYALGTDVYDEKGCQCDVSVELDPLPLKTVIR 514
 Db 469 KERFTAFMKAYAFWQSSD-----DAGTG---DPTAEDRGYNDILEDIMPLTKAIR 520
 QY 515 AIRMKFHVAKRKREKTELPYDVKYDEYQASAGHLMCLCRKSLQTRVDOLGQQTSD 574
 Db 521 AVRIQFLYKKKFKETLRYDKVDYETQYSAHLMCLSRKYLQTRIDMFTPPSPSTP 580
 QY 575 KKSRL-----EKTAHEHT--TDDLSMLGRVYKVKQVQSSIESKLDLL 615
 Db 581 KHKKSQGAFTYPSQSPRNEEYVARPSTSEIEDOSMKGKRVYKQVHMGKKLDLY 640
 QY 616 DIYQVLR-----KSSASLALASFOIPEECQTSYQSPVDSKDLSGSAQN 663
 Db 641 DMHQLQMERLQYHVAQSPSKGASS-----PAEAQOKED-RRDADLKTIIICNYS 689
 QY 664 SGCLSRSTANISRGLOFLTPNEFSAQTFYALSPTHSQAQVPIQSSQSAVAATNTI 723
 Db 690 TG-----APDAPYSFHQVPVK-----VGPYGEF 713
 QY 724 ANQINTAPKPAAPTLQIPPLPAIKHLRPPETLHPNPAGLQESISDVTCLVA-SKENV 782
 Db 714 AHD-----PVNL-----PLGG-----PSSGKHATPYAERPTVLPILTLIDSRGYSR 756
 QY 783 QVAQSNLTKDR---SMRKSFDMDGETLLSVCPMPVDPDLKSLSYQNLIRSTEELNQLSG 839
 Db 757 QVELHGPCSDRYSPPQRNSTRTDSDPLSL-----MSVNH-----EELERSPSG 800
 QY 840 SESSGSRGSDFFP---KWRKSLFTTDEEVGPEETETDTPDAAPAPAREAAFAASDL 894
 Db 801 FSIQODRDYAFGPGSGSSWMREKRLAE-----GETDIDTEPFTPSGLPLSGTGCI 854

RESULT 10
 CIOI_HUMAN
 ID CIOI_HUMAN STANDARD: PRT: 676 AA.
 AC P51787; Q92960; Q00347; Q06007; Q90UM8; Q90UM9; Q94787;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 1 (KVLQT1) (Kv1.9).
 GN KCNQ1 OR KCNA9 OR KVLQT1 OR KCNA8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Kidney;
 RX MEDLINE-97459933; PubMed-9312006;
 RA Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,
 RA Barhanin J.,
 RT "Properties of KVLQT1 K⁺ channel mutations in Romano-Ward and Jervell
 RT and Lange-Nielsen inherited cardiac arrhythmias.";
 RL EMBO J. 16:5472-5479(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS LQT1, AND VARIANT
 RP SRR-643
 RX MEDLINE-99013427; PubMed-9799083;
 RA Itoh T., Tanaka T., Nagai R., Kikuchi K., Ogawa S., Okada S.,
 RA Yamagata S., Yano K., Yazaki Y., Nakamura Y.,
 RT "Genomic organization and mutational analysis of KVLQT1, a gene
 RT responsible for familial long QT syndrome.";
 RL Hum. Genet. 103:290-294(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LQT1 MET-587 AND
 RP HIS-591.
 RX MEDLINE-99147971; PubMed-10024302;
 RA Neyroud N., Richard P., Vignier N., Donger C., Denjoy I., Demay L.,
 RA Shkolnikova M., Pece K., Chevalier P., Hainque B., Coumel P.,
 RA Schwartz K., Guicheney P.,
 RT "Genomic organization of the KCNQ1 K⁺ channel gene and identification
 RT of C-terminal mutations in the long-QT syndrome.";

RL Circ. Res. 84:290-297(1999).
 RN [4]
 RP SEQUENCE OF 96-156 FROM N.A.
 RC TISSUE-Pancreas;
 RX MEDLINE-97055938; PubMed-8900283;
 RA Sanguinetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,
 RA Atkinson D.L., Keating M.T.,
 RT "Coassembly of K(V)LQT1 and minK (Isk) proteins to form cardiac I(Ks)
 RT potassium channel.";
 RL Nature 384:80-83(1996).
 RN [5]
 RP SEQUENCE OF 1-129 FROM N.A.
 RX MEDLINE-97268689; PubMed-9108097;
 RA Yang W.-P., Levesque P.C., Little W.A., Conder M.L., Shalaby F.Y.,
 RA Blamir M.A.,
 RT "KvLQT1, a voltage-gated potassium channel responsible for human
 RT cardiac arrhythmias.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4017-4021(1997).
 RN [6]
 RP SEQUENCE OF 130-676 FROM N.A., AND VARIANTS LQT1.
 RX MEDLINE-9612034; PubMed-8528244;
 RA Wang Q., Curran M.E., Splawski I., Burn T.C., Millholland J.M.,
 RA Varrault T.J., Shen J., Timothy K.W., Vincent G.M., de Jager T.,
 RA Schwartz P.J., Towbin J.A., Moss A.J., Atkinson D.L., Landes G.M.,
 RA Connors T.D., Keating M.T.,
 RT "Positional cloning of a novel potassium channel gene: KVLQT1
 RT mutations cause cardiac arrhythmias.";
 RL Nat. Genet. 12:17-23(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Heart;
 RX MEDLINE-97450920; PubMed-9305853;
 RA Jiang M., Tseng-Crank J., Tseng G.-N.,
 RT "Suppression of slow delayed rectifier current by a truncated isoform
 RT of KVLQT1 cloned from normal human heart.";
 RL J. Biol. Chem. 272:24109-24112(1997).
 RN [8]
 RP MUTAGENESIS OF ALA-178; LEU-273 AND THR-312.
 RX MEDLINE-97462827; PubMed-9323054;
 RA Shalaby F.Y., Levesque P.C., Yang W.-P., Little W.A., Conder M.L.,
 RA Jentsch T.J., Blamir M.A.,
 RT "Dominant-negative KVLQT1 mutations underlie the LQT1 form of long QT
 RT syndrome.";
 RL Circulation 96:1733-1736(1997).
 RN [9]
 RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
 RX MEDLINE-20178300; PubMed-10713961;
 RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
 RA Brown D.A.,
 RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
 RT via M1 muscarinic acetylcholine receptors.";
 RL J. Physiol. (Lond) 522:349-355(2000).
 RN [10]
 RP IDENTIFICATION OF A SUBUNIT ASSEMBLY DOMAIN.
 RX MEDLINE-20120797; PubMed-10654932;
 RA Schmitt N., Schwarz M., Peretz A., Abitbol I., Attali B., Pongs O.,
 RT "A recessive C-terminal Jervell and Lange-Nielsen mutation of the
 RT KCNQ1 channel impairs subunit assembly.";
 RL EMBO J. 19:332-340(2000).
 RN [11]
 RP POSSIBLE INTERACTION WITH KCNE3.
 RX MEDLINE-20110524; PubMed-10646604;
 RA Schroeder B.C., Waldegger S., Fehr S., Bleich M., Warth R.,
 RA Greger R., Jentsch T.J.,
 RT "A constitutively open potassium channel formed by KCNQ1 and KCNE3.";
 RL Nature 403:196-199(2000).
 RN [12]
 RP REVIEW ON VARIANTS.
 RX MEDLINE-20169042; PubMed-10704188;
 RA Tranebjærg L., Bathen J., Tyson J., Bitner-Glindzicz M.,
 RT "Jervell and Lange-Nielsen syndrome: a Norwegian perspective.";
 RL Am. J. Med. Genet. 89:137-146(1999).
 RN [13]

CC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=21114838; PubMed=11220365;
 RA Kunzmann K., Hubner M., Schreiber R., Levy-Holzman R., Garty H.,
 RT Bleich M., Wath T., Slavik M., von Hahn T., Greger R.,
 RT "Cloning and function of the rat colonic epithelial K⁺ channel
 KVLQT1.";
 RL J. Membr. Biol. 179:155-164(2001).
 RN [2]
 RP SEQUENCE OF 134-352 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=97460452; PubMed=9314834;
 RA Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Levitan E.S.;
 RT "Decreased expression of Kv4.2 and novel Kv4.3 K⁺ channel subunit
 RNAs in ventricles of renovascular hypertensive rats.";
 RL Circ. Res. 81:533-539(1997).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
 CC WITH KCNE1 (MINK) TO FORM THE I(Ks) CARDIAC POTASSIUM CURRENT.
 CC ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT.
 CC -1- SUBUNIT: HEPEROMULTIMER WITH KCNE1 (MINK).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -1- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT AT POSITION 321.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ133685; CAB38863.1; -
 DR EMBL: U92655; AAB51395.1; ALT_FRAME.
 DR HSSP: Q54397.1BL8.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR000636; M-channel_nlg.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF03520; Ion_trans. 1.
 DR PRINTS: PR00169; KCNQ1_channel. 1.
 KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 122 142 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 148 168 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 197 217 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 226 248 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 262 282 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 300 320 SEGMENT H5 (POTENTIAL).
 FT TRANSMEM 332 352 SEGMENT S6 (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 170 170 E -> T (IN REF. 2).
 FT CONFLICT 182 182 S -> T (IN REF. 2).
 FT CONFLICT 185 185 V -> L (IN REF. 2).
 FT CONFLICT 255 255 V -> F (IN REF. 2).
 SQ SEQUENCE 669 AA: 74579 MW: 23740CA1290020939 CRC64;

Query Match 23.3%; Score 1101; DB 1; Length 669;
 Best Local Similarity 38.6%; Pred. No. 1.4e-56;
 Matches 275; Conservative 106; Mismatches 190; Indels 142; Gaps 22;

OY 3 RHAG-----GEEGGAAGLVKSGAAAAAGGRLGSGMKVDSGRGVLLSAAARGDG 57
 DB 12 RRAGGRLGARRGSGAGLAKKCPFSLELAGGPTG-----GVYVAVIATPGARG 61

OY 58 LLL-----LGTAAATLGGGGGLRESRGKQAGRMILLKPLSTYSSQSCR 103
 DB 62 LAPPMPSPVSPVAPADLGP-----PRSIDPGR-----VSIYSPR 97
 OY 104 RNKYR-RVONYLYNVLTERPGW-AFIYHAEVFLVPGCLLISVSTPEHRTKSSCLL 161
 DB 98 RPLLRKHIDGRVYNFLERPRGKCFYHFFVFLVLCVLFVSTLEQVAAALAGTLF 157
 OY 162 ILEFVIMVPGLEFIRIRMSAGCCCRKRWGGRFLFARKPCVIDITVLIASIAVSAKT 221
 DB 158 IMEIVLVFEGTEVYVRLMSAGCSKRYGICMGRILFARKPISIDLIYVAVMVLGVCS 217
 OY 222 OGNIPTASRLSRLEQLLWRNRDRGCTKLLGSVYVANSKEITAMTIFVLIRSS 281
 DB 218 KGVFATSAIRGLRLEQLLRHLVDRGGWRLLGSVFIHRQELITLYLIGFLIFSS 277
 OY 282 FLVYLVEKDA-----NKEFSTADALMWGITLTITIGYGDTPPLTWLRLSAGFALGI 336
 DB 278 YFYVLAEKDAVNESGRLEFSGYADALMWGVYTTTIGYGDVPTWVGKTIASCSVRAI 337
 OY 337 SFPAALAGILGSGFALKVQDOROKHFEKRRNPANLIQCVRSYADEKSVIATWPK 396
 DB 338 SFPAALAGILGSGFALKVQDOROKHFEKRRNPANLIQCVRSYADEKSVIATWPK 395
 OY 397 LK---ALHTC-----SPTNKLSEKERVNMASSPRGOSIKRQASV-----GDRRSS 440
 DB 396 VKRPASHTLISPKPKKSVWKKKFKLDDKNGLSGEKIFVNPHTCDPPERRDPH 455
 OY 441 TDTTASGSPFKVQKSMSPNDRTFRPSLRKLSQPKPYIDATLGTDDVYDEKGCQCDV 500
 DB 456 FSI--DGYDSSVRS-----PTL-LevstPH-----FLRTSFMED-----DDL 491
 OY 501.SWEDTLPLP-----KTVIRATLIMFVAKKFKETLRPYDVAKVDEQISAGHLD 550
 DB 492 EETLLTPPTHVSQLDHNRATIKVIRMOYFPAKKRFOQARKYDVADVIEQYSGHLD 551
 OY 551 MLCRIKSLQTRVQILGKG--ITSDKRSREKITAHEHTTDDLMLGVVAVKEQVQSGIE 608
 DB 552 LAMRIKELQRRDQDSIGKPSLFIPISEKSDR-----GSNTIGARLNVEDKVTOLD 603
 OY 609 SKLDCILDIYQOVL-----RKGSAS-ALALASFOIPPE 641
 DB 604 QRLVITIDMLHQLSLQGGPTCNRSQVAVASDERGSINDELFLPNSLPIYE 656

RESULT 12
 CIO1_MOUSE STANDARD; PRT; 604 AA.
 AC P97414; 088702;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 1 (KVLQT1) (Kv1.9).
 GN KCNQ1 OR KCNA9 OR KVLQT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RC TISSUE=Heart;
 RX MEDLINE=97055937; PubMed=8900282;
 RA Barhanin J., Lesage F., Guillemane E., Fink M., Lazdunski M.,
 RT Romy G.;
 RT "KVLQT1 and Isk (mink) proteins associate to form the I(Ks) cardiac
 RT potassium current.";
 RL Nature 384:78-80(1996).
 RN [2]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM II), AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6;
 RX MEDLINE=98282243; PubMed=9618174;
 RA Paulsen M., Davies K.R., Bowden L.M., Villar A.J., Franck O.,

DR EMBL: AJ233714; CA11526.1; -
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF03520; KCNQ1_channel.1.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 MultiGene family.
 FT TRANSMEM 115 135 SEGMENT S1.
 FT TRANSMEM 149 169 SEGMENT S2.
 FT TRANSMEM 190 210 SEGMENT S3.
 FT TRANSMEM 219 241 SEGMENT S4.
 FT TRANSMEM 255 275 SEGMENT S5.
 FT DOMAIN 293 313 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 321 341 SEGMENT S6.
 FT SEQUENCE 660 AA; 74686 MW; 73B416E8BA08A352 CRC64;
 Query Match 22.9%; Score 1083.5; DB 1; Length 660;
 Best Local Similarity 42.0%; Pred. No. 1.4e-55;
 Matches 235; Conservative 105; Mismatches 166; Indels 53; Gaps 11;
 QY 92 KPLSTSSQSCRANKYRV--QNYIXNLEPRGW-AFYHAFFLLVFGCLLSVST 148
 DB 78 KALAPLRLRYGRNPFESKVNIOGRTYNLEPTGKMCFTYHFTVLIVLCLFYSWST 137
 QY 149 IPEHTKLASSCLLLEFVWIVVFGLEFIRIRWSAGCCCRGRMGRLPARKPCVIDTI 208
 DB 138 IEQHYFANRALVMEIYLVFEGITYIVLMSAGCSKTVGEMGRLEFAKPISTIDLI 197
 QY 209 VLASIVASAKTOGNIPTASLSRLRFLQILRMVRDRGRTWKLGSVYVASHKELIT 268
 DB 198 VVASVIVLVCVSGNGOVFTSAIRGIRFLQILRLHVRDGRGFWRLLSGVFIHQELIT 257
 QY 269 AMYIGELVLISSFLVYVEKDA-----NKESTYADALMWGTTLTITIGYDGTPLTWL 323
 DB 258 TLVIGFGLIFSSYVYLAEKDAVDSGQCFSSYADALMWGVYTVTIGYDGVPTWI 317
 QY 324 GRLLSAGFALLGISFALPAGILSGFALVKVOEHOKHPEKRRNPANLIQCWRSYAA 383
 DB 318 GRTIASCFVAFISFALPAGILSGFALKVQOKOKHNRNPALASLIQTSWRCXAA 377
 QY 384 DEKSVIATWPKPHLK---ALHTCSPT-NOKLSFERVRMASPRGQSIKSRQA----- 431
 DB 378 ENH--ESATWKKYVROPTFYVSPKTKKSVGKRKKLTDKDNGINSEKSLVNPITY 435
 QY 432 ----SVGRSRSPSTITAEGPSPTKYOKSMSPNDRTFRPSLRKLSQPKPIYDADTALGT 487
 DB 436 DHVVDKDRKRENSNI--DGYDSVAKSLGILDVNSGALSRRANSYADDLDEGEVYLA 493
 QY 488 DDVYDEKGCOCDSVEDLTPPLKTVIRAIRIMKHFVAKRKEKTELPRDYKDVIEQYSAG 547
 DB 494 -----ITHVSQLRSHRYVYKVIIRBMGYFAKKKFFQAKRKYDVRDVEIQYSOG 542
 QY 548 HLDMLCRKSLQTRVDQILGK----QITSDDKSREKITAHEHTTDDLSMIGRVYVKEQ 603
 DB 543 HLNLMVRKLEQLRRLDOSLGKPTMELSVSEKSDRGKNT-----IGARLNVEEK 592
 QY 604 VQSIKSLDCLLDIYQVL 622
 DB 593 FVHMDQKLTITDMLHLV 611
 RESULT 14
 CIOL_XENLA STANDARD: PRT: 377 AA.
 AC P70057;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Voltage-gated potassium channel protein KQT-like 1 (XKVLOT1)
 DE (Fragment).
 GN KCNQ1 OR KVLOT1.

OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=97055938; Pubmed=8900283;
 RA Sanginetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,
 RT "Coassembly of K(V)LQT and mink (Isk) proteins to form cardiac I(Ks)
 RL Nature 384:80-83(1996).
 CC -1- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
 CC WITH KCNE1 (MINK) TO FORM THE I(Ks) CARDIAC POTASSIUM CURRENT.
 CC ELICITS A RAPIDLY ACTIVATING, K(+)--SELECTIVE OUTWARD CURRENT.
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNE1 (MINK).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY). KQT
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U71076; AAC60042.1; -
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans.1.
 DR PRINTS: PRO0169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 MultiGene family.
 FT TRANSMEM 88 108 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 122 142 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 163 183 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 192 214 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 228 248 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 266 286 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 294 314 SEGMENT S6 (POTENTIAL).
 FT NON_TER 377 377
 FT SEQUENCE 377 AA; 42645 MW; 75524C03F294098F CRC64;
 Query Match 19.0%; Score 899.5; DB 1; Length 377;
 Best Local Similarity 55.38%; Pred. No. 3.1e-45;
 Matches 177; Conservative 53; Mismatches 77; Indels 13; Gaps 5;
 QY 98 SSQSCRNNYVR-RVQNYLVNLEPRGW-AFYHAFFLLVFGCLLSVESTIPEHTL 155
 DB 118 ATEFLFMELIVLVFGAEYVVRMSAGCSKYVGWGRLEFARKPISVIDILVAVSYI 177
 QY 216 VVSAKTOGNIPTASLSRLRFLQILRMVRDRGRTWKLGSVYVASHKELITANYIGFL 275
 DB 178 VLVCGSNGQVFAFSAIRGIRFLQILRLHVRDGRGFWRLLSGVFIHQELITLYIGFL 237
 QY 276 VLIFSEFLVYLVKDA-----NKESTYADALMWGTTLTITIGYDGTPLTWLGRLLSAG 330
 DB 238 GLIFSSFYIYLAEKDALIDSGEYQFSYADALMWGVYTVTITIGYDGVPTWIGTINS 297
 QY 331 FALGISFPALPAGILSGFALKVQEQHOKHPEKRRNPANLIQCWRSYAADKSVSI 390

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Db      298 FSVFAISFFALPACILISGFAIKVQOKORHFNROIPAAASLIOTAMCYAAE--NPDS 355
Qy      391 ATMKPHLKAL----HTCSPT 406
        |||:::|
Db      356 ATKVIYIRKOSRNHHIMSPS 375

RESULT 15
C104_MOUSE
ID C104_MOUSE STANDARD: PRT: 276 AA.
AC 09IK97;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 4 (Fragment).
GN KCNQ4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Brain;
RX MEDLINE=20499211; PubMed=11042367;
RA Beisel K.W., Nelson N.C., Delimont D.C., Fritzsche B.;
RT "Longitudinal gradients of KCNQ4 expression in spiral ganglion and
RT cochlear hair cells correlate with progressive hearing loss in
RT DFNA2(1).";
RL Brain Res. Mol. Brain Res. 82:137-149(2000).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20226104; PubMed=10760300;
RA Kharkevets T., Hardelin J.-P., Safieddine S., Schweizer M.,
RA El-Amraoui A., Petit C., Jentsch T.J.;
RT "KCNQ4, a K+ channel mutated in a form of dominant deafness, is
RT expressed in the inner ear and the central auditory pathway.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4333-4338(2000).
CC -1- FUNCTION: PROBABLY IMPORTANT IN THE REGULATION OF NEURONAL
CC EXCITABILITY. MAY UNDERLIE A POTASSIUM CURRENT INVOLVED IN
CC REGULATING THE EXCITABILITY OF SENSORY CELLS OF THE COCHLEA.
CC -1- SUBUNIT: MAY FORM HETEROMULTIMERS WITH KCNQ3 (BY SIMILARITY).
CC BASAL MEMBRANE OF COCHLEAR OUTER HAIR CELLS.
CC -1- TISSUE SPECIFICITY: IN THE INNER EAR EXPRESSED IN THE OUTER
CC SENSORY HAIR CELLS OF THE COCHLEA AND IN TYPE I HAIR CELLS OF THE
CC VESTIBULAR ORGANS. ALSO EXPRESSED IN THE POSTSYNAPTIC MEMBRANE OF
CC THE CALYX NERVE ENDINGS INNERVATING TYPE I CELLS. IN THE BRAIN
CC EXPRESSED IN NEURONS OF MANY, BUT NOT ALL, NUCLEI OF THE CENTRAL
CC AUDITORY PATHWAY. ABSENT FROM MOST OTHER BRAIN REGIONS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
CC -----
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CC -----
DB EMBL: AF249747; AAF66432.1; -
DB MGD: MGI:1926803; Kcnq4.
DB InterPro: IPR003946; KCNQ1_channel.
DB Pfam: PF03520; KCNQ1_channel; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Multigene family.
FT NON_TER 1
FT NON_TER 276
SEQUENCE 276 AA; 30484 MW; 6F93E70A1D7E08BF CRC64;

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Query Match      13.7%; Score 647; DB 1; Length 276;
Best Local Similarity 53.2%; Pred. No. 8,86-31;
Matches 141; Conservative 49; Mismatches 53; Indels 22; Gaps 7;

Qy      403 CSPTNOKLSKERYRMASPRQGSIKSRQ--ASVDRSRSPSDITAE--GSPTRKQKWSMNF 459
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      24 CPGESSHMGKIDRIKIRISICKRTGPKOHLPAPPIPTSPSSSEQVCEASSPSKVSQSMFN 83
Qy      460 DRTFRFRSLRK---SSQPKYIDADALGTDVDYDEGECQDVSVEELTPKLYIAI 516
        |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      84 DRTFRFRSLRKPRSSAEEGP-----SEVAEEKSYCELTVDVMAVAKTVINISV 134
Qy      517 RIMKFNHAKRKKFETLRPYDVKDYIEQYSAGHLMCLIKISLQTRVQDILGKQITSPDK 576
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      135 RIILFLVAKKFKETLRPYDVKDYIEQYSAGHLMCLIKISLQARVDIVGRG--PGDRK 192
Qy      577 SRE---KITAEHETTDLSMLGRVYKVKQYQSIIESKIDCLLDITYQVLRGASALALA 633
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      193 TREKGDGSPDAEAVDEISMGRVYKVKQYQSIIEHKLDLLGFSRCLRGSTSA--SLG 250
Qy      634 SFQIPPECQGTSPDYSPVDSKDS 658
Db      251 TVQVPLFPDITSDYHSPVDHEDIS 275

RESULT 16
C101_FELCA
ID C101_FELCA STANDARD: PRT: 172 AA.
AC 097531;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Voltage-gated potassium channel protein KQT-like 1 (KVLQ1) (Kv1.9)
DE (Fragment).
GN KCNQ1 OR KVLQ1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Chen L.-S.K.;
RT "Expression of mink and KVLQ1 mRNA in cat tissues: a genetic evidence
RT for the cardiac Iks channel.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
CC WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT.
CC ELICITS A RAPIDLY ACTIVATING, K(+)--SELECTIVE OUTWARD CURRENT (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETEROMULTIMER WITH KCNE1 (MINK) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: AF013961; AAC98890.1; -
DB HSSP: 054397; IHL8.
DB InterPro: IPR001622; K+channel_pore.
DB InterPro: IPR003091; K_channel.
DB InterPro: IPR000636; M+channel_nlg.
DB Pfam: PF00520; Ion_trans; 1.

```


[illegible]

CC WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT.
 CC ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: HETEROMULTIMER WITH KCNE1 (MINK) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AB033207; BAA88580.1; -.
 CC HSSP: Q54397; IBL8.
 CC InterPro: IPR001622; K+channel_pore.
 CC InterPro: IPR003091; K_channel.
 CC InterPro: IPR000636; M+channel_nlg.
 CC Pfam: PF00520; Ion_transf. 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family.
 CC FT NON_TER 1 1
 CC FT TRANSMEM 1 18 SEGMENT S3 (POTENTIAL).
 CC FT TRANSMEM 27 49 SEGMENT S4 (POTENTIAL).
 CC FT TRANSMEM 63 83 SEGMENT S5 (POTENTIAL).
 CC FT DOMAIN 101 121 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 CC FT CARBOHD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT NON_TER 123 123
 CC SQ SEQUENCE 123 AA; 13602 MW; A6CEC4201C6836CA CRC64;
 CC -----
 CC Query Match 8.7%; Score 409.5; DB 1; Length 123;
 CC Best Local Similarity 62.6%; Pred. No. 1.8e-17;
 CC Matches 77; Conservative 20; Mismatches 21; Indels 5; Gaps 1;
 CC -----
 CC QY 204 VIDITVLASIAVSAKTOGNIFATSLRLRLQILIRVMDRGRGTWKLGSVVAHS 263
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:||||:|
 CC 1 IIDIVVAVASNVLCVSGKQGFATSAIGIRLQILRLMHVDRGGTWWLGSVVFTHR 60
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC QY 264 KELLTAWYIGLVLFSSFLVYLVEKDA-----NKEFSYADALMWTITLTITGYGDKT 318
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC Db 61 QELTTTLYIGLIFSSYFYVLAERKDAVNESGOVEFGSYADALMVGVTVTITGYGDKV 120
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC QY 319 PLT 321
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC Db 121 PQT 123
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC -----
 CC RESULT 21
 CC CIRA_HUMAN STANDARD: PRT: 854 AA.
 CC AC 014721:
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Voltage-gated potassium channel protein Kv2.1 (DHK1).
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eulheria; Primates; Catarrhini; Homidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;
 CC Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U02840; AAA36156.1; -.
 CC HSSP: Q54397; IBL8.
 CC Genew: HGNC:6231; KCNB1.
 CC MIM: 600397; -.
 CC InterPro: IPR000210; BTR_PZ.
 CC InterPro: IPR001622; K+channel_pore.
 CC InterPro: IPR003091; K_channel.
 CC InterPro: IPR003131; K_tetra.
 CC InterPro: IPR004350; Kv2channel.
 CC InterPro: IPR004351; Kv2channel.
 CC InterPro: IPR003968; Kv_channel.
 CC InterPro: IPR000636; M+channel_nlg.
 CC InterPro: IPR003973; Shab_channel.
 CC Pfam: PF00520; Ion_transf. 1.
 CC Pfam: PF02214; K_tetra. 1.
 CC Pfam: PF03521; Kv2channel. 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC PRINTS: PR01514; KV2CHANNEL.
 CC PRINTS: PR01491; KVCHANNEL.
 CC PRINTS: PR01495; SHABCHANNEL.
 CC SMART: SM00225; BTR; 1.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation;
 CC FT DOMAIN 1 182
 CC FT TRANSMEM 183 204
 CC FT TRANSMEM 205 224
 CC FT TRANSMEM 225 246
 CC FT TRANSMEM 247 256
 CC FT TRANSMEM 257 278
 CC FT TRANSMEM 279 290
 CC FT TRANSMEM 291 312
 CC FT TRANSMEM 313 326
 CC FT TRANSMEM 327 348
 CC FT TRANSMEM 349 368
 CC FT TRANSMEM 369 389
 CC FT TRANSMEM 390 410
 CC FT TRANSMEM 411 440
 CC FT TRANSMEM 440 440
 CC FT MOD_RES 442 492
 CC FT CARBOHD 279 279
 CC SQ SEQUENCE 854 AA; 95521 MW; 360DEB3E45731EDA CRC64;
 CC -----
 CC Query Match 6.2%; Score 291.5; DB 1; Length 854;
 CC Best Local Similarity 20.2%; Pred. No. 1.5e-09;
 CC Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33;
 CC -----
 CC QY 115 LYNLEPRGMA--FIYHAFVFLVFGCLISVFSFIPHTK-----ASSCLTLE 164
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC Db 171 LMDLEKPNSSVAAKIALIISIMFYLTALSL-NTLPRLQSLDEGQSDNQLAHYE 229
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|
 CC QY 165 FVMIVLEGLFIIRIWSACCCRYRGWGRLEFARKPFCVITIVILASIAVSAKTQGN 224
 CC :|||:||||:|:||||:||||:||||:||||:||||:||||:||||:|

FT MOD_RES 492 492 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 853 AA: 95280 MW: 7A08998839716165 CRC64;
 Query Match 6.1%; Score 289; DB 1; Length 853;
 Match Local Similarity 19.7%; Pred. No. 2.1e-09;
 Matches 176; Conservativity 134; Mismatches 269; Indels 316; Gaps 37;
 115 LYNVLERPRGWA---FYHAFVFLVVGCLLVSFTIPEHTKL-----ASCLLITE 164
 171 LMDLLEKPPSSVAAKLAIISIMFIVLSTALSL-NLPELQSLDEFGSDNPDLAHE 229
 165 FMYIVVGFLEFIRIRISAGCCCRGMQGRLEAPKPCFVIDTVLAVASAKTOGN 224
 230 AVCIAMFTEYELRFLSSP-----KKW-----KFKGFLNADLALILEYV-----T 272
 225 IFATSLARSL-----RFQILMVRDRRGCTMKLLGSVYANSEL-ITAW 270
 273 IFLTSSNKSVLQONVRRVVOAIRIMKLILKLARSTGLQSLGFTLRSYNELGLIL 332
 271 YIGFLVLFFSFLVLYVEKDA-NKESTVADALMWGTITLTIGYDKPTPLTLGLSLA 329
 333 FLAMGIMIPSS-LVFEAKEDDDTKFSIPASFWMATITMTVYGDLYPTLLGKIYG 391
 330 GFALLGISFALPAGLGSFALKVQOHQKHFKERKRNPAANLQCVWRSYADEKSVS 389
 392 LCCINGVLVIALPIPIIVNNSEFEYKQKQKAKIKRR----- 429
 390 IATWPHLKALHTCSPTNOKLSFERVBMASPRGQSIKSRQASVGDNRSPSTDITAEESP 449
 430 -----EALERAKKNGSIY----- 442
 450 TKVQKSWSEFNDTRRFRPSLRKSSQPKVYIDADLTGDDVYDKGCCQDVSVEDLTPPL 509
 443 -----SWNMDAFARSIEM-----MDLYEKN----- 465
 510 KTVIRAIRIMKRVHAKRKKEKETIRPDVDVIEQYSAGHDMCRISLQTRVDOILKG 569
 466 ESIARKDVQDNHLSPLNKKWKWT-----KRALSETSSS-----KSFEK----- 503
 570 QITSKRSKEKITAEHETDDLSMLGRVYVVERVOGIESKLDCLLIYQOVLKRGASA 629
 504 EOGSEPKARSSSPQH-----LNVOOLE-----DMTSMAKTQSQPI 540
 630 L---ALASFOIPPECEQTSYQSPVDSKDLSSAONSGLSRETSANISRGLOFILLPN 686
 541 LNTKEMAPQSKPPELEMS--MSPVAPL---PARTEGVIDMSMSID---SFISAT 592
 687 EFSAQTFALSP--TMHSQATQVPIQO-----SDGSVAATNTTIANQINT-----AP 731
 593 DPEATREFSHSPLASLSSKAGSSTADEVGMRGALGASGRILTEPNIPETSRSGFEVESP 652
 732 KPAAPTITQIP-----PPLPAIKHLPRPETLHPNP-----AGLQESIS 769
 653 RSMKTNPNPIKARLALKVNEVEDPTLLPSL-----GLYHPLNRKGAAVAVAL-ECAS 707
 770 DVTTCGLVASKENVQAQSNLTKDRSMRK-----SFDMG-----GETILSYCP 811
 708 LIDRPVLPESSITYTASARTPPRSPEKHTAIAFNFEAGVHHYIDTPTDEGQLLYSVDS 767
 812 MVRPDIGKSLSVONLIRSTEELINQLSGSESSSRSSQDPYPRKRESKFLTDEVEGPEE 871
 768 SPSPASLHGSTSPK-----FSTGAR----- 786
 872 TETDTPDAPOPAR-----EAAFASDSLRTGSRSSQICKAGEST--DALSLP 918
 787 TEKNHFESEPLPTSPKFLRPNCVYSSEGL-TGKGPQAOEKCKLNNHTPPVHMLP 840

RESULT 23
 CIRC_HUMAN
 ID CIRC_HUMAN STANDARD: PRT: 806 AA.
 AC 092953;
 DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv2.2.
 GN KCNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98275219; PubMed:9612272;
 RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
 RA Flynn E.R., Kenyon J.L., Horowitz B.;
 RT "Molecular identification of a component of delayed rectifier current
 in gastrointestinal smooth muscles."
 RL Am. J. Physiol. 274:G901-G911(1998).
 CC - FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC - DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U69962; AAB08433.1; -.
 DR HSSP: Q54397; IBL8.
 DR GeneW: HGNC:6232; KCNB2.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR004351; Kv22channel.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF005520; Ion_trans.1.
 DR Pfam: PF02214; K_tetra.1.
 DR Pfam: PF03521; Kv2channel.1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01515; KV22CHANNEL.
 DR PRINTS: PR01491; KYCHANNEL.
 DR PRINTS: PR01495; SHABCHANNEL.
 DR SMART: SM00225; BTB; 1.
 DR K+ channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT DOMAIN 1 190
 FT TRANSMEM 191 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 254
 FT DOMAIN 255 264
 FT TRANSMEM 265 286
 FT DOMAIN 287 298
 FT TRANSMEM 299 320
 FT DOMAIN 321 334
 FT TRANSMEM 335 356
 FT DOMAIN 357 396
 FT TRANSMEM 397 418

FT DOMAIN 419 806 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 806 AA; 90990 MW; 2ABEBCE05A90E6 CRC64;
 Query Match 6.0%; Score 282; DB 1; Length 806;
 Best Local Similarity 22.2%; Pred. No. 5e-09;
 Matches 150; Conservative 105; Mismatches 238; Indels 182; Gaps 28;
 115 LYNLEPRRGA---FYHAFVFLVFGCLLSVSTIPE-----HTKLASSC 159
 179 LMDLEKPNSSVAAKILAIIVSLFTLSTALST-NLPELOETDEFGQNDNRQLAH-- 235
 160 LLLLEFVIVVGFLEFIRWSAGCCCRVGRGRLRFARKPCVDTVLIASIIVASA 219
 236 ---VEANCIAFMETMEYLRFLSS-----PNMKKFFKGLVNDLAILPYV---- 279
 220 KTGONIFATSAKRLS-----RFLQILNRVMDRGRGKWLGLSVYVAHAKEL 266
 280 ---TIFLESNKSVLQFQNVRRVQVIFRIMRLILKLARHSTGLQSLGFTLRISYNEL 335
 267 -ITAMYIGFLVLISSFLVYLVKEND--KESTYADALIMWGTLITLTIGYDKTPLTWIG 324
 336 GLILFLFAMGIMITS-LVFEAKEDKATKFTSIPASEFWATITMTVGIDYPTKLIG 394
 325 RLISAGFALLGISFEALPAGILSGFALKVQDHRQKHFEKRRNP-----AANL 373
 395 KIVGGLGCIACIVVIALPIPIIVNFSFEYKQKQKQKAKIKREALERAKRNGSIYMN 454
 374 IQCVWRST-----AADEKSVSTATKPKHLKALHTGSPYNOCKLFKER 415
 455 KDAFARSMLIDVAVERKAGESANTKDSADDNHLSRMRKARKAL---SETSSNKSPENK 511
 416 VRMASPRQSIKRSQASVGDNRSPSTDTIAGESS--TKYOK-SWSFNDTRFRPSRLKS 472
 512 YQESYQKKS-----HEQILNNTFSSPOHLSQKLEMLYNEITKTQP-----H 553
 473 SQPKVIDADTALGTDVYDEKGCOCQDVSEDLTPPLKTVIRA-----IRIMKF 521
 554 SHPN--DCQEKPERPSAYEE-----EIMEEVYVQDEQLAVQTEVYDMKSTSSIDSF 606
 522 HVAKKEKETLRYPVYKVDIYEOYSAGHDLMLCRISLQTRVQDILKGOITSPKSKSEKI 581
 607 TSCATDFETETER-----SPLPPPSASHLOM-----KEPTDLPG-- 639
 582 TAEHETTDLSMLGIVNVEKQVQVQSTESKID-CLLDIYQVLRKGSASALALASFOIPE 640
 640 TEEHORANGPPPL--TLSEKGPAPARDGTLLEAPVITVNLASGSGOGL----- 687
 641 ECEQTSYQSPYDSKDLSSAONSGLSRSTSANISRGLOFILTPEFSAQTEFALSPIM 700
 688 -----HSPLOSONATDPSKSS--LKGSNPLKRSRLKVNKKNRNGSA-----PQT 730
 701 HSOATOVPISSODGS 715
 731 PSTARPLPVTTADFS 745
 RESULT 24
 CTRB_CANFA STANDARD; PRT; 806 AA.
 ID CTRB_CANFA 095167;
 AC 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Voltage-gated potassium channel protein Kv2.2.
 GN KCNB2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98275219; PubMed=9612272;

RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A.,
 RA Flynn E.R., Kenyon J.L., Horowitz B.;
 RT "Molecular identification of a component of delayed rectifier current
 RT in gastrointestinal smooth muscles";
 RL Am. J. Physiol. 274:G901-G911(1998).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; U69963; AB08432.1; -.
 DR HSSP; Q54397; 1BL8.
 DR InterPro: IPR000210; BTP_PQZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K channel.
 DR InterPro: IPR003131; K tetra.
 DR InterPro: IPR004351; Kv2channel.
 DR InterPro: IPR003968; Kv channel.
 DR InterPro: IPR006366; M+channel_nlg.
 DR InterPro: IPR003973; Shab channel.
 DR Pfam; PF00520; Ion trans. 1.
 DR Pfam; PF02214; K tetra. 1.
 DR Pfam; PF03521; Kv2channel. 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01491; KCHANNEL.
 DR PRINTS; PR01495; SHABCHANNEL.
 DR SMART; SM00225; BTP. 1.
 DR K+ ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family;
 FT DOMAIN 1 190
 FT TRANSMEM 213 212
 FT DOMAIN 213 232
 FT TRANSMEM 233 254
 FT DOMAIN 255 264
 FT TRANSMEM 265 286
 FT DOMAIN 287 298
 FT TRANSMEM 299 320
 FT DOMAIN 321 334
 FT TRANSMEM 335 356
 FT TRANSMEM 357 396
 FT DOMAIN 397 418
 FT TRANSMEM 419 806
 FT CARBOHYD 287 287
 SQ SEQUENCE 806 AA; 90283 MW; D962EC256760B743 CRC64;
 Query Match 5.8%; Score 276.5; DB 1; Length 806;
 Best Local Similarity 22.2%; Pred. No. 1e-08;
 Matches 162; Conservative 99; Mismatches 248; Indels 221; Gaps 31;
 117 NVLEPRRG-----NAFYHAFVFLVFGCLLSVSTIPEHTKL-----ASSCLLIL 163
 181 DLEKPNSSVAAKILAIIVSNLFI---VLSIALST-NLPELOEMDEFGQPNNDQLAHV 236


```

0Y 220 KTOGIGFPTSALRSL-----RFLIOILRWBRMDRCGTMKLGSVYAHSEL 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 ----TIFLETESKSVLOFONARRVYOIFIRIMRLIRLILKLARHSTGLQSGFTLLRSYNEL 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 267 -ITAWYIGFLVLIFSSFLVYLEEKDAN-KEFSTYADALWMGFTTLLTIGYGDKTPLTWLG 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 GLLILFLAMGINIFES-LVFEAKEDDARKFTSIPASFEMATITMTTVGIDLYPKTLIG 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 325 RLNSGFFLLIGISFALPAGILGSGFALKVBOHROKHEKRRNP-----AANL 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 KIVGGLICIAGLVIALPLPIIVNNSEFEYKEQKROEKAIKREALEKARNGSIVSMNL 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 374 IQCVWRSY-----AADEKSVSITATMKPHLKALTTCSTNOKLSKEVRYMASPFGOSIKSR 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 KDAPARSKELLIDVAEAKGESANITDSVDNHI-TSPSRKMKARKALSETSNKSYENKYQ 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 430 QASVGDRRSPSTUDIATIEGSP--TKYOK-SWSNDRRFRPPLRLKSOPKRPVIDADTALG 466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 EVSQKDSHQOLNNT-ISSSSPQHLKSQKLEMLYNEITKYQ-----TSHRNP--DCEQPE 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 487 TDDVYDEKGCOCODSVEDLTPPLKTVIRA-----IRIMKPHVAKRKEETLRLPY 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 566 RPSAYEE-----ETEMEVEVCPQEOALAVQAOTEVIVDMKSTSIDSTSCATDPTETER-- 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 536 DVKDVIIEQYSAGHLDM 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 ---SPLPPPSASHLOM 631
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 26	
CIKF_MOUSE	
ID	CIKF_MOUSE
	STANDARD;
	PRT;
	769 AA

AC Q03593; Q02068;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv3.3 (KSHIID).
 GN KCNC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 NCBI_TaxID=10090;

SEQUENCE FROM N.A. (ISOFORM RV3.3B).
MEDLINE-94132879; PubMed-8301351.
Goldman-Wohl D.S., Chan E., Baird D., Heintz N.;
"Kv3.3b: a novel Shaw type potassium channel expressed in terminally
differentiated cerebellar Purkinje cells and deep cerebellar
nuclei." J. Neurosci. 14:511-522(1994).

SEQUENCE OF 78-769 FROM N.A. (ISOFORM KV3.3A).
 (2)
 RP
 PC

RX MEDLINE=92155707; Pubmed=1740329;

RA Ghanshani S., Pak M., McPherson J.D., Strong M., Dethlefs B.,
RA Wasmuth J.J., Salkoff L.A., Gutman G.A., Chandv G.K.?

RT of a Shaw-related potassium channel gene, Kv3.3, and mapping of Kv3.3

RT and Kv3.4 to human chromosomes 19 and 1.";
RL Genomics 12:190-196(1992)

-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES, INCREASING CURRENTS OF ACTION

CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE AND PROPOSED THAT THE

CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROU
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.

CC GRADIENT.
CC -I- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A

CC HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE)
CC -|- SUBCELLULAR LOCATION: Integral membrane protein
CC

- 1- ALTERNATIVE PRODUCTS: 2 isoforms; KV3.3A and KV3.3B (shown here), are produced by alternative splicing

CC -1- TISSUE SPECIFICITY: THE KV3.3B ISOFORM IS HIGHLY ENRICHED IN THE

CC BRAIN PARTICULARLY IN THE CEREBELLUM, WHERE ITS EXPRESSION IS
CC CONFINED TO PURKINJE CELLS AND DEEP CEREBELLAR NUCLEI. ISOFORM
CC KV3.3A IS NOT EXPRESSED IN CEREBELLUM.
CC
CC -I- DEVELOPMENTAL STAGE: EXPRESSION OF KV3.3B BEGINS IN CEREBELLAR
CC PURKINJE CELLS BETWEEN POSTNATAL DAY 8 (P8) AND P10 AND CONTINUES
CC THROUGH ADULTHOOD.
CC
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC
CC -I- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC
CC -----
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CC
DR EMBL: S69381; AAC60679.1; -,
DR EMBL: X60796; CAA43209.1; -,
DR EMBL: X60797; CAA43209.1; JOINED.
DR HSSP: O54397; 1BL8.
DR MCD: MGI:96650; KCNC3.
DR
Tel: +359 2 9600000
Fax: +359 2 9600001

```
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000210; BTH_PoZ.
DR InterPro; IPR001622; K+channel_pore.
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```
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
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```
DR InterPro; IPR003968; kv_channel.
DR InterPro; IPR000636; M+channel_nlg.
```

```
DR InterPro; IPR003974; Shaw_channel.  
DR Pfam; PF00520; ion_trans_1.
```

DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNE1.

DR PRINTS: PRO1491; KVCHANNEL.
DR PRINTS: PRO1408; CURECHANNEL.

DR PRINTS; PRO1496; SHAWCHANNEL.
DR SMART; SM00225; BTB; 1.

KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Alternative splicing; Phosphorylation.

FT	DOMAIN	1	290	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	291	309	SEGMENT S1 (POTENTIAL).

FT	DOMAIN	310	350	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	351	370	SEGMENT S2 (POTENTIAL)

FT	DOMAIN	FT	TRANSMEM	FT	DOMAIN	FT	TRANSMEM
371	379	371	379	371	379	371	379
380	398	380	398	380	398	380	398
398	406	398	406	398	406	398	406
406	414	406	414	406	414	406	414
414	422	414	422	414	422	414	422
422	430	422	430	422	430	422	430
430	438	430	438	430	438	430	438
438	446	438	446	438	446	438	446
446	454	446	454	446	454	446	454
454	462	454	462	454	462	454	462
462	470	462	470	462	470	462	470
470	478	470	478	470	478	470	478
478	486	478	486	478	486	478	486
486	494	486	494	486	494	486	494
494	502	494	502	494	502	494	502
502	510	502	510	502	510	502	510
510	518	510	518	510	518	510	518
518	526	518	526	518	526	518	526
526	534	526	534	526	534	526	534
534	542	534	542	534	542	534	542
542	550	542	550	542	550	542	550
550	558	550	558	550	558	550	558
558	566	558	566	558	566	558	566
566	574	566	574	566	574	566	574
574	582	574	582	574	582	574	582
582	590	582	590	582	590	582	590
590	598	590	598	590	598	590	598
598	606	598	606	598	606	598	606
606	614	606	614	606	614	606	614
614	622	614	622	614	622	614	622
622	630	622	630	622	630	622	630
630	638	630	638	630	638	630	638
638	646	638	646	638	646	638	646
646	654	646	654	646	654	646	654
654	662	654	662	654	662	654	662
662	670	662	670	662	670	662	670
670	678	670	678	670	678	670	678
678	686	678	686	678	686	678	686
686	694	686	694	686	694	686	694
694	702	694	702	694	702	694	702
702	710	702	710	702	710	702	710
710	718	710	718	710	718	710	718
718	726	718	726	718	726	718	726
726	734	726	734	726	734	726	734
734	742	734	742	734	742	734	742
742	750	742	750	742	750	742	750
750	758	750	758	750	758	750	758
758	766	758	766	758	766	758	766
766	774	766	774	766	774	766	774
774	782	774	782	774	782	774	782
782	790	782	790	782	790	782	

EM	DOMAIN	FT	SEGMENT	33 (FOLENTIAL)	EXTRACELLULAR (POTENTIAL)
413	413	413	413	413	413

FT	DOMAIN	435	447	458	469	480	491	502	513	524	535	546	557	568	579	590	601	612	623	634	645	656	667	678	689	700	711	722	733	744	755	766	777	788	799	810	821	832	843	854	865	876	887	898	909	920	931	942	953	964	975	986	997	1008	1019	1030	1041	1052	1063	1074	1085	1096	1107	1118	1129	1140	1151	1162	1173	1184	1195	1206	1217	1228	1239	1250	1261	1272	1283	1294	1305	1316	1327	1338	1349	1360	1371	1382	1393	1404	1415	1426	1437	1448	1459	1470	1481	1492	1503	1514	1525	1536	1547	1558	1569	1580	1591	1602	1613	1624	1635	1646	1657	1668	1679	1690	1701	1712	1723	1734	1745	1756	1767	1778	1789	1800	1811	1822	1833	1844	1855	1866	1877	1888	1899	1910	1921	1932	1943	1954	1965	1976	1987	1998	2009	2020	2031	2042	2053	2064	2075	2086	2097	2108	2119	2130	2141	2152	2163	2174	2185	2196	2207	2218	2229	2240	2251	2262	2273	2284	2295	2306	2317	2328	2339	2350	2361	2372	2383	2394	2405	2416	2427	2438	2449	2460	2471	2482	2493	2504	2515	2526	2537	2548	2559	2570	2581	2592	2603	2614	2625	2636	2647	2658	2669	2680	2691	2702	2713	2724	2735	2746	2757	2768	2779	2790	2801	2812	2823	2834	2845	2856	2867	2878	2889	2900	2911	2922	2933	2944	2955	2966	2977	2988	2999	3010	3021	3032	3043	3054	3065	3076	3087	3098	3109	3120	3131	3142	3153	3164	3175	3186	3197	3208	3219	3230	3241	3252	3263	3274	3285	3296	3307	3318	3329	3340	3351	3362	3373	3384	3395	3406	3417	3428	3439	3450	3461	3472	3483	3494	3505	3516	3527	3538	3549	3560	3571	3582	3593	3604	3615	3626	3637	3648	3659	3670	3681	3692	3703	3714	3725	3736	3747	3758	3769	3780	3791	3802	3813	3824	3835	3846	3857	3868	3879	3890	3901	3912	3923	3934	3945	3956	3967	3978	3989	4000	4011	4022	4033	4044	4055	4066	4077	4088	4099	4110	4121	4132	4143	4154	4165	4176	4187	4198	4209	4220	4231	4242	4253	4264	4275	4286	4297	4308	4319	4330	4341	4352	4363	4374	4385	4396	4407	4418	4429	4440	4451	4462	4473	4484	4495	4506	4517	4528	4539	4550	4561	4572	4583	4594	4605	4616	4627	4638	4649	4660	4671	4682	4693	4704	4715	4726	4737	4748	4759	4770	4781	4792	4803	4814	4825	4836	4847	4858	4869	4880	4891	4902	4913	4924	4935	4946	4957	
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FT	TRANSMEM	448	469	SEGMENT S5 (POTENTIAL).
FT	DOMAIN	470	517	EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	518	539	SEGMENT S6 (POTENTIAL).
FT	DOMAIN	540	769	CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	41	44	POLY-GLN,
FT	DOMAIN	82	86	POLY-GLY.

FT	DOMAIN	229	234	POLY-GLY.
FT	DOMAIN	577	587	POLY-DPO

FTT	DOMAIN	596	599	600	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900
FTT	DOMAIN	596	599	600	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889											

FT	DOMAIN	POLY-ALA.	N-LINKED (GLCNAC. . .) (POTENTIAL).
320	009	0/4	
320	320		

FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	483	483	N-LINKED (GLCNAC. . .)	(POTENTIAL).

FTT	660	769	VDPRNGDPAALAHEDCPAIDQPA MSPEDKSPITPGSRG RYSRDRACFLVTDYAPSPDGSIRKGYEKSRSLSSIVGLSGV
-----	-----	-----	--

FT SLRLAPLAPPPGSPRATRRAPPTLPSTL -> GEAGARTGG
FT VGRSGGKVAGIEGMGGGFLGSGRGVWEATADKDKWLECW
FT

FT TPPTKSHNRRIPTTRACEHGFQPGCSQRLPLVRSVRRTGE
FT DSEETQV / TN TSOEQDM NVZ 2A)

CONFLICT	256	256	G -> D (IN REF. 2).
CONFLICT	260	260	
CONFLICT	266	266	

FI CONF LCI . 200 200 GAGGAG -> AKAAGA (IN REF. 2).

1

50	SEQUENCE	769 AA;	82116 MW;	BCACD5AB2D66D9DEC	CRC64;	
	Query Match	5.38;	Score 251;	DB 1;	Length 769;	
	Best Local Similarity	23.28;	Pred. No. 3e-07;			
	Matches	96;	Conservative	65;	Mismatches 162;	Indels 90; Gaps 13;
QY	3	RHHAGGEEGGAAGLWVSGAAAAAAGGGRGSGKMDVESSGGRVLLNSAARGDGLLLTG	62			
DB	191	KQHRDAEEALDSEFAPDPSSANANANNAGGADHAGDLD--EAGAG-----GGGLDAG	239			
QY	63	TRAAITL-----GGGGGGIRESRRKQGAQMSLGLPLSYSSQSCRNNKRYRQVNYLYN	117			
DB	240	GELKRLCFODAGGAGGLPGGAGGAGG-----TMMRRMQPRYWA	278			
QY	118	VLEKRP---RGNAFLYHAFVLLVYGCILLSY-----FSTIPEHTKLASS-----	158			
DB	279	LFEDPYSSRAARYAFASFLFFILSTITTFCELEHGFHISNKIVTQASPIPGAPPENIT	338			
QY	159	-----CLLIEFWNIIVVFGLEFETIRIMSAGCCCRYRGMQGRLFARFAPCEYDITVL	210			
DB	339	NVEVETPEPLLYVEGVCVWMTPEFELMRV---TFC-----PDKVEFLKSLNIIDCVAI	389			
QY	211	I-----ASIAVNSAKKTQGNIFATISALSKRLQLLRWAMRMRRGCTWLLGSVYAHNSKE	265			
DB	390	LPFLYLEVGLSGLSSSKAAKDVY--GELRVRPFRVILRIEKLIRHVGVLGHTLPLASTNE	447			
QY	266	-LITAWYIGFVLITFFSFLVLYVEKDANKE-----FSTYADALMWGITITLTITIG	315			
DB	448	FLLIILFLALGVLFEMFMYYAEKHIGADPPDILGSNHYFENINIDGFMMAVVMTTIGYG	507			
QY	316	DKPLPLWKLRLSAGFALLGISFPALPGAILGSGFALKVQDQKHOKKEFRKN	368			
DB	508	DMEPKTSGMLVGGICLAGVLTITAMPYPIVNNFGMYSLAMAKOKLPPKKN	560			
RESULT 27						
CIRK_HUMAN						
ID	CIRK_HUMAN	STANDARD:	PRT;	582 AA.		
AC	003721;					
DT	15-JUL-1998 (Rel. 36, Created)					
DT	15-JUL-1998 (Rel. 36, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Voltage-gated potassium channel protein Kv3.4 (KSH11C).					
GN	KCNK4.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RX	MEDLINE=92396711; Pubmed=1381835;					
RA	Vega-Ssenz de Miera E., Moreno H., Fruhling D., Kentros C., Rudy B.;					
RT	"Cloning of Shii (Shaw-like) cDNAs encoding a novel high-voltage-					
RT	activating, TEA-sensitive, type-A K ⁺ channel.";					
RL	Proc. R. Soc. Lond., B, Biol. Sci., 248:9-18(1992).					
CC	-!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM					
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED					
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE					
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH					
CC	WHICH K ⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL					
CC	GRADIENT.					
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS					
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT					
CC	EVERY THIRD POSITION.					
CC	-!- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL					
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR					
CC	COMPARTMENTS.					
CC	-!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER					
CC	CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					

[illegible]

DB 481 LAMAKOKLPRKKHVPAPQLESMPYCKSEET-----SPRSTYCSPTSPAREGMIE 534
 OY 415 RVRASPRGOSIKS 428
 DB 535 RKRAGEIRGWEKGS 548

RESULT 28
 CIRK_DROME STANDARD: PRT: 985 AA.
 ID C1R7970; 076805; 091779; 091700;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Shab.
 CN SHAB OR CG1066.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-Oregon-R;
 RX MEDLINE=9146139; PubMed=2493160;
 RA Butler A., Wei A.G., Baker K., Salkoff L.;
 RT "A family of putative potassium channel genes in Drosophila.";
 RL Science 243:943-947(1989).
 [2]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RX MEDLINE=9023553; PubMed=233511;
 RA Wei A.G., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RL Science 248:599-603(1990).
 [3]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RX MEDLINE=9024568; PubMed=2336395;
 RA Butler A., Wei A.G., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila.";
 RL Nucleic Acids Res. 18:2173-2174(1990).
 [4]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND MUTAGENESIS.
 RC STRAIN-Canton-S;
 RX MEDLINE=99348357; PubMed=10419540;
 RA Hegde P., Gu G.G., Chen D., Free S.J., Singh S.;
 RT "Mutational analysis of the Shab-encoded delayed rectifier K(+)
 channels in Drosophila.";
 RL J. Biol. Chem. 274:22109-22113(1999).
 [5]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borovoy D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P.E., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusseren D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -1- DEVELOPMENTAL STAGE: Expressed in late embryos and pupae.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AT
 CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AND
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: BELONGS TO THE DELAYED RECTIFIER CLASS. SHAB POTASSIUM
 CC CHANNEL SUBFAMILY.
 CC -1- CAUTION: Ref.5 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M32659; AAA28896.1; -;
 DR EMBL: AF084525; AAC33365.1; -;
 DR EMBL: AE003476; AAG32237.1; ALT-SEQ.
 DR EMBL: AE003476; AAG22233.1; ALT-INIT.
 DR PIR: S15058; S15058.
 DR HSSP: Q54397; 1BL8.
 DR Flybase: FBgn0003383; Shab.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003969; kv8_channel.
 DR InterPro: IPR003970; kv8_channel.
 DR InterPro: IPR003971; kv9_channel.
 DR InterPro: IPR003978; kv9_channel.
 DR InterPro: IPR003981; kv_channel.
 DR InterPro: IPR000636; M+channel_n1g.
 DR InterPro: IPR003973; Shab_channel.
 DR InterPro: IPR003975; Shal_channel.
 DR Pfam: PF00520; Ion_trans_3.
 DR Pfam: PF02214; Ion_tetra_2.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01492; KV6CHANNEL.
 DR PRINTS: PR01493; KV8CHANNEL.

DR PRINTS; PRO1494; KV9CHANNEL.
 DR PRINTS; PRO1491; KVCHANNEL.
 DR PRINTS; PRO1495; SHABCHANNEL.
 DR PRINTS; PRO1497; SHALCHANNEL.
 DR SMART; SM00225; BTB; 1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation; Alternative splicing.

FT TRANSMEM 436 454
 FT TRANSMEM 474 495
 FT TRANSMEM 506 527
 FT TRANSMEM 536 561
 FT TRANSMEM 577 598
 FT TRANSMEM 638 659
 FT CARBOHYD 245 245
 FT CARBOHYD 429 429
 FT CARBOHYD 530 530
 FT CARBOHYD 749 749
 FT CARBOHYD 766 766
 FT CARBOHYD 885 885
 FT CARBOHYD 888 888
 FT CARBOHYD 914 914
 FT MOD_RES 690 690
 FT MOD_RES 731 731
 FT MOD_RES 796 796
 FT VARSPLIT 717 746
 FT MUTAGEN 435 435
 FT MUTAGEN 608 608
 FT CONFLICT 31 31
 FT CONFLICT 220 220
 FT CONFLICT 307 307
 FT CONFLICT 362 362
 FT CONFLICT 414 415
 FT CONFLICT 495 495
 FT CONFLICT 553 553
 FT CONFLICT 613 613
 FT CONFLICT 630 630
 FT CONFLICT 651 651
 FT CONFLICT 827 828
 FT CONFLICT 877 877
 FT CONFLICT 903 985
 FT CONFLICT 911 913
 FT SEQUENCE 985 AA; 106359 MM; 59E38AD35F064AC8 CRC64;
 Query Match 5.2%; Score 248; DB 1; Length 985;
 Best Local Similarity 28.6%; Pred. No. 6,1e-07;
 Matches 81; Conservative 54; Mismatches 110; Indels 38; Gaps 10;

107 KYRVRQNTLYNVLRLP-----RGNAFIYHAFVLLVFGCLILSVSTIPE-----HTK 154
 413 KFESEQKYLMELEKRPNTSEFARVIAVILFIIVL-----STALTLNTLPLQLOHIIDGTP 468
 155 LASSCLILIEVMIVYEGLEFIIRIWSAGCCCRKRGWGLRPARRPFVIVTIVLIA-S 213
 469 QDNQPLAMVEAVCTMTFLEYIL-----RFSASPKMKFKFGGLNITDLAIIPYF 519
 214 IAAVSATKQNIPTASRLS-----RFLILRLVRMDRRCGTWKMLGSVYAHSKEL 266
 520 VSLFLLETKNK--ATDQFODARVYQVFRIMILRLKLARHSTGLQSLGFTLRNSYKEL 577
 267 -TAMVIGELVLISSFLVLYVEKD--ANKESFYADALMGITLTITIGGDKTPTLWLG 324
 578 GLMLFLAMGLIPRS-LAYFAEKEDKTKFVSIPFAFMAGITMTTGGDLCPTTALG 636
 325 RLISAGFALLGISFPALDAGILGSPALKVQDQHRKHFEKRR 367
 637 KVIQTVCCICGLVVALPIPIIVNNFAEYKQNMREKALKRR 679

RESULT 29
 CIRK_HUMAN
 ID CIRK_HUMAN STANDARD: PRT: 757 AA.
 AC Q14003;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein Kv3.3 (KSHI1D).
 GN KCNC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens epithelium;
 RA MEDLINE=20179629; PubMed=10712820;
 RT Rae J.L., Shepard A.R.;
 RT "Kv3.3 potassium channels in lens epithelium and corneal
 endothelium";
 RL Exp. Eye Res. 70:339-348(2000).
 RN [2]
 RP SEQUENCE OF 291-651 FROM N.A.
 RA Lee J.E., Garbutt J.H., Phillips K.L., Roses A.D.;
 RT "A human chromosome 19 Shaw type potassium channel gene";
 RT Submitted (JAN-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CONFORMATION IN RESPONSE TO THE VOLTAGE-DIFFERENCE ACROSS THE
 MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
 HETEROPOLYMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSITIVE AND IS
 CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF05989; AAC24118.1; -
 CC EMBL: Z11585; CA77671.1; -
 CC HSPF: Q54397; 1BL7.
 CC HSPF: Q54397; 1BL7.
 CC GeneW: HGNC:6235; KCNC3.
 CC MIM: 176264; -
 CC InterPro: IPR000210; BTB_POZ.
 CC InterPro: IPR001622; K_channel_pore.
 CC InterPro: IPR003091; K_channel.
 CC InterPro: IPR003131; K_tetra.
 CC InterPro: IPR003968; KV_channel.
 CC InterPro: IPR00636; M+channel_nlg.
 CC InterPro: IPR003974; Shaw_channel.
 CC Pfam: PF00520; Ion_trans_1.
 CC DR pfam: PF02214; K_tetra_1.
 CC DR PRINTS; PRO2214; K_tetra_1.
 CC DR PRINTS; PRO1491; KVCHANNEL.
 CC PRINTS; PRO1491; KVCHANNEL.
 CC PRINTS; PRO1495; SHABCHANNEL.
 CC PRINTS; PRO1497; SHALCHANNEL.
 CC SMART; SM00225; BTB; 1.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation;
 KW CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 290

FT TRANSMEM 291 309 SEGMENT S1 (POTENTIAL).
 FT DOMAIN 310 350 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 351 370 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 371 379 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 380 398 SEGMENT S3 (POTENTIAL).
 FT DOMAIN 399 411 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 412 434 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 435 447 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 448 469 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 470 517 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 518 539 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 540 757 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 39 38 POLY-PRO.
 FT DOMAIN 39 42 POLY-GLN.
 FT TRANSMEM 81 85 POLY-GLY.
 FT DOMAIN 229 234 POLY-GLY.
 FT TRANSMEM 577 587 POLY-PRO.
 FT DOMAIN 596 599 POLY-PRO.
 FT TRANSMEM 668 673 POLY-ALA.
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 757 AA; 80520 MW; 266F6B2B2AC5A52 CRC64;

Query Match 5.2%; Score 247; DB 1; Length 757;
 Best Local Similarity 23.5%; Pred. No. 4,9e-07;
 Matches 93; Conservative 63; Mismatches 150; Indels 90; Gaps 13;

QY 20 SGAAAAAGGRLSGMKDVGSGRGRVYLNSAARGDGLLLGTRATL-----GGGGGG 74
 DB 208 AGAANNAAGAHGDLDD-EGAG-----GGGIDGAGGELKLCFODAGGAGG 256
 QY 75 LRESRRGQAGRMILGRLPLSTSSQSCRNRKYRVQNYLVNLERP---RQMATIYHA 131
 DB 257 PPGAGGAGG-----TWRRWQRPVALFEDPYSSRARVAF 295
 QY 132 FVFLVFLFCILISV-----FSTIPHTKLASS-----CLLLEFVW 167
 DB 296 SLFLILISITTFCLTEHGFHISNKTYQASPIGAPPPENTINVEVEPEFLTYEGVC 355
 QY 168 IVFGELETTIRWSAGCCCRRGWGRRLFRAPKPCVIDTYLI-----ASIAVVSAKTQ 222
 DB 356 VVWFEEFELMRI---TFC-----PDKVEFLKSLNIIDCVALLPYLEVGSLGSKAA 406
 QY 223 GNIFATSLRSRLPQILRMVMDRGRGTWKLGSVVAHSKE-LITAWYIGFLVIESS 281
 DB 407 KDVL--GFLRVAREVRLITKFLRHENGRLVGLHTRASTNEFLLLITFLAIGVLFAT 464
 QY 282 FLVYLVERDANK-----FSTYADALMWGTLITIGYGDKTPLTWLGRILSNGFA 332
 DB 465 MIYVAERIGADDDLLGSNHYFKNIPIGFWMAVYMTLIGYGDMPKTMGMLVGAICA 524
 QY 333 LLGISFFALPAGILGSGFALKVOEORHOKHFERRN 368
 DB 525 LAGVLTIAMPVYIVNNGMYSLAMAKOLPKKK 560
 RESULT 30
 CITE_RAT STANDARD; PRT; 889 AA.
 AC Q01956;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv3.3 (KSHIID).
 GN KCNC3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS KSHIID.1 AND KSHIID.2).
 RC TISSUE=Brain;

RX MEDLINE=92396711; PubMed=1381835;
 RA de Mera E.V.-S., Moreno H., Fruhling D., Kentros C., Rudy B.;
 RT "Cloning of Shil1 (Shaw Like) cDNAs encoding a novel high-voltage-
 RT activating, TEA-sensitive, type-A K⁺ channel.";
 RL Proc. R. Soc. Lond., B. Biol. Sci. 248:9-16(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
 CC HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; KSHIID.1 (shown here) and
 CC KSHIID.2; are produced by alternative splicing.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC
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Query Match 5.2%; Score 244; DB 1; Length 889;
 Best Local Similarity 23.0%; Pred. No. 9.1e-07;
 Matches 95; Conservative 65; Mismatches 163; Indels 90; Gaps 13;

QY 378 WRSTAADKSVSIATWPKLALHTCSPTNOKLSFKERVAMASPRGOSIKSROASVGD RR 437
 DB 505 SPICKSEET-----SPDSTYSDTSPAPREGEVMEKRRADSKON-----GDAN 548
 QY 438 SPSDITAE-----SPTXOKSSEFDRTRFR 465
 DB 549 AVLSDEGAGLTOPLASPTPERRRALRRSGTRDR 583

RESULT 33
 CIRK_MOUSE STANDARD: PRT: 654 AA.

AC 061423;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.4.
 GN KCNA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AKR;
 RX MEDLINE=94292198; PubMed=8020965;
 RA Wyome R.S., Korenberg J.R., Kinoshita K.D., Aiyar J., Coyne C.,
 RA Chen X.N., Hustad C.M., Copeland N.G., Gutman G.A., Jenkins N.A.,
 RA Chandy K.G.;
 RT "Genomic organization, nucleotide sequence, biophysical properties,
 RT and localization of the voltage-gated K⁺ channel gene KCNA4/Kv1.4 to
 RT mouse chromosome 2/human 11p14 and mapping of KCNC1/Kv3.1 to mouse
 RT 7/human 11p14.3-p15.2 and KCNA1/Kv1.1 to human 12p13.";
 RL Genomics 20:191-202(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: 003723; AAB60668.1;
 CC DR HSSP: P15385; 1270.
 DR MGD: MGI:96661; Kcna4.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004051; KV14channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003966; Kv_channel.
 DR InterPro: IPR000636; Kv_channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.

DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1511; KV14CHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 309 327 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 372 393 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 405 425 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 444 462 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 479 498 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 540 562 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 38 50 POLY-ALA.
 FT DOMAIN 62 65 POLY-HIS.
 FT DOMAIN 83 89 POLY-ARG.
 FT DOMAIN 123 137 POLY-GLU.
 FT DOMAIN 162 166 POLY-GLN.
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 600 600 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 654 AA; 73473 MW; 8693651A30BD36D4 CRC64;

Query Match 5.1%; Score 240.5; DB 1; Length 654;
 Best Local Similarity 19.7%; Pred. No 9.7e-07;
 Matches 105; Conservative 75; Mismatches 163; Indels 191; Gaps 17;

QY 37 KVESGRGVNLNSAARGDGLLLGTRAAITGGGG-----GLRES 78
 DB 133 EEEBEGR---FYSEEDHGDCSYTDLDPQEDGGGGYSVRYSDCCERVYVNSGLNFE 189
 QY 79 RRGKQGRM-SLGRPLSYTSQSCRN----- 105
 DB 190 TOMKTLAOPPELLGPERKTOYFDPLRNEYFEDRNPSPDALIYYQSGRLRPVNP 249
 QY 106 -----VKYRVQNY-----LYNVLERP-----RG 124
 DB 250 FDIETEVVYQGEELALKFRDEGVFREEDRALPENFKKIMLFEPESSPRNG 309
 QY 125 WAFIHAFFVLVPGCLISVSTPE-----HTKLASSC----- 159
 DB 310 IAIV-----SVILIVISIVFCTETLEPFRRDRLIMALSAGHSRLINDTSAPHLENSGH 365
 QY 160 -----LILFEVMIYFGLEFTRILMSAGCCCRVGMQRLRPARKFCYIDITVIT-- 211
 DB 366 TIFNDPFLVEVCIWFSFEVYRCFAC-----TSQALFFKIMNITIDIVSTILPY 416
 QY 212 -ASIAVSAKTQG-----NIFATSLSLRFLOILRMVMDRGGTWMKLGSSVYAHS 263
 DB 417 FTLTGDLAQQGGGNGGQQQAMSFALIRILRVRFRIKLSRHSKGLDIGHTLNASM 476
 QY 264 KELITAWITGLVLFSSFLVLYVEND-ANKESTYADALAMWGTITLTITGKGKPLTW 322
 DB 477 RELGLLIFFLGVILFSSAVYFAEADPTHTQSLPDAFWMVVMTTGVGGMKPIV 536
 QY 323 LGRLLSAGFALLIGIFFALPAIGLISGFALKVQEOHRKFEKRRNPANILICVWMSYA 382
 DB 537 GGIIVGSLCINALGVLTIALPVPYIVSNFN---YFIRETNEQOTOLTQNAVSC----- 587
 QY 383 ADEKSVSIATWPKLALHTCSPTNOKLSFKERVAMASPRGOSIKSROASVGD RR 436
 DB 588 -----PVL-----PSNLKKFR-----SSVSSSLGDK 609

RESULT 34
 CIRK_RAT STANDARD: PRT: 655 AA.
 AC P15385;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Voltage-gated potassium channel protein Kv1.4 (RCK4) (RHK1) (RK4).
 GN KCNA4.
 ON Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain:
 RX MEDLINE=90059914; PubMed=2555158;
 RA Stuenkel W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Gleese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Heart;
 RX MEDLINE=90346174; PubMed=2384173;
 RA Tseng-Crank J., Tseng G.-N., Schwartz A., Tanouye M.A.;
 RT "Molecular cloning and functional expression of a potassium channel
 RT cDNA isolated from a rat cardiac library.";
 RL FEBS Lett. 268:63-68(1990).
 RN [3]
 RP STRUCTURE BY NMR OF 1-37.
 RX MEDLINE=97152495; PubMed=9000078;
 RA Artz C., Geyer M., Fakler B., Schott M.K., Guy H.R., Frank R.,
 RA Ruppersberg J.P., Kalbitzer H.R.;
 RT "NMR structure of inactivation gates from mammalian voltage-dependent
 RT potassium channels.";
 RL Nature 385:272-275(1997).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: HEART AND BRAIN
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; X16002; CA34133.1; -;
 DR EMBL; M32867; AAA41469.1; -;
 DR PIR; S06710; S06710.
 DR PDB; 1ZTO; 05-JUN-97.
 DR InterPro: IPR0000210; BMB_P0Z.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004051; KV14channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; KV_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.

DR PRINTS; PR01511; KV14CHANNEL.
 DR PRINTS; PR01491; KCHANNEL.
 DR PRINTS; PR01496; SHAKERCHANNEL.
 DR SMART; SM00225; BTF; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation; 3D-structure.
 FT TRANSMEM 310 328 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 373 394 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 406 426 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 445 463 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 480 499 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 541 563 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 38 50 POLY-ALA.
 FT DOMAIN 62 65 POLY-HIS.
 FT DOMAIN 92 95 POLY-GLY.
 FT DOMAIN 124 138 POLY-GLU.
 FT DOMAIN 163 167 POLY-GLY.
 FT DOMAIN 435 438 POLY-GLN.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 601 601 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CONFLICT 42 42 A -> L (IN REF. 2).
 FT CONFLICT 84 88 EEEAT -> RRRQ (IN REF. 2).
 FT CONFLICT 95 95 MISSING (IN REF. 2).
 FT CONFLICT 310 310 G -> A (IN REF. 2).
 SQ SEQUENCE 655 AA; 73390 MW; 40AEF2F901A05F43 CRC64;
 Query Match 5.1%; Score 240.5; DB 1; Length 655;
 Best Local Similarity 19.7%; Pred. No. 9.7e-07;
 Matches 105; Conservative 75; Mismatches 163; Indels 191; Gaps 17;
 QY 37 KDVSGRGVYLNAAAGDGLLLGTRATLVGGG-----GLRES 78
 DB 134 EEEEGEGR---FYEEEDHGGCSTYDILLPODDGGGGGSSVRYSDCCERYVNVSGLRE 190
 QY 79 RRGKGARM--SLGKPLSYTSSQSCRN-----105
 DB 191 TQMTLAFPEPTLLGDPEKPYQFDPLRNEYFDNRPSFDALYYQSGRLKRPVNP 250
 QY 106 -----VKRRVQNT-----LYNVIERP-----RG 124
 DB 251 FDIPEEYKPYQLEALIKFREDEGFVREEDRALPENRKKQIWLFEYESSSPARG 310
 QY 125 WAFIYHAFVFLVGCCLLYESTYPE-----HTKLASCC-----159
 DB 311 IAIY-----SVLVILISIVFCELTIDPEPRDROLIMALSAGSHSLNDTSAPHLENGH 366
 QY 160 -----LLIEFVMIIVFGLFEIIRIMSGCCCRVYRGNGRLRFARKPCVDTIVL-- 211
 DB 367 TIFNDPFVIVTCIVWFSFEVYVRCFAC-----PSQALFFKNIMNIIIDIVSLPY 417
 QY 212 -ASIAVVSATKQG-----NIFATSRLSLRFLOILMVRNDRRGGTAKLLGSVYVARS 263
 DB 418 FITLGTDLAQOOGGNGGQOQAMSPALIRIIRLVVFREFIKLSRSHSGIQLIIGHTLRASM 477
 QY 264 KELLTAMVIGFLVIFSSFLVYLYVEKD--ANKEFSYADALMGTTLTIGYGDRTPLM 322
 DB 478 RELGLLIFFLITGVILSSAVYFPADEPTTHFQSIIDPAFMVAVYMTTIVGIDMKPTIV 537
 QY 323 LGRLLSAGFALLIGISFFALPAGILGSGFALKVQEOHRKHFEKRRNPANLIIQCVWRSYA 382
 DB 538 GGRITVGLCAIAGVATIALPVPVIVSNFN--YFYHRETFENDEQQLQPNVAVS-----588
 QY 383 ADEKSVSIATVKKPHLKAHTCSPTNOKLSFKERVMAASPRGSIISROASVDR 436
 DB 589 -----PYL-----PSNLKKFR-----STSSSLDCK 610
 RESULT 35
 CIRK3_HUMAN STANDARD; PRT; 523 AA.
 ID CIRK3_HUMAN
 AC P22001;

DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.3 (HPCN3) (HGK5) (HUKIII)
 DE (HGK3)
 GN KCNA3 OR HGK5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=91095456; PubMed=1986382;
 RA Phillips L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
 RA Nelson D.J., Steiner D.F.;
 RT "Sequence and functional expression in *Xenopus* oocytes of a human
 RT Insulinoma and Islet potassium channel.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymphocytes;
 RX MEDLINE=92189730; PubMed=1547020;
 RA Cai Y.-C., Osborne P.B., North R.A., Dooley D.C., Douglass J.;
 RT "Characterization and functional expression of genomic DNA encoding
 RT the human lymphocyte type n potassium channel.";
 RL DNA Cell Biol. 11:163-172(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92235098; PubMed=1373731;
 RA Attali B., Romey G., Honore E., Schmid-Alliana A., Mattei M.-G.,
 RA Lesage F., Ricard P., Barhanin J., Lazdunski M.;
 RT "Cloning, functional expression, and regulation of two K⁺ channels in
 RT human T lymphocytes.";
 RL J. Biol. Chem. 267:8650-8657(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE=95130104; PubMed=7829094;
 RA Foldander K., Douglass J., Swanson R.;
 RT "Confirmation of the assignment of the gene encoding Kv1.3, a
 RT voltage-gated potassium channel (KCNA3) to the proximal short arm of
 RT human chromosome 1.";
 RL Genomics 23:295-296(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 CC EMBL: M55515; AAA36425.1; -
 CC DR EMBL: M38217; AAB88073.1; -
 CC EMBL: M85217; AAA59457.1; -

DR EMBL: L23499; AAC31761.1; -
 DR HSSP: Q54397; 1BL8
 DR Genew; HGNC:6221; KCNA3.
 DR MIM: 176263; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K⁺channel_pore.
 DR InterPro: IPR004050; Kv1.3channel.
 DR InterPro: IPR003091; K⁺channel.
 DR InterPro: IPR003131; K⁺tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M⁺channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF02214; K_tetra. 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1510; KV13CHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 183 201
 FT TRANSMEM 243 264
 FT TRANSMEM 276 296
 FT TRANSMEM 311 329
 FT TRANSMEM 346 365
 FT TRANSMEM 407 429
 FT CARBOHYD 57 57
 FT CARBOHYD 227 227
 FT MOD_RES 468 468
 FT CONFLICT 20 20
 FT CONFLICT 37 37
 FT CONFLICT 61 61
 FT CONFLICT 91 91
 FT CONFLICT 257 257
 FT CONFLICT 338 338
 FT CONFLICT 419 419
 FT CONFLICT 488 488
 FT SEQUENCE 523 AA; 58303 MW; 8BA2F1C7C802B411 CMC64;
 Query Match 5.0%; Score 237; DB 1; Length 523;
 Best Local Similarity 22.2%; Pred. No. 1.2e-06;
 Matches 68; Conservative 64; Mismatches 114; Indels 60; Gaps 8;

QY 104 RAVKRYRQNYLYNVLERP-----RCMATIYHAFVLYVGCILTSFSTIPEH----- 152
 DB 157 RFLPRDFORQYWLLEYPSSGPARGIATV---SVLVITISTVICLETLPFERDEKD 212
 QY 153 -----TKLASSCLLLEFVMIYVFGLEFIIRWSAGCCCHYR 189
 DB 213 YPASTSODSFEAAGNSTSGSRAGASSDFFVETICITWFSELLVRFAC----- 265
 QY 190 QMGQRLRFPRKPCVVDITVLT---ASIAVYSAKTQGN---IFATSALRSIRPLQILMV 243
 DB 266 --PSKATFERNIMNLNDIIVAIIPYFTLTGTELAEKQNGQOAMSLAIRVIRLVFRIF 323
 QY 244 RMDRGGTAKLIGSVYVYVSKEL-ITAWYTGFLVYIPSSFLVYLVENDAKESFTYDAL 302
 DB 324 KLSRHSKGLIIGQITKASMKRELGLIFLFTGVILSSAVYFEADDPISGFSIPAF 383
 QY 303 WMGITLTITIGYGDKPTLWLGRLSAGFALLGISFPALPAGILSGF-----ALKVOE 356
 DB 384 WMAVVTMTVVGDMHVPITIGKIVGSLACIAGVLTALPVPYIVSNFNRYHRETESEE 443
 QY 357 QHRQKH 362
 DB 444 OSQYMH 449
 RESULT 36
 CIRC_RAT
 ID CIRC_RAT
 AC P15384;
 STANDARD; PRT; 525 AA.

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Voltage-gated potassium channel protein Kv1.3 (RGK5) (RCK3) (KV3).
 GN KCNA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=90059914; PubMed=2555158;
 RA Stuehmer M., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stuehmer M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=90297965; PubMed=2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=90278098; PubMed=2351830;
 RA Douglass J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J.,
 RA Adelman J.P.;
 RT "Characterization and functional expression of a rat genomic DNA
 RT clone encoding a lymphocyte potassium channel.";
 RL J. Immunol. 144:4841-4850(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
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 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
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 DR EMBL: X16001; CAA34132.1; -;
 DR EMBL: M30312; AAA42035.1; -;
 DR EMBL: M31744; AAA41500.1; -;
 DR PIR: S06708; S06708.
 DR PIR: JH0168; JH0168.
 DR HSSP: O54397; 1BL8.
 DR InterPro: IPR000210; BTH_POZ.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR004050; KV13channel.
 DR InterPro: IPR003091; K_channel.

DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans_1.
 DR Pfam: PF02214; K_tetra_1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01510; KV13CHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 185 203 SEGMENT S1.
 FT TRANSMEM 245 266 SEGMENT S2.
 FT TRANSMEM 278 298 SEGMENT S3.
 FT TRANSMEM 313 331 SEGMENT S4.
 FT TRANSMEM 348 367 SEGMENT S5.
 FT TRANSMEM 409 431 SEGMENT S6.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 470 470 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CONFLICT 106 106 F -> L (IN REF. 1).
 FT CONFLICT 181 181 G -> R (IN REF. 3).
 FT CONFLICT 430 430 V -> L (IN REF. 3).
 SQ SEQUENCE 525 AA; 58424 MW; 6DA8869D5471C401 CRC64;
 Query Match 5.08; Score 237; DB 1; Length 525;
 Best Local Similarity 23.38; Pred. No. 1.2e-06;
 Matches 67; Conservative 63; Mismatches 104; Indels 54; Gaps 8;
 QY 104 RNVKRYRYOVYLVNLERP-----RGMAFYHAFVLVGCILSVSTIPE----- 151
 DB 159 RPLPRDFQKQVWLFEPSSSGPARKAIY----SVLVISIVIFCLELTFPERDND 214
 QY 152 -----HTKLASS-----CLILEFYAVFGEFLIRWSAGCCRRY 189
 DB 215 YPASPQDVEAANNSTSGASSGSFSDPEFVETICIIWFSELLVRFAC----- 267
 QY 190 GNGRLFAKPCVIDTYVLI---ASLAVSACTQGN---IFATSAKSLFLQILMV 243
 DB 268 --PSKATFSRNINMLDIDVAIIPEYITLIGTELARQGGQAMSLALIRLVKVFRTF 325
 QY 244 RMDRGSTWKLDSVYAHKEU-ITAMYIGFLVLFSPFLVYKDNKEFTYADAL 302
 DB 326 KLSRHSKGLDILGTLASMRLEGLLFFLTGYLTSSAVYFAPADPPSGFNSIPDAF 385
 QY 303 WMCITLTITIGYGDKPPLTWLGRLLSAGFALLGISFFALPAGILGSGF 350
 DB 386 WMAVVTITVGYGDMHPVTIGKIVGSLCAIAGVLTALPVPVIVSNF 433
 RESULT 37
 CIR4_BOVIN STANDARD; PRT; 660 AA.
 AC 005037;
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Voltage-gated potassium channel protein Kv1.4 (BAR4).
 GN KCNA4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=92371645; PubMed=1505668;
 RA Garcia-Guzman M., Calvo S., Cena V., Criado M.;
 RT "Molecular cloning and permanent expression in a neuroblastoma cell

RT line of a fast inactivating potassium channel from bovine adrenal
 RT medulla.
 RL FEBS Lett. 308:283-289(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X57033; CAA40349.1; -
 CC DR HSSP: P15385; 1270. B7B_POZ.
 CC DR InterPro: IPR000210; B7B_POZ.
 CC DR InterPro: IPR001622; K+channel_pore.
 CC DR InterPro: IPR004051; KV14channel.
 CC DR InterPro: IPR003091; K_channel.
 CC DR InterPro: IPR003131; K_tetra.
 CC DR InterPro: IPR003968; KV_channel.
 CC DR InterPro: IPR000636; M+channel_nlg.
 CC DR InterPro: IPR003972; Shaker_channel.
 CC DR Pfam: PF00520; Ion_trans.1.
 CC DR Pfam: PF02214; K_tetra.1.
 CC DR PRINTS: PRO0169; KCHANNEL.
 CC DR PRINTS: PRO1511; KV14CHANNEL.
 CC DR PRINTS: PRO1491; KCHANNEL.
 CC DR PRINTS: PRO1496; SHAKERCHANNEL.
 CC DR SMART: SM00225; B7B.1.
 CC DR SMART: SM00225; B7B.1.
 CC DR GlycoProfile: Multigene family: Ion transport: Voltage-gated channel;
 CC KW GlycoProfile: Multigene family: Phosphorylation.
 CC FT TRANSMEM 316 334 SEGMENT S1 (POTENTIAL).
 CC FT TRANSMEM 379 400 SEGMENT S2 (POTENTIAL).
 CC FT TRANSMEM 412 432 SEGMENT S3 (POTENTIAL).
 CC FT TRANSMEM 451 469 SEGMENT S4 (POTENTIAL).
 CC FT TRANSMEM 486 505 SEGMENT S5 (POTENTIAL).
 CC FT TRANSMEM 547 569 SEGMENT S6 (POTENTIAL).
 CC FT TRANSMEM 38 50 POLY-ALA.
 CC FT DOMAIN 53 59 POLY-GLY.
 CC FT DOMAIN 62 65 POLY-HIS.
 CC FT DOMAIN 83 87 POLY-ARG.
 CC FT DOMAIN 131 137 POLY-GLY.
 CC FT DOMAIN 162 173 POLY-GLY.
 CC FT DOMAIN 441 444 POLY-GLN.
 CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 607 607 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT SEQUENCE 660 AA; 73512 MW; ALFAE59677929D5 CRC64;

Query Match 5.08; Score 235.5; DB 1; Length 660;
 Best Local Similarity 23.78; Pred. No. 1.9e-06;
 Matches 74; Conservative 57; Mismatches 116; Indels 65; Gaps 10;

DB 139 GCLTLEVFSTPE---HTKLASSCLLIEFPMIVFGLFETIRMSAGCCCTRMGQGL 195
 356 GGLINDTSAHPENSGHT-IFNDPFIVETVCIWFSEFVRCFAC-----PSQA 405

QY 196 RFARKPCVYIDRTVL---ASIAVSAKTOG-----NIFATSALRSLRELQILRM/RM 245
 DB 406 LFFKNIMNIDIVSILPYFTLTGDLAQOQGGGQOQOAMSFALIRILRVFRIRKL 465
 QY 246 DRGGTKWLLGSSVYVNAHKKELITAWYIGFVLVFFSSFLVLYEVD-ANKESFYADALMW 304
 DB 466 SHRSKGLQILGHTLRASMRLEGLLIFPLFGVILFSSAVFAEADPTTHQSPDAPMW 525
 QY 305 GTITLTITGYGDKPTLWGLRLLSAGFALLGISFPALPAGILGSGFALKVOEHRQKHE 364
 DB 526 AVYMTWTGCGDKPRTYVGKIVGSLCAIGVLTALPVPVYSNFN---YFYHRETFNE 582
 QY 365 KRRNPANILQCVWRSYADERSVSTATMPHKLALTCSPNTOKLSPEKEVRASPRQ 424
 DB 583 EPTQLQNMVSC-----PYL-----PSNLKFR----- 606
 QY 425 SIKSRQASVGR 436
 DB 607 --STSSSLGDK 616

RESULT 38
 CIR4_MUSPF STANDARD; PRT; 654 AA.
 AC Q28527;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Kv1.4 (FK1).
 GN KCNA4.
 OS Muscula putorius furo (Ferret).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 CC Muscula.
 OX NCBI_TaxID=9669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart ventricle;
 RX MEDLINE=95029958; PubMed=7943383;
 RA Comer M.B., Campbell D.L., Rasmussen R.L., Lamson D.R.,
 RA Morales M.J., Zhang Y., Strauss H.C.;
 RT "Cloning and characterization of an Ito-like potassium channel from
 RT ferret ventricle."
 RL Am. J. Physiol. 267:H1383-H1395(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. LEFT AND RIGHT
 CC VENTRICLE, AND KIDNEY BUT NOT IN SKELETAL MUSCLE, ENDOTHELIAL
 CC CELLS, AORTA, AND LIVER.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

Query Match	Best Local Similarity	4.9%; Score 233; DB 1; Length 656;
Matches 67; Conservative 48; Mismatches 99; Indels 46; Gaps 7		
QY 128	IYHAEVFLLL--VFQGL-----ILVSFTPEHETKL-----ASSCLLIEFMAIYF 171	DR Pfam: PF00520; Ion trans; 1.
Db 231	IISVEVILLSTIYFCELETLPEKHKYKVFNTTNGKRIEDEVDYDIDPFLIEITCLIMF 290	DR Pfam: PF02214; K lettra; 1.
QY 172	GLEFIRIRMSAGCCCRKRGMGQRLLFAKRPFCYIDITVL---ASIAVVA----- 219	DR PRINTS: PRO1508; KVILCHANNEL.
Db 291	TFEELTV-----RFLACPKNLFCRDVNVNVDIAIILPYFITLATYVAEEDTLNP 341	DR PRINTS: PRO1491; KVCHANNEL.
QY 220	-----KTQGNIFATSLRSLRFQLDIRMVRMDRGGTWKLGSVVAASHKEL--ITAW 270	DR PRINTS: PRO1496; SHAKECHANNEL.
Db 342	KAPVSPQKFSNQAMSLAILNIVRIYLRVPRIRKLSHSGLDQIDIGTLAKASMELGLITF 400	DR SMART: SM00225; BTB; 1.
QY 271	YIGFLVYLIFSSFLVLYLVEKDANKERFSYADALIMGCTITVLTITGYGDKTFLTWLGRLLSAG 330	KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
Db 402	FLFLGVVLYESSAVYFAEAGSENSFPKSIDPAFMVAWVMTFTVGYGDMTEPVGWGIIVGSL 461	KT Ion channel; Transmembrane; Ion transport; Voltage-gated channel;
QY 331	FALIGSFPAIPAGILGSGF 350	KT Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
Db 462	CAIAGVLTIALPVPYIVSNF 481	KT Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;

ID	CIRK MOUSE	STANDARD:	PRT:	528 AA.
AC	P16390:			
DT	01-AUG-1990 (rel. 15, Created)			
DT	01-FEB-1996 (rel. 33, Last sequence update)			
DT	15-JUN-2002 (rel. 41, Last annotation update)			
DE	Voltage-gated potassium channel protein Kv1.3 (MK3).			
GN	KCNA3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90161996; PubMed=2305265;			
RA	Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,			
RA	Shanshali S., Tempel B.L., Gutman G.A.;			
RT	A family of three mouse potassium channel genes with intronless			
RT	coding regions.";			
RL	Science 247:973-975(1990).			
CC	-I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	-I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE			
CC	RATE OF INACTIVATION OF THE CHANNEL, WHILE THE TAIL MAY PLAY A ROLE			
CC	IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL			
CC	TO SPECIFIC SUBCELLULAR COMPARTMENTS.			
CC	-I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	-I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@lsb-sib.ch).			
CC	-----			
CC	EMBL: M30441; AAA39716.1; -.			
DR	HSSP: Q54397; 1BL8.			
DR	MGI: 96660; Kcnab.			
DR	InterPro: IPR000210; RTB_POZ.			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR004050; KV13channel.			
DR	InterPro: IPR003091; K_channel.			
DR	InterPro: IPR003131; K_tetra.			
DR	InterPro: IPR003968; kv_channel.			
DR	InterPro: IPR000636; M+channel_nig.			
DR	InterPro: IPR003972; Shaker_channel.			
DR	Pfam: PF00520; Ion_trans; 1.			
DR	Pfam: PF02214; K_tetra; 1.			
DR	PRINTS: PRO0169; KCHANNEL.			
DR	PRINTS: PRO1510; KV13CHANNEL.			
DR	PRINTS: PRO1491; KVCHANNEL.			
DR	PRINTS: PRO1496; SHAKERCHANNEL.			
DR	SMART: SM00225; RTB; 1.			
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;			
KW	Glycoprotein; Multigene family; Phosphorylation.			
FT	TRANSMEM 188 206 SEGMENT S1.			
FT	TRANSMEM 248 269 SEGMENT S2.			
FT	TRANSMEM 281 301 SEGMENT S3.			
FT	TRANSMEM 316 334 SEGMENT S4.			
FT	TRANSMEM 351 370 SEGMENT S5.			
FT	TRANSMEM 412 434 SEGMENT S6.			
FT	CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).			

[illegible]

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CC -----
 DR EMBL: X12589; CAA31102.1; -
 DR EMBL: M26161; AAA41982.1; -
 DR PIR: A41353; A41353.
 DR PIR: S01161; S01161.
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR004048; K+channel.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003972; Shaker_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1508; KYLCHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1496; SHAKERCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 FT Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 168 186 SEGMENT S1.
 FT TRANSMEM 221 242 SEGMENT S2.
 FT TRANSMEM 254 274 SEGMENT S3.
 FT TRANSMEM 290 309 SEGMENT S4.
 FT TRANSMEM 326 345 SEGMENT S5.
 FT TRANSMEM 387 408 SEGMENT S6.
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RSS 322 322 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD_RSS 445 445 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64;

Query Match 4.9%; Score 230; DB 1; Length 495;
 Best Local Similarity 19.6%; Pred. No. 2.7e-06;
 Matches 75; Conservative 80; Mismatches 142; Indels 86; Gaps 10;
 Oy 104 RNKYYRRQNYLYNLEBR--GNAFIYHAFYFLVFGCLLSVFSTIE----- 151
 Db 142 RPLPEKEYQROVWLLFEYPSSGPARVIAIVSVWVLLISVIFCLETLELDDKDFGT 201
 Oy 152 -----HTKLASSCLLLEFVMIVVEGLEFIIRISAGCCCRYGMOGRLEFPARK 200
 Db 202 IHRIDNTVITYTNSFTDPFIVERLCTIWFSEFLVREFAC-----PSKDFPKN 252
 Oy 201 PCVVIDITVL--ASIAVVSAGTOGN-----IFATSLRSLRFLOILRMVRDRRGTV 252
 Db 253 IMNFIDIAIIPYFTLTLEIEOENOGEOATSLAIRVIRLIVAVFRIFKLRSKGL 312
 Oy 253 KLLGSVVAHAKEL-ITAMVIGFLVLITSSFLVLYVERKANKEFSTYAAALMGTTITLT 311
 Db 313 QILGTLTASMEKELGELLFELTGVILFSSAVYFAEAEESHFSSIPAFMVAVSMVT 372
 Oy 312 IGYGDKPLTWLGRLLSAGFALLGISFPAIGILSSGPAKLVQEOHROKHFEKRNPAA 371
 Db 373 VGYGMYVTYIGKIVGSLCAIAGVLTIALPVPVIVSNN--YFHRREGSEQ----- 424
 Oy 372 NLIOCVMSYADEKSVSIATWPKPHIKALHTCSP-----TNOKLSFEKRYMAS 420
 Db 425 -----AQLHVSPPNLASDSDLRRSSSTLSKSEYMEIEE 459
 Oy 421 PRGOSIKS-ROASVGDRRSPSTD 442
 Db 460 DMNNSIAHYRQANIRGTCTATD 482

RESULT 43
 CIRD_HUMAN
 ID CIRD_HUMAN STANDARD; PRT; 511 AA.
 AC P48347;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Voltage-gated potassium channel protein Kv3.1 (Kv4) (NGK2).
 GN KCNC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93194190; PubMed=8449507;
 RA Ried T., Rudy B., de Miera E., Lau D., Ward D.C., Sen K.,
 RT "Localization of a highly conserved human potassium channel gene
 RT (NGK2-KV4; KCNC1) to chromosome 11p15.";
 RL Genomics 15:405-411(1993).
 RN [2]
 RP SEQUENCE OF 244-475 FROM N.A.
 RX MEDLINE=93016011; PubMed=1400413;
 RA Griesmer S., Ghanshani S., Dehlefs B., McPherson J.D.,
 RA Wasmuth J.J., Gutman G.A., Cahalan M.D., Chandy K.G.;
 RT "The Shaw-related potassium channel gene, Kv3.1, on human chromosome
 RT 11, encodes the type 1 K+ channel in T cells.";
 RL J. Biol. Chem. 267:20971-20979(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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CC -----
 DR EMBL: S56770; AAB25764.1; -
 DR EMBL: M96747; AAA59458.1; -
 DR HSSP: Q54397; 1BL8.
 DR Genew: HGNC:6233; KCNC1.
 DR MIM: 176258; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003091; K+channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003974; Shaw_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PRO0169; KCHANNEL.
 DR PRINTS: PRO1491; KVCHANNEL.
 DR PRINTS: PRO1496; SHAWCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family.
 FT DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).
 FT

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FT TRANSMEM 191 209 SEGMENT S1 (POTENTIAL).
FT DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 267 SEGMENT S2 (POTENTIAL).
FT DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 295 SEGMENT S3 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 309 331 SEGMENT S4 (POTENTIAL).
FT DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 345 366 SEGMENT S5 (POTENTIAL).
FT DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 415 436 SEGMENT S6 (POTENTIAL).
FT DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57942 MW: 10A93478F7120AB CRC64;

Query Match 4.9%; Score 230; DB 1; Length 511;
Best Local Similarity 21.8%; Pred. No. 2.8e-06;
Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

3 RHHAGEEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVLLNSAARGDGLLLG 62
110 RQHRDAE-----ALDSFGAPLDNSAD-----ADADGFG----- 140
63 TRAAITGGGGGGLRSGRKGARMSILGKPLSTYSQSCRNVKRYRVONYLYNTERP 122
141 -----DSGDEDELEMT-----KRLALSDSPDRPGGFWRRMQPRIVALFEDP 183
123 RGMAFI-YHAFVELLVFGLISV-----FSTIPRHTKL----- 155
184 YSSRARVYAFASLPF---ILVSITTFCTETHERFNPVTKTELENVNGTOVRYREAE 240
156 ASSCLLLEFVNIIVVGLFETIRISAGCCCRYGNOGRILFARKPCVIDTYILI--- 211
241 TEAFLEYIEGVCVVFTEFELKRV---IFC-----PNKVEFKNSLIIDFVALDPYLL 291
212 -ASIAVSAKQGNIFATISALSLRFLQILRMVRMDRGGTMMKLLGCVYVAHSE-LITA 269
292 EVGSGISSKAKADVL--GFLRVYRVRILRIKFLRHFGVLGHTLHASTNEFLILLI 349
270 WYGFVLVIFSEFLVYVEK-----DANKETSTADALMWGITLTITIGYDXT 319
350 IFALGVILFNF-MIYIERIGAOQRPDPASETHKRNIPIGWMAVYMTLTIGDYMP 408
320 LTLWGLRLSAGFALIGISFFALPAGILSGFALKVO--EOROKHFEKRRNPANLLOCW 378
409 QTWGGMVLGALCALAGVLTIAMPVPIYVNNFGMYSLAAMAKKLPKKKKHPRPOLGS 468
379 RSYADEKSVSIATWKPRLKALHTCSPTNOKLSFKERVRAVSRGCSI 426
469 PNICK-----SVNSPHHSTOSDTCPLAGEELLEINRAGRKRPLRGMSI 511

RESULT 44
CIRK_MOUSE ID STANDARD; PRT: 511 AA.
AC P15388;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv3.1 (Kv4) (NGK2).
GN KCNC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=90092535; PubMed=2599109;
RA Tokoyama S.; Imoto K.; Kawamura T.; Higashida H.; Iwabe N.; Miyata T.;
RT Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells.
RT Primary structure and functional expression from cDNAs."

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RL FEBS Lett. 259:37-42(1989).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; Kv3.1 (shown here) and Kv4;
CC are produced by alternative splicing.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL: Y07521; CAA68814.1; -
DR PIR: S07095; S07095.
DR HSSP: Q54397; 1BL8.
DR MGD: MGI:96667; Kcnc1.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K+channel.
DR InterPro: IPR003131; K+channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003974; Shaw_channel.
DR Pfam: PF00520; Ion_trans. 1.
DR Pfam: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01491; KCHANNEL.
DR PRINTS: PR01498; SHAWCHANNEL.
DR SMART: SM00225; BTB; 1.
DR K+ ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
DR Glycoprotein; Multigene family; Alternative splicing;
DR DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 191 209 SEGMENT S1 (POTENTIAL).
FT DOMAIN 210 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 267 SEGMENT S2 (POTENTIAL).
FT DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 295 SEGMENT S3 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 309 331 SEGMENT S4 (POTENTIAL).
FT DOMAIN 332 344 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 345 366 SEGMENT S5 (POTENTIAL).
FT DOMAIN 367 414 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 415 436 SEGMENT S6 (POTENTIAL).
FT DOMAIN 437 511 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 511 AA: 57928 MW: 50A939E8F7120F37 CRC64;

Query Match 4.9%; Score 230; DB 1; Length 511;
Best Local Similarity 21.8%; Pred. No. 2.8e-06;
Matches 102; Conservative 76; Mismatches 180; Indels 110; Gaps 17;

3 RHHAGEEGGAAGLWVKSAAAAAGGRLSGMKDVEGRGVLLNSAARGDGLLLG 62
110 RQHRDAE-----ALDSFGAPLDNSAD-----ADADGFG----- 140
63 TRAAITGGGGGGLRSGRKGARMSILGKPLSTYSQSCRNVKRYRVONYLYNTERP 122

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Db 142 RPLPEKEQROVWLFEPYESSGPANVAIVSVVILISVIFCLELPLPELKDQDEFTGT 201
 QY 152 -----HTKLASCLLLEFYMIVVGFLEFIRIMSAGCCCRVGRWGRLREARK 200
 Db 202 VHRIDNTVIVSNFTDPEFIVETLCIWFSEFLVVRPAC-----PSTDFEKN 252
 QY 201 PCVYDITVL---ASIAVSAKTOGN-----IFATSLRSLRPLQLLRVMDRGGTW 252
 Db 253 IMNFIDYAIIPFYTLGTEIAEOENOGEOATSLAILVIRIVRFRFKLSRHSKGL 312
 QY 253 KLLGSVVAHSKEL-ITAWYIGFVLVIFSSFLVYLVEKDKNKPESTADLMNGTITLT 311
 Db 313 QILGOTLASHRELGLLFFLFGVLFSSAVFAAEAEBSHSPSPDAFWMAVVSMTT 372
 QY 312 IGYGDKTPLTWLGRLLSAGFALLGISFALPAGILSGFALKVOEORHOKHFERRNPA 371
 Db 373 VGYGDMYPTIGKIVGSLCAGVLTALPVPVIVSNEN---YFYHREGEQD---A 425
 QY 372 NLICQVMSYAAD-----EKSVAIATWPKPHLKALHTCSPTNOKL 410
 Db 426 QLLHVVSPNLASDLSLRSSSTMSKEYMEIEEDMNNSTAHYKOVNIRTANCTTANQC 485
 QY 411 SFKEV 416
 Db 486 VNKSKL 491

RESULT 46

CIRK_RAT STANDARD: PRT: 585 AA.
 ID P25122;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Voltage-gated potassium channel protein KV3.1 (KV4) (NGK2) (RAM2).
 GN KCNC1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91219486; PubMed=2023941;
 RA Lüneau C.J., Williams J.B., Marshall J., Levitan E.S., Oliva C.,
 RA Smith J.S., Antanavage J., Folander K., Stein R.B., Swanson R.,
 RA Kaczmarek L.K., Buhrow S.A.;
 RT "Alternative splicing contributes to K⁺ channel diversity in the
 RT mammalian central nervous system";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3932-3936(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92331599; PubMed=1378392;
 RA Rettig J., Wunder F., Stocker M., Lichtenhagen R., Mastiaux F.,
 RA Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,
 RA Vohr R., Pongs O.;
 RT "Characterization of a Shaw-related potassium channel family in rat
 RT brain";
 RL EMBO J. 11:2473-2486(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR

CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS, BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M68880; AAA41501.1; -;
 CC EMBL: X62840; CAA44644.1; -;
 CC PIR: A39395; A39395.
 CC PIR: S22704; S22704.
 CC HSSP: Q54397; 1BL8.
 CC InterPro: IPR002210; BTB_POZ.
 CC InterPro: IPR001622; K_channel_pore.
 CC InterPro: IPR003091; K_channel.
 CC InterPro: IPR003131; K_tetra.
 CC InterPro: IPR003968; KV_channel.
 CC InterPro: IPR000636; M_channel_nig.
 CC InterPro: IPR003974; Shaw_channel.
 CC Pfam: PF00520; Ion_trans_1.
 CC Pfam: PF02214; K_tetra_1.
 CC PRINTS: PR00169; KCHANNEL.
 CC PRINTS: PR01491; KVCCHANNEL.
 CC PRINTS: PR01498; SHAWCHANNEL.
 CC SMART: SM00225; BTB; 1.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Alternative splicing.
 CC DOMAIN 1 190
 CC TRANSMEM 191 209
 CC DOMAIN 210 247
 CC TRANSMEM 248 267
 CC DOMAIN 268 276
 CC TRANSMEM 277 295
 CC DOMAIN 296 308
 CC TRANSMEM 309 331
 CC DOMAIN 332 344
 CC TRANSMEM 345 366
 CC DOMAIN 367 414
 CC TRANSMEM 415 436
 CC DOMAIN 437 585
 CC CARBOHYD 220 220
 CC CARBOHYD 229 229
 CC VARSPLIC 502 511
 CC VARSPLIC 512 585
 CC SEQUENCE 585 AA; 65857 MW; DD4E2D32848B2DCE CRC64;
 SQ
 Query Match 4.88; Score 227; DB 1; Length 585;
 Best Local Similarity 22.28; Pred. No. 5, 1e-06;
 Matches 92; Conservative 72; Mismatches 138; Indels 112; Gaps 17;
 QY 3 RHAGGEGGAAGLWVSGAAAGGGRGSGKDVESGRGVILNSAARGDILLG 62
 Db 110 RQHRDAE-----ALDSFGARPLDNSMD-----ADADGR----- 140
 QY 63 TRAAITGGGGGGLRESRRKGARMSLLKPLSTYSQSCRRNVKRYRVQYLVNLERP 122
 Db 141 -----DSGDGEDELEMT-----KRLALSDSPDGRPGGFWRCPRIVALFDP 183
 QY 123 RGMATF-YHAFVFLVFGLLISV-----FSIIPETKL----- 155
 Db 184 YSSRAYVAFAFLF-----ILVSTTFCTETHERFNIVKTLETENVNGTVRYREAE 240
 QY 156 ASSCLLLEFYMIVVGFLEFIRIMSAGCCCRVGRWGRLREARKPCVIDTIVL----- 211
 Db 241 TEAFITLIEGVCVWMTFFELKRV-----VFC-----PNKEFLKNSLNIIDFVAILPPYL 291
 QY 212 -ASIAVSAKTOGNIFATSLRSLRPLQLLRVMDRGGTWLLGSVVAHSKE-LITA 269

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Db 292 EVGLISGLSSKAAKVDL--GFLRVRFVRLIRFKLRHFVGLVGLTGLASTNEFLLLI 349
Oy 270 WYIGLVLFVFSFLVYLVK-----DANKESTADALMWGITITITGGYKTP 319
Db 350 IFLALVGLIFAF-MIYARICGAOPNPDSASETHRKNPICGPMVAVVTITGGYGMYP 408
Oy 320 LTVLGRLLSAGFALLGISFALPAGIL---GSGFALKVQEO---HROKHFEK 365
Db 409 OTWSGMLVGLCALCALCVLTITAMPVIVNNFGMYISLAMAKOKLPKKKKHTRP 462

RESULT 47
CIRK_MOUSE STANDARD; PRT; 495 AA.
AC P16388.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Voltage-gated potassium channel protein Kv1.1 (MK1) (MK1).
GN KCNA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90161996; PubMed=2305265;
RA Chandu K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ghanshani S., Tempel B.C., Gutman G.A.;
RT "A family of three mouse potassium channel genes with intronless
RT coding regions."
RT Science 247:973-975(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=88189348; PubMed=2451788;
RA Tempel B.L., Jan Y.N., Jan L.Y.;
RT "Cloning of a probable potassium channel gene from mouse brain."
RT Nature 332:837-839(1988).
RL
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL, M30439; AAA39711.1; -
CC EMBL, Y00305; CAA68408.1; -
CC PIR, S06378; S06378.
CC PIR, A40090; A40090.
CC HSSP, G34397; 1BL8.
CC MGD; MG1:96654; Kcna1.
CC InterPro; IPR000210; BTB_P0Z.

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DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR004048; Kv11channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR000636; M-channel_n19.
DR InterPro; IPR003972; Shaker_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01508; KV11CHANNEL.
DR PRINTS; PR01491; KVCCHANNEL.
DR PRINTS; PR01496; SHAKERCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT 51.
FT TRANSMEM 221 242 SEGMENT 52.
FT TRANSMEM 254 274 SEGMENT 53.
FT TRANSMEM 290 309 SEGMENT 54.
FT TRANSMEM 326 345 SEGMENT 55.
FT TRANSMEM 367 408 SEGMENT 56.
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT MOD_RES 446 446 PHOSPHORYLATION (BY PKA) (POTENTIAL).
SO SEQUENCE 495 AA; 56409 MW; C9249F130E943D3D CRC64;

Query Match 4.8%; Score 226; DB 1; Length 495;
Best Local Similarity 21.1%; Pred. No. 4,7e-06;
Matches 66; Conservative 74; Mismatches 125; Indels 48; Gaps 8;

Oy 104 RNKVRARQVNYLVNLERP--GMAFIYAFVFLVFGCLISVFSTPE-----151
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 142 RPLPEKRYQROYWLIFETPESSGPARYAIVSVMVLISIVFCLTTEBLADKDKFTGT 201
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Oy 152 -----HTKLASSCLITLFEVMIVFGELFIRITMSAGCCCRKMGORLPARK 200
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 202 IHRIDNTVITYTSNFTDPEFVETLCIMFSELCVRRFAC-----PSKTDPFKN 252
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Oy 201 PCVYIDTIVL---ASIAVYSAKTQGN-----IFATSAIRSLRFLDILRMVRRDRGGTW 252
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 253 IMNFEDIYAIIPYFTLTGTEIAEOGNQGEQATSAIRLVIRLVVFRFKLSRSKGL 312
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Oy 253 KLGSSVVAHSHKEL-ITAVYIGFVILFESSFLVYLVKANKNEFSYADALMWGITITTT 311
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 313 QILGOTLRASMRDLILFELTGYLFSAYFAEAERESHFSIPDAFMVAVVSMTT 372
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Oy 312 IGYGDKPTLVGLRLSAGFALLGISFALPAGIILSGFALKVQEOHROKHFEKRRNPAA 371
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 373 VGYGMYVTVTIGKIVGSLCAIGVLTALPVPVIVSNFN---YFHYRTEGEQ-----A 425
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Oy 372 NLIQCWRSYAAD 384
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 426 QLLHVSSPNLASD 438

RESULT 48
CIRK_MOUSE STANDARD; PRT; 601 AA.
AC P79197.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Voltage-gated potassium channel protein Kv1.5.
GN KCNA5.
OS Musceta putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9669;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart atrium;

```


DR SMART: SM00225; BTR: 1.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycine channel; Multigene family; Phosphorylation.
 FT TRANSSEM 242 260 SEGMENT S1.
 FT TRANSSEM 316 336 SEGMENT S2.
 FT TRANSSEM 347 368 SEGMENT S3.
 FT TRANSSEM 387 408 SEGMENT S4.
 FT TRANSSEM 423 444 SEGMENT S5.
 FT TRANSSEM 484 505 SEGMENT S6.
 FT DOMAIN 373 376 POLY-GLY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD.RES 81 81 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 FT MOD.RES 535 535 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 546 546 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT MOD.RES 569 569 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 602 AA; 66552 MW; 6A784535FE226ED7 CRC64;
 Query Match 4.7%; Score 223.5; DB: 1; Length 602;
 Best Local Similarity 24.9%; Pred. No. 8.4e-06;
 Matches 68; Conservative 49; Mismatches 111; Indels 45; Gaps 8;
 QY 162 ILEFWIIVGEGLEPIRIMSAGCCCRGRWGRLRFARKPCVIDIYL---IASIAVVS 218
 DB 317 IVETTCVMTFFELVFFAC-----PSKAEFSNNINIIDVAFPIYFIIIGEL 367
 QY 219 AKQY-----GNIFATSLRSIRFIQILRMVMDRGKWKILGSVVAHSEKELTAW 270
 DB 368 AEQPGGGGONGOAMSLALRYLRVRFIFKLSRSKGLQILGKTLQASMRLEGLLI 427
 QY 271 YICFLVLISSFLVYVEKDN--KEFSTYADALWMGTTITLTIGYDOKPLTWGRILSA 329
 DB 428 FLEFIVILSSAVYFAEADNHGSHSPSIDAFWMAVYMTTGTGDMRPITVGKIVGS 487
 QY 330 GFALLISFPALDAGILGSGF-----ALKVDBHROKHREKRRNPANLIQ 375
 DB 488 LCALACVLTALPVLVSNFNYFHRETDHEQOALK--EEQGNQRRSGIDTGGQRKVS 546
 QY 376 CVMRSYAAD-----EKSVSTATW-----KPIHKA 399
 DB 547 CSMASCKTGSGLESSDSIRSGSCPLEKHLKA 579
 RESULT 50
 CIKL.DROME STANDARD; PRT: 490 AA.
 AC P17971; Q9YV11.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Voltage-gated potassium channel protein Shal (Shal12).
 GN SHAL OR SHAL2 OR CG9262.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90233953; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RL Science 248:599-603(1990).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9024568; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila.";

RL Nucleic Acids Res. 18:2173-2174(1990).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle E.C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
 RA Abail J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brottler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon S., Nuskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svetska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -I- SUBUNIT: HETEROTRIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CURRENT CLASS.
 CC -I- CAUTION: Ref.3 sequence differs from that shown due to erroneous
 gene model prediction.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 or send an email to license@isb-sib.ch).

CC -----
DR EMBL: M32660; AAA28895.1; -
DR EMBL: AE003516; AAF49144.1; ALT_SEQ.
DR PIR: A35312; A35312.
DR PIR: S12747; S12747.
DR FLYBase: FBgn0005564; Shal.
DR InterPro: IPR000210; BTR_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003975; Shal_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1491; KCHANNEL.
DR PRINTS: PRO1497; SHALCHANNEL.
DR SMART: SM00225; BTR; 1.
DR SMART: SM00225; BTR; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Alternative splicing.
FT TRANSMEM 186 204 SEGMENT S1.
FT TRANSMEM 229 250 SEGMENT S2.
FT TRANSMEM 261 282 SEGMENT S3.
FT TRANSMEM 290 308 SEGMENT S4.
FT TRANSMEM 324 345 SEGMENT S5.
FT TRANSMEM 385 406 SEGMENT S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA; 55918 MW; E178E1C9B07DA74 CRC64;

Query Match 4.78; Score 222.5; DB 1; Length 490;
Best Local Similarity 23.48; Pred. No. 7.3e-06;
Matches 78; Conservative 65; Mismatches 136; Indels 55; Gaps 13;

QY 89 LGGKPLSTSSOSCRANVKYRVQNYLVNERPR---GNAFIYHAFVFLVFGCLLS 144
DB 148 LMDDKLSENGDQNLQQLTNMQ---KMKRAFENPHSTISALVYVYTGFIIV--SYMAN 202
QY 145 VFSTIP-----EHTKLASSCLLLEFVMIIVFGLEFIIRIWSAGCCCRYRG 190
DB 203 VVEVPCGHRPGRAGTLPCGERYKIVFC---LDTACVMIETAEYLLRLFAA----- 251
QY 191 WQGLRFRARPFQYIDTVLSTAVSAKQGNIEATSAISRFLQILRMVRMDRGG 250
DB 252 -PDCKFVRSVMSLIDVAIMP--YYIGLITDNDVSGAEVTLRFRVFRIFKFSRHSQ 308
QY 251 TWKLLGSVVAHAKELITAWYIGFLV-----LISSFVLYLVLEKDN--KEFSTYADAL 302
DB 309 GLRIIGTLKSCASEL-----GLVYFLAMAIITFATVMFY-AEKNVNGTNTSIPAAF 361
QY 303 WMGTTITLTIGYDKPTLTWLGRLLSAGPALIGISFPALPAGILGSGFA-LKVOEQRQK 361
DB 362 WYTLVWTTLTIGYDMVEPTIAGKIYGVCSLSGVLYIALPVPIVYNSFSRIYHQNRADK 421
QY 362 HFERRRNPANLIGQVMSYAA--DEKSVSTATW 393
DB 422 RKAQRKARLARIRIAKASSGAAPVSKKKAAREARW 455

Search completed: June 14, 2003, 17:41:11
Job time : 36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2003, 17:40:28 ; Search time 96 Seconds
(without alignments)
1981.057 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHHAGGEGGAAGLWVKS.....SICKAGESTDLSPHYKTK 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1810.5	38.3	842	11	Q923N2 mus musculu
2	1801.5	38.1	870	11	Q8R498 mus musculu
3	1795	37.9	723	11	Q923N4 mus musculu
4	1791.5	37.9	840	11	Q923N1 mus musculu
5	1767	37.3	759	11	Q923M5 mus musculu
6	1753	37.0	747	11	Q923M6 mus musculu
7	1614	34.1	623	11	Q923M0 mus musculu
8	1613	34.1	570	11	Q923M3 mus musculu
9	1234	26.1	473	11	Q923M9 mus musculu
10	1226	25.9	692	5	Q967F8 caenorhabd1
11	1199	25.3	347	11	Q923M7 mus musculu
12	1199	25.3	349	11	Q923M8 mus musculu
13	1181	25.0	409	4	Q9BX08 homo sapien
14	1064.5	22.5	294	4	Q9BX07 homo sapien
15	1040	22.0	338	11	Q923M6 mus musculu
16	950	20.1	645	5	Q9XWG9 caenorhabd1

17	697	14.7	343	5	Q9V5H7	Q9V5H7 drosophila
18	549.5	11.6	392	4	Q96A19	Q96A19 homo sapien
19	452.5	9.6	363	4	Q9BQU4	Q9BQU4 homo sapien
20	437	9.2	97	11	Q9CTU2	Q9CTU2 mus musculu
21	430	9.1	675	5	Q96YX8	Q96YX8 caenorhabd1
22	424.5	9.0	399	4	Q9BQU5	Q9BQU5 homo sapien
23	311	6.6	469	5	Q9V5H6	Q9V5H6 drosophila
24	308.5	6.5	911	4	Q9BXD3	Q9BXD3 homo sapien
25	297.5	6.3	858	6	Q9M219	Q9M219 oryctolagus
26	291.5	6.2	858	4	Q14193	Q14193 homo sapien
27	287.5	6.1	858	6	Q18668	Q18668 sus scrofa
28	285	6.0	611	6	Q8WNQ3	Q8WNQ3 sus scrofa
29	281.5	5.9	876	13	Q91593	Q91593 xenopus lae
30	280	5.9	898	13	Q91592	Q91592 xenopus lae
31	279	5.9	857	11	Q03717	Q03717 mus musculu
32	274.5	5.8	816	13	Q98SV4	Q98SV4 ictalurus p
33	274.5	5.8	911	6	Q95L11	Q95L11 oryctolagus
34	267	5.6	959	5	Q97045	Q97045 halocynthia
35	262.5	5.5	575	11	Q9QUU4	Q9QUU4 rattus sp.
36	260.5	5.5	478	5	P91784	P91784 polyorchis
37	260.5	5.5	582	4	Q9H1V7	Q9H1V7 homo sapien
38	256.5	5.4	582	4	Q9H1V7	Q9H1V7 homo sapien
39	256	5.4	908	5	Q18476	Q18476 loligo peal
40	254	5.4	606	4	Q9H1V6	Q9H1V6 homo sapien
41	248.5	5.3	528	5	P91256	P91256 caenorhabd1
42	246	5.2	609	5	Q95XD1	Q95XD1 caenorhabd1
43	245.5	5.2	905	5	Q26344	Q26344 aplysia sp.
44	245	5.2	484	5	Q22012	Q22012 caenorhabd1
45	245	5.2	647	4	Q9NSA2	Q9NSA2 homo sapien
46	245	5.2	647	4	Q75671	Q75671 homo sapien
47	243.5	5.1	662	13	Q90W36	Q90W36 columba liv
48	243	5.1	613	4	Q96PR0	Q96PR0 homo sapien
49	243	5.1	638	4	Q96PR1	Q96PR1 homo sapien
50	242.5	5.1	490	5	Q9XND1	Q9XND1 caenorhabd1
51	241.5	5.1	344	16	Q98QES	Q98QES mycoplasma
52	241	5.1	263	16	Q8YND3	Q8YND3 anabaena sp
53	240.5	5.1	480	11	Q9QYU3	Q9QYU3 rattus ratt
54	240.5	5.1	628	11	Q8R1C0	Q8R1C0 mus musculu
55	240.5	5.1	662	13	Q9VX8	Q9VX8 gallus gall
56	239	5.0	510	5	Q26095	Q26095 polyorchis
57	237.5	5.0	515	5	Q16968	Q16968 aplysia cal
58	236	5.0	488	5	Q25376	Q25376 loligo opal
59	235.5	5.0	661	6	Q9GLF1	Q9GLF1 bos taurus
60	233.5	4.9	587	13	Q91A29	Q91A29 oncorhynch
61	233.5	4.9	655	6	Q8WN02	Q8WN02 mustela put
62	233.5	4.9	655	11	Q08723	Q08723 rattus norv
63	233	4.9	516	6	Q28656	Q28656 oryctolagus
64	232.5	4.9	512	5	Q26597	Q26597 schistosoma
65	232.5	4.9	651	13	Q9DDN7	Q9DDN7 apteronotus
66	232.5	4.9	655	4	Q9UH85	Q9UH85 homo sapien
67	231.5	4.9	655	6	Q9T7M5	Q9T7M5 oryctolagus
68	230.5	4.9	655	11	Q920V1	Q920V1 mus musculu
69	230.5	4.9	655	11	Q99P42	Q99P42 rattus norv
70	230	4.9	280	16	Q9RM39	Q9RM39 delinococcus
71	230	4.9	592	13	Q9PVD1	Q9PVD1 xenopus lae
72	230	4.9	636	11	P70622	P70622 rattus norv
73	230	4.9	658	13	Q9PMD3	Q9PMD3 gallus gall
74	229.5	4.8	630	4	Q9NZV8	Q9NZV8 homo sapien
75	229.5	4.8	635	4	Q9UK17	Q9UK17 homo sapien
76	229	4.8	494	13	Q91830	Q91830 oncorhynch
77	229	4.8	561	5	Q95PC9	Q95PC9 panulirus i
78	229	4.8	636	4	Q9UH86	Q9UH86 homo sapien
79	228.5	4.8	485	13	Q90YV3	Q90YV3 xenopus lae
80	228.5	4.8	630	4	Q9UNH9	Q9UNH9 homo sapien
81	228	4.8	279	17	Q8TP82	Q8TP82 methanosarc
82	228	4.8	585	6	Q9XSJ8	Q9XSJ8 canis fam11
83	228	4.8	651	11	Q03719	Q03719 mus musculu
84	227.5	4.8	630	4	Q9UBV7	Q9UBV7 homo sapien
85	227.5	4.8	630	11	Q63881	Q63881 rattus sp.
86	227	4.8	490	11	Q99249	Q99249 rattus norv
87	227	4.8	611	11	Q63286	Q63286 rattus norv
88	227	4.8	636	11	Q920V0	Q920V0 mus musculu
89	227	4.8	636	11	Q62897	Q62897 rattus norv

90	226.5	4.8	518	13	073606	073606 gallus gall
91	226.5	4.8	540	11	09J9760	09J9760 mus musculu
92	226.5	4.8	558	5	062350	062350 caenorhabdi
93	226.5	4.8	630	11	0920V2	0920V2 mus musculu
94	226	4.8	556	5	017535	017535 caenorhabdi
95	226	4.8	636	4	09UK16	09UK16 homo sapien
96	225.5	4.8	632	13	08UW33	08UW33 gallus gall
97	225	4.8	477	11	035174	035174 mus musculu
98	225	4.8	477	11	09ER26	09ER26 rattus norv
99	225	4.8	546	5	026040	026040 panulirus i
100	225	4.8	551	5	095PD0	095PD0 panulirus i
101	225	4.8	579	5	095PC5	095PC5 panulirus i
102	225	4.8	585	5	095PC4	095PC4 panulirus i
103	225	4.8	660	5	095PC8	095PC8 panulirus i
104	225	4.8	660	5	095PC7	095PC7 panulirus i
105	225	4.8	680	5	095PC6	095PC6 panulirus i
106	224	4.7	489	4	09ULS6	09ULS6 homo sapien
107	223.5	4.7	522	5	061335	061335 panulirus i
108	223	4.7	466	4	09UJ96	09UJ96 homo sapien
109	223	4.7	500	4	09GHJ4	09GHJ4 homo sapien
110	223	4.7	500	6	09GKU7	09GKU7 macaca fasc
111	221.5	4.7	295	17	09YDF8	09YDF8 aeryopyrum p
112	221.5	4.7	608	5	095PC3	095PC3 panulirus i
113	221	4.7	409	5	091783	091783 polychelis
114	220.5	4.7	597	6	09TS07	09TS07 bos taurus
115	220	4.6	519	4	08TDM1	08TDM1 homo sapien
116	219.5	4.6	489	13	098TMD	098TMD xenopus lae
117	219	4.6	725	6	028649	028649 oryctolagus
118	218.5	4.6	357	5	026039	026039 panulirus i
119	218	4.6	602	11	0921R6	0921R6 mus musculu
120	217.5	4.6	655	4	060577	060577 homo sapien
121	217	4.6	504	11	060565	060565 mesocricetu
122	216	4.6	593	6	028248	028248 canis famli
123	215.5	4.6	460	5	009658	009658 caenorhabdi
124	214.5	4.5	280	16	09KMX2	09KMX2 vibrlo chol
125	214.5	4.5	455	16	067715	067715 aquifex aeo
126	214.5	4.5	489	13	091781	091781 xenopus lae
127	214.5	4.5	494	4	09H3M0	09H3M0 homo sapien
128	214.5	4.5	514	5	076457	076457 aplysia cal
129	214	4.5	489	4	026041	026041 panulirus i
130	214	4.5	636	4	060576	060576 homo sapien
131	213.5	4.5	511	4	016322	016322 homo sapien
132	213.5	4.5	677	13	098TW3	098TW3 xenopus lae
133	213	4.5	503	11	097557	097557 rattus norv
134	212.5	4.5	499	6	09MYX3	09MYX3 oryctolagus
135	212.5	4.5	499	6	028293	028293 canis famli
136	212	4.5	577	5	016976	016976 aplysia cal
137	212	4.5	604	5	08SYL2	08SYL2 dtrosophila
138	211.5	4.5	476	6	008635	008635 bos taurus
139	211	4.5	204	11	099NR6	099NR6 mus musculu
140	211	4.5	278	16	082P47	082P47 salmonella
141	211	4.5	278	16	0827E6	0827E6 salmonella
142	211	4.5	503	11	09CZRL	09CZRL mus musculu
143	211	4.5	529	11	061923	061923 mus musculu
144	211	4.5	776	5	019464	019464 caenorhabdi
145	210	4.4	483	13	091829	091829 oncorhynch
146	208.5	4.4	659	13	057662	057662 xenopus lae
147	207.5	4.4	491	4	09BOJ1	09BOJ1 homo sapien
148	207.5	4.4	499	13	098TW4	098TW4 xenopus lae
149	207	4.4	521	5	095XV8	095XV8 caenorhabdi
150	207	4.4	583	5	09YXX0	09YXX0 halocynthia

ALIGNMENTS

RESULT 1
 O923N2
 AC O923N2: PRELIMINARY; PRT; 842 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE	BM40117.3.1 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 1)).
GN	KCNQ2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Wall M.
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AL450341; CAC40730.1; -
DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR003946; KCNQ1_channel.
DR	InterPro; IPR000636; M+channel_nlg.
DR	Pfam; PF00520; Ion_trans.1.
DR	Pfam; PF03520; KCNQ1_channel.1.
SQ	SEQUENCE 842 AA; 92928 MW; C62B86CA8898735 CRC64;
Query Match	
Best local similarity 48.4%; Pred. No. 2,7e-122; Length 842;	
Matches 414; Conservative 99; Mismatches 210; Indels 133; Gaps 23;	
OY	21 GAAAAAGGRLGSGMKDVESSGRGVLLNSAARGDLLLGTAAATLGCGGGLRESRR 80
DB	9 GYPTSGEKKLVGEVGLDPGA-----PDSTRDGLLIAGSEAPK---RGSVLSKPR 59
OY	81 GGGAGMSLLGRLSTSSQSCRNVKRRQNTLVNLEPRGAFVYHAFVLLVGC 140
DB	60 GGAGA-----GKP-----PKNAYFRKLQNLVNLLEPRGAFVYHAFVLLVSC 106
OY	141 LILSVSTPEHTKLASSCLLLEFVMIIVGELFIIRMSAGCCCRGGRGRLEFR 200
DB	107 LVLSVSTIKEYKSSGALVILEITVIVGVEYFPRVMAAGCCCRGRGRLEFR 166
OY	201 PCGVDTIVLASIVASATQGNIFATSLRSLRFLQILRMVRRDRRGTWKLLGSVY 260
DB	167 PCGVDTIVLASIVASATQGNIFATSLRSLRFLQILRMVRRDRRGTWKLLGSVY 226
OY	261 ASKELITVMIYIGFLVLIIFSSFLVLYLEKANKREFSYADALMMGTILTTIGYDKPL 320
DB	227 ASKELITVMIYIGFLVLIIFSSFLVLYLEKANKREFSYADALMMGTILTTIGYDKPL 286
OY	321 TWLGRLLSAGFALLGISFALPAGILSGFALKVQEQHROKHFERRRPAANLLOCVRS 380
DB	287 TWNGRLLAATFTLIGVSEFALPAGILSGFALKVQEQHROKHFERRRPAAGLIGSARF 346
OY	381 YAAD-----EKSVSIATWK--PHKALHMC-----SPT 406
DB	347 YATNLSRTDLHSTWQYERTVTPMYRLIPLNQLLELRNLSKSGLTFRRKEPOPEPSP- 405
OY	407 NOKLSFERRMASPRGOSIKRSQASVGD--RRSPSTDIYEGSPPTKQKSMFDRPRF 464
DB	406 SOKVSLKDRV-FSSPRGMAKKGSPQAOQVRRSPSDQSIDSDSPKPKMSFGEDRSRT 464
OY	465 RSLRLKSSQPKVIDADTALGTDDVYDEKGCOCQDVSEDLTPPLKTVIRAIRMKFVA 524
DB	465 ROAFRIKGAASRQNSSEASLPGEDIVEDNKSCEFEYTEDLPGLKVISIRAVCVARFLVS 524
OY	525 KKKFKETLPRPYKDVTEQYSAGHLDMLCKIKSLQTRVDQLGQITSDKKSREKITA 584
DB	525 KKKFKESLRPYDMVDVIEQYSAGHLDMLSRKISLQSRVDQIVGCRPTTD-KDRKGP 583
OY	585 HETTDLSMLGRVYKVKQVQSIKSLDCLDITQOVLKRSASALALASQIPEPEC-- 642
DB	584 TELPEPSSMGRGKVEKQVLSMEKIDFLVSYITO--RMC-----IPAELEA 630
OY	643 -----EQTSYQSPVDSKDLGSAQNSGC---LSRSTANISRGLOFILTPEEFSQ 692
DB	631 YFGAKEPEBPAPYHSPEDSRD---HADKHCICIKIVSTSS-----TGR 672
OY	693 FALSPHMSQATQVVISQSDGSAVAATNTIANQINAPPAFTTQIIPPLA----- 747


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Db 673 NYAAPPA-----IPPAOCPPS--TSWOOSHQHGTSYPVGDHSLVRIPPP-PAHERSL 722
QY 748 -----IKHLPRPETHLPNPAAGLOESI.DVTCYLVAKENOVQAOSNLTKDRSM 795
Db 723 SAVGGNNRSTEFLERLGCTPACRPSSEALKDSDTSTISPV-DHEELERSFGFSISOS- 780
QY 796 RKSFDMGGETILSVCP 811
Db 781 KENLDALGSCYAANVP 796

RESULT 2
OBR498
ID 08R498 PRELIMINARY; PRT; 870 AA.
AC 08R498:
DT 01-JUN-2002 (TREMUREL. 21, Created)
DT 01-JUN-2002 (TREMUREL. 21, Last sequence update)
DE Potassium channel KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Men H., Levitan I.B.;
RT "Calmodulin is an auxiliary subunit of KCNQ channels.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490773; AAM09696.1; -
SQ SEQUENCE 870 AA; 95742 MW; 9C6106C27CE70C5F CRC64;

Query Match 38.1%; Score 1801.5; DB 11; Length 870;
Best Local Similarity 46.8%; Pred. No. 1.3e-121;
Matches 413; Conservative 100; Mismatches 211; Indels 159; Gaps 22;

QY 21 GAAAAAAGGRLSGMKDVESEGRVLLNSAANGDGLLIGTRAATLGGGGGGLRESRR 80
Db 9 GYVPGTSGEKKLWGFGLDPGA-----PDSTRDGLALLINGSEAPK---RGSVLSKPT 59
QY 81 GKGARMSLLGKPLSTYSSOSCRNNVRRVQNTLYNLEPRGKAFIYHAFVLLVGC 140
Db 60 GGAGA-----GKP-----PKRNAFYRKLNFLYNLEPRGAFIYHAFVLLVSC 106
QY 141 LIIVSFTIPEHRTKLASSCLLIEFVMIYVGLFEITIRMSAGCCCRVGMGRRLRFARK 200
Db 107 LVISVFTIPEHRTKLASSCLLIEFVMIYVGLFEITIRMSAGCCCRVGMGRRLRFARK 166
QY 201 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVMDRDRGGTWKLLGSVY 260
Db 167 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVMDRDRGGTWKLLGSVY 226
QY 261 AHSKELITAVYIGFLVLIFFSFLVYVEKANKFEFTADALMWGITLTITIGYDCKPL 320
Db 227 AHSKELITAVYIGFLVLIFFSFLVYVEKANKFEFTADALMWGITLTITIGYDCKPL 286
QY 321 TWIGRLISAGFALGISEFFAPAGILGSGFALKVOEQRHKKFEKRRPAAMLICVMS 380
Db 287 TWIGRLISAGFALGISEFFAPAGILGSGFALKVOEQRHKKFEKRRPAAMLICVMS 346
QY 381 YAAD-----EKSVSIATW----- 393
Db 347 YATNITDLSHTLSTWQYERVTVMYSSQOTYGASRLIPLNQLLELNLKSKSLRPR 406
QY 394 -----KPHLALHTGSP--TWOKLSFKERVMAASPRGOSISRSQASVD--RR 437
Db 407 KEPQPEPSKGRKRCGLCGCCPGHSSQKVLAKRV--FSSPRGMAAGKGSPOAQTVRR 465
QY 438 SPSTIDITAEAGSPYVOKSMSPFNDRTRFRPSRLIKSSQPKPVADATALCTDQVYDEKGO 497
Db 466 SPADQSLDSDPSKVPKSMSPFGDSRTROAFRIKGAARONSEKSLPEDIVEDKSKSN 525
QY 498 CDVSVEDELTPPLKTVIRAIRIMKRFHVAARKKFEKRLRPYDKVDEIYOYSAGHLDMLCRIKS 557

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Db 526 CEFEVEDLTPGLKVSIRAVCYMRFVLSKRRFKESLPRYDWDVIEQYSACHLMLSRKIS 585
QY 558 IOTRVQOIIIGKQIITSDKKSREKITAHEHTDLSMGRVYKQVQIESKLDCLDI 617
Db 586 IQSRVDQIVRGRTIYD-KORTKGPATELPEDEPSMGRGKQVLSMEKKLIDFLVSI 644
QY 618 YQVLEKSGSALALASFOIPEPEC-----EQTSDYQSPVSDKLSGSAQNSGC-- 666
Db 645 YQV--RMG-----IPPAETEYFGAKPEPAPYPHSPEDSD--HADKHCIT 688
QY 667 -LSRSTSANISRGLOFLIPNEPSAOTFVALSPHMSOANOVPIQSODGSAVATNTIAN 725
Db 689 KIVRSTSS-----TGORNYAAPPA-----IPPAOCPPS--TSWOOSHQ 724
QY 726 QINTAKRPAAPTLOIIPPLPA-----IKHLPRPETHLPNPAAGLOESI 768
Db 725 RKGTSVPGDHGSLVLRIPPP-PAHERSLSAVGGNNRSTEFLERLGCTPACRPSSEALKDSD 783
QY 769 SDVTTCLVASKENYQVQAOSNLTKDRSMRKSFDMGGETILSVCP 811
Db 784 TSTISPSV-DHEELERSFGFSISOS-KENLDALGSCYAANVP 824

RESULT 3
O923N4
ID 0923N4 PRELIMINARY; PRT; 723 AA.
AC 0923N4:
DT 01-DEC-2001 (TREMUREL. 19, Created)
DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)
DE 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE BM401117.3.8 (potassium voltage-gated channel, subfamily O, member 2 (isoform 8)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL450341; CAC40728.1; -
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000346; KCNQ1_channel.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans.1.
DR Pfam; PF03520; KCNQ1_channel.1.
DR SEQUENCE 723 AA; 80540 MW; 0F8738B23EAD7DC3 CRC64;

Query Match 37.9%; Score 1795; DB 11; Length 723;
Best Local Similarity 53.2%; Pred. No. 2.9e-121;
Matches 394; Conservative 77; Mismatches 163; Indels 106; Gaps 18;

QY 21 GAAAAAAGGRLSGMKDVESEGRVLLNSAANGDGLLIGTRAATLGGGGGGLRESRR 80
Db 9 GYVPGTSGEKKLWGFGLDPGA-----PDSTRDGLALLINGSEAPK---RGSVLSKPT 59
QY 81 GKGARMSLLGKPLSTYSSOSCRNNVRRVQNTLYNLEPRGKAFIYHAFVLLVGC 140
Db 60 GGAGA-----GKP-----PKRNAFYRKLNFLYNLEPRGAFIYHAFVLLVSC 106
QY 141 LIIVSFTIPEHRTKLASSCLLIEFVMIYVGLFEITIRMSAGCCCRVGMGRRLRFARK 200
Db 107 LVISVFTIPEHRTKLASSCLLIEFVMIYVGLFEITIRMSAGCCCRVGMGRRLRFARK 166
QY 201 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVMDRDRGGTWKLLGSVY 260
Db 167 PFCVIDITVLIAIAVSAKTQGNIFATSLRFLDILRMVMDRDRGGTWKLLGSVY 226
QY 261 AHSKELITAVYIGFLVLIFFSFLVYVEKANKFEFTADALMWGITLTITIGYDCKPL 320
Db 227 AHSKELITAVYIGFLVLIFFSFLVYVEKANKFEFTADALMWGITLTITIGYDCKPL 286

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[illegible]

RESULT 5	
0923N5	
ID	Q923N5
AC	Q923N5
DT	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE	BM40117.3.11 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 1)).
GN	KCNQ2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
XX	NCBI_TaxID=10090;
RP	[1]
RP	SEQUENCE FROM N.A.
RA	Wall M.;
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL450341; CAC40727.1; -
DR	InterPro; IPR001622; K+channel_pore.
DR	InterPro; IPR003946; KCNQ1_channel.

DR InterPro: IPR000636; M-channel_n19.

DR Pfam: PF00520; Ion_trans; 1.

DR Pfam: PF03520; KCNQ1_channel; 1.

DR SEQUENCE 759 AA; 84494 MW; D828BE47D0DE3C4A CRC64;

Query Match 37.3%; Score 1767; DB 11; Length 759;
Best Local Similarity 50.8%; Pred. No. 3.3e-119;
Matches 394; Conservative 77; Mismatches 163; Indels 142; Gaps 19;

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OY 21 GAAAAAGGRLSGMKDVGSGRGVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 GVPETSEKKLVGFVGLDPGA-----PDSTRDGLALLIAGSEAK---RGSVLKPR 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 81 GKGARMSLGRPLSTSSQCRNVKRYRNVLYNVLEPRGMAFIYHAEVLLVFGC 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFYVLEPRGMAFIYHAEVLLVFGC 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 141 LILSVFTPTPEHTKLASSCLLLEFMYIVFGLEFIIRISAGCCCRYRMOGRLEPARK 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 107 LVLSTFTIKEYEKSEGLTYLEIYTVFGEYEVRIWMAACCCCRKRGRLKPRARK 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 201 PFCVIDITVLASIVASAKTOGNIFATSLNSRLQLIRVMRDRGGTWMKLLGSVY 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 167 PFCVIDITVLASIVASAKTOGNIFATSLNSRLQLIRVMRDRGGTWMKLLGSVY 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 261 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTIGYGDKPTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 227 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTIGYGDKPTL 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 321 TWLGRLLSAGFALLIGISFPALPAGILGSGFALKVOBOHOKHFEKRRNPANLIOCWRS 380
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 287 TWNGRLAATFTLLIGVSPFALPAGILGSGFALKVOBOHOKHFEKRRNPANLIOCWRS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 361 YAAD-----EKSVSIATWK--PHLKALHTC-----SPT 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 347 YATNLSRDLHSTWQYERTVYPMYRLPLNQLLELRMLKSKSLTFKPEQPEBSP- 405
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 407 NOKLSFERVRMASPGOSIKSRQASVGD--RRSPDTITAEGSPTRYOKSMSPNDTRF 464
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 406 SOKVSLKADNV-FSSPGMAKKGSPQAOQTVKRSPPSADOSLSDSPSKVPSMSGDSKRT 464
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 465 RPSRLKSSQPKPVVIDADTALGTDVYDEKGCOCODSVEDLTPPLKTVIRAIRIMKTHVA 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 465 RQAFRIKGAASRONSEASIPGEDIVEDNKCNEFEVTEDLTPGLKVISRAVCVWRFLVS 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 525 KKKFKETLAPYDYKVIDEYASAGHLDMLSKISLQSRIDMIVGPPRSTPRHKKYPTKGP 584
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 525 KKKFKETLAPYDYKVIDEYASAGHLDMLSKISLQSRIDMIVGPPRSTPRHKKYPTKGP 584
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 561 -----RVDOIILGQITSDKSKREKITAHEHTDDLSMLGRVNVVEKOVOSIE 608
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 585 TAPRSRSPQSPRVDDIVGRPTITD-KDRTKGAPELPEPDSMGRGLGVEKQVLSME 643
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 609 SKLDCLDIYQOVLKRGASALALASFOIPPEFC-----EOTS DYOSPVDSKDLISG 659
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 644 KLIDFLVSIYTO--RMG-----IPPAETEAFFGAKEPPAPYHSPEDSRD--- 687
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 660 SAONSGC---LSNSTANISRGLOFILTPEFSAQTYALSPTMHSQATQVPISOS 712
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 688 HADKHGCIILKIYVSTSS-----TGQRNYAAPRAL--PPACCPSTPS 726
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 6

OY 0923N6 PRELIMINARY; PRT: 747 AA.
AC 0923N6;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE BM401L17.3.10 (potassium voltage-gated channel, subfamily O, member 2 (isoform 10)).
GN KCNQ2.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA Wall M.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL450341; CAC40726.1; -.

DR InterPro: IPR001622; K-channel_pore.

DR InterPro: IPR003946; KCNQ1_channel.

DR InterPro: IPR000636; M-channel_n19.

DR Pfam: PF00520; Ion_trans; 1.

DR Pfam: PF03520; KCNQ1_channel; 1.

DR SEQUENCE 747 AA; 83118 MW; E5714B98A18A7E60 CRC64;

Query Match 37.0%; Score 1753; DB 11; Length 747;
Best Local Similarity 51.0%; Pred. No. 3.3e-118;
Matches 389; Conservative 77; Mismatches 170; Indels 126; Gaps 18;

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OY 21 GAAAAAGGRLSGMKDVGSGRGVLLNSAARGDGLLLGTRATLGGGGGLRESRR 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 GVPETSEKKLVGFVGLDPGA-----PDSTRDGLALLIAGSEAK---RGSVLKPR 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 81 GKGARMSLGRPLSTSSQCRNVKRYRNVLYNVLEPRGMAFIYHAEVLLVFGC 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNFYVLEPRGMAFIYHAEVLLVFGC 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 141 LILSVFTPTPEHTKLASSCLLLEFMYIVFGLEFIIRISAGCCCRYRMOGRLEPARK 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 107 LVLSTFTIKEYEKSEGLTYLEIYTVFGEYEVRIWMAACCCCRKRGRLKPRARK 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 201 PFCVIDITVLASIVASAKTOGNIFATSLNSRLQLIRVMRDRGGTWMKLLGSVY 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 167 PFCVIDITVLASIVASAKTOGNIFATSLNSRLQLIRVMRDRGGTWMKLLGSVY 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 261 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTIGYGDKPTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 227 AHSKELITAWYIGFLVLFSSFLVLYVEKDANKFESTYADALMWGITLTIGYGDKPTL 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 321 TWLGRLLSAGFALLIGISFPALPAGILGSGFALKVOBOHOKHFEKRRNPANLIOCWRS 380
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 287 TWNGRLAATFTLLIGVSPFALPAGILGSGFALKVOBOHOKHFEKRRNPANLIOCWRS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 361 YAAD-----EKSVSIATWK--PHLKALHTCSPTNOK--LSFERVR--MAS 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 347 YATNLSRDLHSTWQYERTVYPMYRLPLNQLLELRMLKSKSLTFKPEQPEBSPS 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 421 PRGOSIKSRQASVGD--RRSPDTITAEGSPTRYOKSMSPNDTRPRPSLRKSSQPKV 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 407 PRGMAKKGSPQAOQTVKRSPPSADOSLSDSPSKVPSMSGDSKRTQAFRIKGAASRON 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 479 IDADTALGTDVYDEKGCOCODSVEDLTPPLKTVIRAIRIMKTHVAIRIMKTHVA 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 467 SEASLPGEDIVEDNKCNEFEVTEDLTPGLKVISRAVCVWRFLVSRRKESLRPDVM 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 539 DVIEQYSAGHLDMLCRISLOT-----RV 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 527 DVIEQYSAGHLDMLSKISLQSRIDMIVGPPRSTPRHKKYPTKGPAPRSRSPQSPRV 586
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 563 DOIILGQITSDKSKREKITAHEHTDDLSMLGRVNVVEKOVOSIEKLDCLDIYQOVL 622
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 587 DOIIVGRPTITD-KDRTKGAPELPEPDSMGRGLGVEKQVLSMEKRLFLVSIYTO-- 643
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 623 RKGASALALASFOIPPEFC-----EOTS DYOSPVDSKDLISGSAONSGC---LSRS 670
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 644 RMG-----IPPAETEAFFGAKEPPAPYHSPEDSRD---HADKHGCIILKIVRS 689
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 671 TSANISRGLOFILTPEFSAQTYALSPTMHSQATQVPISOS 712
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 690 TSS-----TGQRNYAAPRAL--PPACCPSTPS 714
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

0923N0
ID 0923N0 PRELIMINARY: PRT: 623 AA.
AC 0923N0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BM401L17.3.5 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 5)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL450341; CAC40732.1; -;
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF03520; KCNQ1_channel.1.
SO SEQUENCE 623 AA; 69764 MW; C05D2F023DA32D26 CRC64;

Query Match 34.1%; Score 1614; DB 11; Length 623;
Best Local Similarity 57.3%; Pred. No. 2.9e-108;
Matches 333; Conservative 66; Mismatches 122; Indels 60; Gaps 10;

QY 21 GAAAAAGGRLGSGMKDVGSGRVLNSAARGDGLLGTAAATLGGGGGGLRESRR 80
DB 9 GYPTSGEKKLVKGFVGLDPGA-----PDSTRDGLLLGASEAPK--RGSVLSKPR 59
QY 81 GKOGARMSLLGKPLSTYSOSGRNVKRYRQVNYLVLEPRGMAFYHAFFVLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNLVLEPRGMAFYHAFFVLVFGC 106
QY 141 LILSVSTIPEHTKLASSCLLLEFVMIYVGLFEITIRMSAGCCCRYGMGRFARK 200
DB 107 LVLSVESTIKEYEKSESGALYILEYIVVGEYEVIRIWAAGCCCRYGMGRFARK 166
QY 201 PCVIDITVLASIAVSAKTQGNIFATSAIRSLRFLQILRMVRMDRGGTWKLLGSVY 260
DB 167 PCVIDIMVLASIAVLAAGSGNVFATSLRFLQILRMVRMDRGGTWKLLGSVY 226
QY 261 AHSKELITAMWYIGFLVLIFFSFLVLYVEKDANKFESTYADALMWGITLTITIGYDKPTL 320
DB 227 AHSKELVTAMWYIGFLVLIFFSFLVLYVEKDANKFESTYADALMWGITLTITIGYDKPTL 286
QY 321 TWLGRLLSAGFALLGISFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVRS 380
DB 287 TWNGRLLAATFTLLIGVSFFALPAGILGSGFALKVQEQHROKHFEKRRNPAGLIQSAWRF 346
QY 381 YAAD-----EKSVSIAATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRDLHSTWYERTVTPMYRLPLNQLLELRNLKSGTLFRKEPPEPSP- 405
QY 407 NOKLSFERVMAAPRGOSIKSRQASVGD--RRSPSTIDITAEQSPTKVQKSMSEFNDRTRE 464
DB 406 SOKVSLDKRV--FSSPRGMAAKGSGPQAGVVRNSPADQSLDSDPSKVPKSMSEFNDRTRE 464
QY 465 RPSRLKSSQKRPVIDADTALGTDVYDEKGCOCQDVSEDLTPPLKTVIRAIRIMKFEVA 524
DB 465 RQAFRIKGAASRONSSEASLPGEDIVEDNKSCEFEYEDLTPLKVISIRAVCVARFLVS 524
QY 525 KRKFETLRPYDVKYDIEOYSAGHLDMLCRISLQTRVDQI 565
DB 525 KRKFESLRPYDVMDVIEOYSAGHLDMLSRISLQSRQEP 565

RESULT 8
ID 0923N3 PRELIMINARY: PRT: 570 AA.

AC 0923N3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE BM401L17.3.3 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 3)).
GN KCNQ2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL450341; CAC40729.1; -;
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003946; KCNQ1_channel.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF03520; KCNQ1_channel.1.
SO SEQUENCE 570 AA; 63835 MW; 6BEDA2952C1C7178 CRC64;

Query Match 34.1%; Score 1613; DB 11; Length 570;
Best Local Similarity 57.7%; Pred. No. 3e-108;
Matches 333; Conservative 64; Mismatches 120; Indels 60; Gaps 10;

QY 21 GAAAAAGGRLGSGMKDVGSGRVLNSAARGDGLLGTAAATLGGGGGGLRESRR 80
DB 9 GYPTSGEKKLVKGFVGLDPGA-----PDSTRDGLLLGASEAPK--RGSVLSKPR 59
QY 81 GKOGARMSLLGKPLSTYSOSGRNVKRYRQVNYLVLEPRGMAFYHAFFVLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAFYRKLQNLVLEPRGMAFYHAFFVLVFGC 106
QY 141 LILSVSTIPEHTKLASSCLLLEFVMIYVGLFEITIRMSAGCCCRYGMGRFARK 200
DB 107 LVLSVESTIKEYEKSESGALYILEYIVVGEYEVIRIWAAGCCCRYGMGRFARK 166
QY 201 PCVIDITVLASIAVSAKTQGNIFATSAIRSLRFLQILRMVRMDRGGTWKLLGSVY 260
DB 167 PCVIDIMVLASIAVLAAGSGNVFATSLRFLQILRMVRMDRGGTWKLLGSVY 226
QY 261 AHSKELITAMWYIGFLVLIFFSFLVLYVEKDANKFESTYADALMWGITLTITIGYDKPTL 320
DB 227 AHSKELVTAMWYIGFLVLIFFSFLVLYVEKDANKFESTYADALMWGITLTITIGYDKPTL 286
QY 321 TWLGRLLSAGFALLGISFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVRS 380
DB 287 TWNGRLLAATFTLLIGVSFFALPAGILGSGFALKVQEQHROKHFEKRRNPAGLIQSAWRF 346
QY 381 YAAD-----EKSVSIAATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSTRDLHSTWYERTVTPMYRLPLNQLLELRNLKSGTLFRKEPPEPSP- 405
QY 407 NOKLSFERVMAAPRGOSIKSRQASVGD--RRSPSTIDITAEQSPTKVQKSMSEFNDRTRE 464
DB 406 SOKVSLDKRV--FSSPRGMAAKGSGPQAGVVRNSPADQSLDSDPSKVPKSMSEFNDRTRE 464
QY 465 RPSRLKSSQKRPVIDADTALGTDVYDEKGCOCQDVSEDLTPPLKTVIRAIRIMKFEVA 524
DB 465 RQAFRIKGAASRONSSEASLPGEDIVEDNKSCEFEYEDLTPLKVISIRAVCVARFLVS 524
QY 525 KRKFETLRPYDVKYDIEOYSAGHLDMLCRISLQTRVDQI 561
DB 525 KRKFESLRPYDVMDVIEOYSAGHLDMLSRISLQSR 561

RESULT 9
ID 0923M9 PRELIMINARY: PRT: 473 AA.
AC 0923M9;
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE BM40L17.3.7 (potassium voltage-gated channel, subfamily Q,
 member 2 (isoform 7)).
 GN KCN02.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wall M.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL450341; CAC40733.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans; 1.
 DR SEQUENCE 473 AA; 52682 MW; 3AFC95E6946FA57 CRC64;

Query Match 26.1%; Score 1234; DB 11; Length 473;
 Best Local Similarity 58.2%; Pred. No. 6.4e-81;
 Matches 235; Conservative 51; Mismatches 98; Indels 34; Gaps 9;

OY 21 GAAAAAGGGRGCGMKVDSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESKR 80
 Db 9 GYVPGTSGEKKLVGFGLDPGA-----PDSTRDGLALINGSEAPK---RGVLSKRPRT 59
 OY 81 GKGAGMSLLGKPLSTSSQSCRRNRYRYRYQNTLYNLEPRRGMAFYHAFFLLVFGC 140
 Db 60 GGAGA-----GKP-----PKRNAFYRKLNFLNLYLERPRRGMAFYHAFFLLVFGC 106
 OY 141 LLSVSTPEHTKHLASSCLLLEFVAVVGFLEFIRIRWSAGCCCRYGMOGRLEFARK 200
 Db 107 LVLSVSTPEHTKHLASSCLLLEFVAVVGFLEFIRIRWSAGCCCRYGMOGRLEFARK 166
 OY 201 PFCVIDTIVLIASIAVYSAKQGNIFATSALRSIRFQILRMVMDRGGTCKLLGSVY 260
 Db 167 PFCVIDTIVLIASIAVYSAKQGNIFATSALRSIRFQILRMVMDRGGTCKLLGSVY 226
 OY 261 AHSKELITAVYIGLVLISSFLVLYLEKDNKESTYADALMKGITITLTGYGDKTFL 320
 Db 227 AHSKELITAVYIGLVLISSFLVLYLEKDNKESTYADALMKGITITLTGYGDKTFL 286
 OY 321 TWIGRLSAGPALGISFFALPAGILGSGFALKVOEORHOKHFEKRRNPANLIOCVRMS 380
 Db 287 TWIGRLSAGPALGISFFALPAGILGSGFALKVOEORHOKHFEKRRNPANLIOCVRMS 346
 OY 381 YAADEKSVSI-ATWKPMLKALHTCSPTNOKLSFKERVMAASPRGQ-----SIKSRQASVG 434
 Db 347 YATNLSTDLHSTQYVERVTVPMYSSQOTQYGAS-RLIPPLNQLLELRNLKSK-SGLT 404
 OY 435 DRSPSTDTAEGSPTKY 452
 Db 405 FRKEPQ---PEPSPRV 418

RESULT 10

O967F8 PRELIMINARY; PRT; 692 AA.
 AC O967F8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE C25B8.1 protein.
 GN C25B8.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peioderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 MEDLINE=99069613; PubMed=9851916;

RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA W1cox L.;
 RT "The sequence of C. elegans cosmid C25B8.";
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41556; AAK3192.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF03520; KCNQ1_channel; 1.
 DR SEQUENCE 692 AA; 77486 MW; 6A69D9B21D059BF8 CRC64;

Query Match 25.9%; Score 1226; DB 5; Length 692;
 Best Local Similarity 41.1%; Pred. No. 4.3e-80;
 Matches 276; Conservative 121; Mismatches 184; Indels 90; Gaps 17;

OY 75 LRSRRGKQCARMSILGKPLSTSSQSCRRNRYRYRYQNTLYNLEPRRGMAFYHAFF 133
 Db 54 LHDSEBGR--KMSLVGKPLTY--KNYRDFRRMKNHNLFRGKMAATYHLAV 108
 OY 134 FLVFGCLLSVSTPEHTKHLASSCLLLEFVAVVGFLEFIRIRWSAGCCCRYGMOGR 193
 Db 109 LPMVLMCLALSVSTPMDFEVMAFYLYLYEIVVIMATPYICRVMSAGGSRXRGISG 168
 OY 194 RLFPARKPFCVIDTIVLIASIAVYSAKQGNIFATSALRSIRFQILRMVMDRGGTCK 253
 Db 169 RLFPARKPFCVIDTIVLIASIAVYSAKQGNIFATSALRSIRFQILRMVMDRGGTCK 228
 OY 254 LLSGVYAAHSEKELITAVYIGLVLISSFLVLYLEKDNKESTYADALMKGITITLT 313
 Db 229 LLSGVYAAHSEKELITAVYIGLVLISSFLVLYLEKDNKESTYADALMKGITITLT 288
 OY 314 YGDKTPTLWIGRLSAGPALGISFFALPAGILGSGFALKVOEORHOKHFEKRRNPANL 373
 Db 289 YGDKTPTLWIGRLSAGPALGISFFALPAGILGSGFALKVOEORHOKHFEKRRNPANL 348
 OY 374 IQCVWRSYAADEKSVSIATWKPMLKALHTCSPTNOKLSFKERVMAASPRGQSIK 427
 Db 349 IQCVWRSYAADEKSVSIATWKPMLKALHTCSPTNOKLSFKERVMAASPRGQSIK 408
 OY 428 SROASVDRRS-----PSYDTAEGSPTKYQKMSFMDRGRFRLSLR-- 469
 Db 409 SROASVDRRS-----PSYDTAEGSPTKYQKMSFMDRGRFRLSLR-- 468
 OY 470 ----LKSSQRPV---IDADTALGTDVYDEKGGQCDVSDVLDLPTLVIRAIRIMFH 522
 Db 469 DSVYLSQRMALPNAHDEEAVG---YQPG-----TIEFFPALNCVVAIRRIOLL 518
 OY 523 VAKRKEKTLRPYVQVQVYIEOYSAGHLDMLCRISLSLQTRVQIIGKGOITSKREKIT 582
 Db 519 VAKRKEKTLRPYVQVQVYIEOYSAGHLDMLCRISLSLQTRVQIIGKGOITSKREKIT 570
 OY 583 AEHTTDDLSMLGVVYVEKOVOSIESKLDLDLDYQOVLLRKSASALATLSFQIAPFEC 642
 Db 571 PK-----ISMFTIATLETTVGKMDKLDLMEVEM-----GRASQRVESQNSP--- 616
 OY 643 EQTSYDQSPVDSKDLSSAQNQSLSRSTANISRGLOFLTPNFSQOTYALSPYMH 702
 Db 617 --RGFESEPTSAQ-----DLTRSRSMVSTDMEM-----YTAARSH---SPGYHG 656
 OY 703 QATVQPISSQD 713

Db 657 DARPI-IAQID 666

RESULT 11

0923M7 PRELIMINARY; PRT: 347 AA.

AC 0923M7; 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DE BM401117.3.6 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 6)).

GN KCNQ2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA Wall M.;

RP SEQUENCE FROM N.A.

DR InterPro: IPR000636; K+channel_pore.

DR Pfam: PF00520; Ion_trans; 1.

SQ SEQUENCE 347 AA; 38461 MW; 93BEA660ADB82103 CRC64;

Query Match 25.3%; Score 1199; DB 11; Length 347;

Best Local Similarity 66.8%; Pred. No. 1.4e-78;

Matches 237; Conservative 33; Mismatches 63; Indels 22; Gaps 4;

QY 21 GAAAAAGGRLGSGMKDVGSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESRR 80

DB 9 GYVPGTSGEKKLVGVGLDGA-----PDSTRDGLLLINGSEAPK---RGSVLSKRT 59

QY 81 GKGARMSLKGKPLSTSSGCRNRVRYRQNYLYVLERPGMAFYHAFVFLVFGC 140

DB 60 GGAGA-----GKP-----PKRNAFYRKLFNLYVLERPGMAFYHAFVFLVFGC 106

QY 141 LLSVFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGRLEFARK 200

DB 107 LVLVSFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGRLEFARK 166

QY 201 PCVVIDIVLIVLAVVSAKTQGNIPATSLRSLRFLQILRMVMDRGRGTWKLGSVY 260

DB 167 PCVVIDIVLIVLAVVSAKTQGNIPATSLRSLRFLQILRMVMDRGRGTWKLGSVY 226

QY 261 AHSKELITVWYIGFLVIFSSFLVLYVEKANKERSTADALMWGTTLTITGDKTPL 320

DB 227 AHSKELITVWYIGFLVIFSSFLVLYVEKANKERSTADALMWGTTLTITGDKTPL 286

QY 321 TWLGRLLSAGFALLGISFPALPAGILGSGFALKVOEHOHRKHFEKRRNPANLIO 375

DB 287 TWNGRLLAATFTLLIGVSEFPALPAGILGSGFALKVOEHOHRKHFEKRRNPANLIO 341

RESULT 12

0923M8 PRELIMINARY; PRT: 349 AA.

AC 0923M8; 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DE BM401117.3.2 (potassium voltage-gated channel, subfamily Q, member 2 (isoform 2)).

GN KCNQ2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RA Wall M.;

RP SEQUENCE FROM N.A.

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL450341; CAC40734.1; -

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR000636; M+channel_nlg.

DR Pfam: PF00520; Ion_trans; 1.

SQ SEQUENCE 349 AA; 38683 MW; A35A50C777C54EC2 CRC64;

Query Match 25.3%; Score 1199; DB 11; Length 349;

Best Local Similarity 66.8%; Pred. No. 1.4e-78;

Matches 237; Conservative 33; Mismatches 63; Indels 22; Gaps 4;

QY 21 GAAAAAGGRLGSGMKDVGSGRGVLLNSAARGDGLLGTAAATLGGGGGGLRESRR 80

DB 9 GYVPGTSGEKKLVGVGLDGA-----PDSTRDGLLLINGSEAPK---RGSVLSKRT 59

QY 81 GKGARMSLKGKPLSTSSGCRNRVRYRQNYLYVLERPGMAFYHAFVFLVFGC 140

DB 60 GGAGA-----GKP-----PKRNAFYRKLFNLYVLERPGMAFYHAFVFLVFGC 106

QY 141 LLSVFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGRLEFARK 200

DB 107 LVLVSFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGRLEFARK 166

QY 201 PCVVIDIVLIVLAVVSAKTQGNIPATSLRSLRFLQILRMVMDRGRGTWKLGSVY 260

DB 167 PCVVIDIVLIVLAVVSAKTQGNIPATSLRSLRFLQILRMVMDRGRGTWKLGSVY 226

QY 261 AHSKELITVWYIGFLVIFSSFLVLYVEKANKERSTADALMWGTTLTITGDKTPL 320

DB 227 AHSKELITVWYIGFLVIFSSFLVLYVEKANKERSTADALMWGTTLTITGDKTPL 286

QY 321 TWLGRLLSAGFALLGISFPALPAGILGSGFALKVOEHOHRKHFEKRRNPANLIO 375

DB 287 TWNGRLLAATFTLLIGVSEFPALPAGILGSGFALKVOEHOHRKHFEKRRNPANLIO 341

RESULT 13

09BX08 PRELIMINARY; PRT: 409 AA.

AC 09BX08; 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

DE BA358D14.1.1 (Potassium voltage-gated channel, KQT-like subfamily, member 2, isoform 1) (Fragment).

GN KCNQ2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RA Wall M.;

RP SEQUENCE FROM N.A.

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR003091; K+channel.

DR InterPro: IPR000636; M+channel_nlg.

DR Pfam: PF00520; Ion_trans; 1.

DR PRINTS: PR00169; KCHANNEL.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 409 AA; 45645 MW; 5D828C0EFA31649A CRC64;

Query Match 25.0%; Score 1181; DB 4; Length 409;

Best Local Similarity 59.1%; Pred. No. 3.5e-77;

Matches 238; Conservative 40; Mismatches 61; Indels 64; Gaps 6;

QY 134 FLVFGCLLSVFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGR 193

DB 1 FLVFGCLLSVFTIPEHTKLASSCLLLEFVIVVEGLEFIIRIMSAGCCCRGWRGR 60

RA Sme R.
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; AL032648; CAA21699.1; .
 DR HSSP; Q54397; 1BL8.
 DR InterPro: IPR000048; IO_region.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003846; KCNQ1_channel.
 DR InterPro: IPR003091; K_channel.
 DR Pfam; PF00520; Ion_trans_1.
 DR Pfam; PF00612; IO_1.
 DR Pfam; PF03520; KCNQ1_channel; 1.
 DR PRINTS; PRO0169; KCHANNEL.
 DR SMART; SM00015; IO; 1.
 DR SEQUENCE 645 AA; 73569 MW; B30BA20FCOD7AEB8 CRC64;
 SQ
 Query Match 20.1%; Score 950; DB 5; Length 645;
 Best Local Similarity 36.2%; Pred.No.3,7e-60;
 Matches 247; Conservative 92; Mismatches 175; Indels 168; Gaps 22;
 108 YRRVONTLYNLEREGM-AFIYHAFVFLVFCGLISVSTPEHTKLASSCLLIEFV 166
 3 YRAM---IYNCLERTGKCELYHFSVFLIVLCILSLVSTVEHSHFAELLITIEIV 59
 167 MIYVGFLEFIRISAGCCCRRCRMOGRIRAPKPCVT----- 205
 60 LVFFSVFIVRLMSAGCRSKYIGYGRLEKFRKPTLLIGRFGRLQLIRDMLRHGGS 119
 206 -----DTI-----VLASTAVS--AKTQGNIFATSA-----L 231
 120 FCGKRDAGDIYASSEDAPRPSAGMWEIRISKIPKIEFSLKIGIFENFMNFOQF 179
 232 RSLRFLQILR-----MVMEDRGCTWKLGSVYVAHSKE 265
 180 RKLFFSKILKKNLAGRVHWGSAATPSSGDPDLDVCGFRLHQLASRRLLGSVVFTHRE 239
 266 LITFMYIGFLVLISSFLVLYLEK-----DANKESTYADALMWGITTLTIGYDKTPL 320
 240 LITLTYIGFLGLISSYFVLAEKDHIGVDGROAFTSYADALMWGITTLTIGYDVVPQ 299
 321 TWIGRLISAGFALLGISFPFALPAGILGSGFALKVOEHOKHPEKRRNPANLIQCWRS 380
 300 TWIGRIYASCSIFRISFALPAGILGSGFALKVOEHOKHPEKRRNPANLIQCWRS 359
 381 YAADKSVSTATWPKPHLAL-HTCSPTNOKLSFKERVRMA--PRGQSIKRSQASVGD- 435
 360 HAA-EKRVS-ATWNAHIDPLAHETKETHHMMNKGKHAASSMDSNNLTKRQLDFKQSSLYNT 417
 436 ---RRSSTITLTAAGSPTKYOKSMSEFNRTFRPRLKLSQSPKPYTDALACTDD--- 489
 418 FRKKSSTV-----EMGEIDQERLLRHERNSDTDEKR 452
 490 VYDEKGGCCQCVSVE-----DLPPKLTIVRAIRIMEFVAKKREKET 531
 453 IY-RVAGDIDIDYEPTTPTRPOGHISHYCELDIAIRNAIRLRVYVFAARRFOOA 511
 512 RKPYDVADVIEYOXGQHLMNMVRIKELQRLDQTLGKGOYDGKSRK---GHVPT--- 564
 532 LRPIYDVADVIEYOXGQHLMNCRISLQTRVQDLGKGOITSDKRSREKITAHEHTDDL 591
 512 RKPYDVADVIEYOXGQHLMNMVRIKELQRLDQTLGKGOYDGKSRK---GHVPT--- 564
 592 SMIGRVYKVKOVOSIESKID---CLLDIYQOYLKRG---SASALALASQIIPPECE 643
 565 -IGSRISRLLEOMSSLDKRVKSSNRTNALYRLMADRNSLTISPSPALRPVSPACL 623
 644 QTSDYOSPVDSKDLGSAONSG 665

DB 624 SPRDQLSPT-----SISSQSSG 640
 RESULT 17
 ID 09VSH7 PRELIMINARY; PRT; 343 AA.
 AC 09VSH7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CG12215 protein.
 GN CG12215.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Adysani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Beeson K.Y., Beeson P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dyrin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster K., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iobagyan C.,
 RA Jatalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003830; AAF5829.1; .
 DR FLYBase; FBgn003494; CG12215.
 DR InterPro; IPR000636; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans_1.
 DR SEQUENCE 343 AA; 38755 MW; C8B8CA56540F4164 CRC64;
 Query Match 14.7%; Score 697; DB 5; Length 343;
 Best Local Similarity 61.3%; Pred.No.3e-42;
 Matches 138; Conservative 33; Mismatches 50; Indels 4; Gaps 3;
 87 MSLLGKPLSYSSQCRNRVYKRVQNTLYNLERPG-WAFIYHAFVFLVFCGLISV 145
 1 MSLLGKPLSYNT---NRGTRDVRKTRRLQSLNLEFRGRLHAIRYHAFVFLVFCGLISV 58

QY 146 FSTPEHTKLASSCLLLEFEVIVFGLFIRIRMSAGCCCRGRMGRLREAPKPCVY 205
 DB 59 FSTIKETEDAVYLLFRMLIVIMTFEFGARLSSGCRSRYQCLGRLKVKRPFCL 118
 QY 206 DTIVLASIAVSAKTOGNIPATSLRSLRQLIRVYMDRGGTWMKLGSVYAH-SK 264
 DB 119 DIVIILASIVYLGMTSGOVFATSLRGLREFQILRMVMDRGGTWMKLGSVYAH-RQ 178
 QY 265 ELITAMVIGFLVLFSSFLVYLVEKDANKFESTYDALMWGITL 309
 DB 179 ELITMVGIFGLIFASFLVYMEKVDNKFENFQALMWGDHLL 223

RESULT 18

Q96A19 PRELIMINARY; PRT; 392 AA.
 AC Q96A19; PRELIMINARY; PRT; 392 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Similar to potassium voltage-gated channel, KQT-like subfamily, member 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strauberg R.;
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC017074.1; AAI1074.1;
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR00636; M-channel_nlg.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF03520; KCNQ1_channel. 1.
 FT NON_TER
 SQ SEQUENCE 392 AA; 43727 MW; E0E8CBF2C56FF62C CRC64;

Query Match 11.6%; Score 549.5; DB 4; Length 392;
 Best Local Similarity 34.4%; Pred. No. 1.8e-31;
 Matches 138; Conservative 75; Mismatches 117; Indels 71; Gaps 13;

QY 287 VEXDANKFSTYADALMWGITLITIGYDRTPLMWGLSAGFLLGSEFALPAGL 346
 DB 4 VNESGRVEFGSYADALMWGVYVTTIGYDQVPTWVGKTLASCFSEVAFSPFALPAGL 63
 QY 347 GSGFALKVQEOHROKHFERRRNPANLQCVRSYAADEKSVSIATMKPHLAL--HT- 402
 DB 64 GSGFALKVQOKOROKHFNROIPAAASLIOTANRCVAAENPDS--TWKIYIRKAPSHL 121
 QY 403 CSPTNOKLSFKERVYMASPRGOSIKRSQASVGDNRSPDTITAEISPTKVKQKSW--FN 459
 DB 122 LSPSPKRP--KKSYYVKKKKFKLIDKNGVTPGEKMLTVPHITCDPPEERLDFHSDGYD 178
 QY 460 DTRRREPLRLKSSQPKPIYDADTALGTDVYDEKCCQDDVSYEDLTPPL----- 509
 DB 179 SSVKSPPL-LEVSMPH-----FRTNSFAD-----DLLEGTLTPTHISQLEHH 226
 QY 510 KTVIRAIIMKFKVKKRKEKTLRPYDVADVYEQYSAGHLDIMCRISLQTRVDLIGK 569
 DB 227 RATIVIRMOYFVAKKKRQOAKRPYDVADVYEQYSOGHNLNMLVRIKELORRIDQSIGK 286
 QY 570 Q--ITSDDKSRKRTAEHETTDLSMLGVVYKVKOVQSTIESLDCLDLIYQVY----- 622
 DB 287 SLFISVSEKSKDR-----GSNTIGARLNREVEDVTOLODRLALITDMLHOLLSDHGC 338
 QY 623 -----RKGS-----SALALASPDIPPE 641
 DB 339 STPGSGGPPREGAHITPOCGSGGSVDPELFLPSNTLPTYE 379

RESULT 19

Q9B0U4 PRELIMINARY; PRT; 363 AA.
 AC Q9B0U4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE BA261N11.6.1 (Potassium voltage-gated channel, KQT-like subfamily, member 2, isoform 1) (Fragment).
 GN KCNQ2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL121827; CAC36121.1;
 DR InterPro: IPR003946; KCNQ1_channel.
 DR Pfam: PF03520; KCNQ1_channel. 1.
 FT NON_TER
 SQ SEQUENCE 363 AA; 39479 MW; 90862BB0E36097FB CRC64;

Query Match 9.6%; Score 452.5; DB 4; Length 363;
 Best Local Similarity 36.8%; Pred. No. 1.7e-24;
 Matches 130; Conservative 36; Mismatches 94; Indels 93; Gaps 14;

QY 484 ALGTDVYDEKGCOCNVSVDLTPPLKTVIRAIRIMKFKVKKRKEKTLRPYDVADVYQ 543
 DB 2 SLPEDEIVDDKSCPEFEFTEDLTGELIKYSIRAVCWRLVSRKPKESLRPYDMDVYQ 61
 QY 544 YSAGHLDMLCRKISLQTFVDDIIGQITSDPKSRKRTAEHETTDLSMLGVVYKVK 603
 DB 62 YSAGHLDMLSRKISLQSVYDVOIVGRRPALT-DKRTKPAEALDEDPDMARKLVEKQ 120
 QY 604 VQSTESKLDCLDIYQVYQVLRKGSASALALASFPDPFC-----EQTSDYQSPVS 654
 DB 121 VLSMEKKLDPLVNIYMQ--RMG-----IPETEAIFYGAKEPPAPPHSPEDS 167
 QY 655 KDLGSAONSGCLSRSTANISRGLOFILTPEFSNQTFYALSPYHSQATQVPISQ-- 712
 DB 168 RE--HVDHRCICIVKIVRSSSTG-----QKNFAP--AAP-----VCCPSTSMQ 210
 QY 713 -----DGSAAVANTNTIANQINTAPKPAAPTLOI-----P-- 743
 DB 211 PQSHRQGHGSPVGDHGLVHIPPFAHRSLSAYGGNRSAMERTLRQEDTPGCRPPSG 270
 QY 744 -----PLPAIKHLRPPETLHPNPAGLQESISDYVTCIVASKENVOAQS 787
 DB 271 NLKRDSTISIPSYDH-----FELERSFGF--SISQ-----SKENLDALNS 310

RESULT 20

Q9CTU2 PRELIMINARY; PRT; 97 AA.
 AC Q9CTU2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 9230107005RIK protein (Fragment).
 GN KCNQ5 OR 9230107005RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EPIDIDYMIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinglich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001)
 DR EMBL; AK020325; BAB32071.1; -
 DR MGI; MGI:1924937; Kcnq5.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10547 MW; 6317ED3AC977B7A CRC64;

Query Match 9.2%; Score 437; DB 11; Length 97;
 Best Local Similarity 88.5%; Pred. No. 3e-24; Mismatches 0; Gaps 0;
 Matches 85; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 827 IRSTELNQLSGSSSGSGSGSODFPYKWRKSLFTDEVEGPEETDTPDAPAPARE 886
 DB 1 IRSTELNQLSGSSSGSGSGSODFPYKWRKSLFTDEVEGPEETDTPDAPAPARE 60
 QY 887 AAFASDSLRTGSRSSQSLCKAGESTDALSLPHVKL 922
 DB 61 AAFSSDSLRTGSRSSQSLCKAGESTDALSLPHVKL 96

RESULT 21
 QY 09GYM8 PRELIMINARY; PRT; 675 AA.
 AC 09GYM8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-JUN-2002 (Tremblrel. 21, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Hypothetical 78.0 kDa protein.
 GN M60.5
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE=99069613; PubMed=9851916;
 RX None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Steillys L.;
 RT "The sequence of C. elegans cosmid M60.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U39995; AAF99993.2; -
 KW Hypothetical protein.
 SQ SEQUENCE 675 AA; 77981 MW; 3A5E193769BD1FA2 CRC64;

Query Match 9.1%; Score 430; DB 5; Length 675;

Best Local Similarity 25.0%; Pred. No. 1.8e-22;
 Matches 144; Conservative 103; Mismatches 233; Indels 96; Gaps 15;

QY 103 RRRNKKRVONYLYNLERPRGMAFY-YHAFVLLVFGCLISVSTPEHTKLASSCLL 161
 DB 69 QORNLRRIRLKVNFLEKPLMAASAPYHFFGLIVIANIILGAATN--DNDSTVSKIH 126
 QY 162 ILLEFVWVGLFEITIRWSAGCCORRGWOGRLFAKRPVIDITVILASAVASAT 221
 DB 127 FLEIFKVFILFEAVLMSVRADAKTKYGRLLVHTVYLIDILIPATILLIVER- 185
 QY 222 QGNIFATLSRLFLIOLIRVMDRGGTWKLLGSVYVANSKELLTAYVIGLIFSS 281
 DB 186 -GHDVOSTDLTLRFILIRFHYDRQAMATKLLKMLIIGWQMATYITLVVGLSLA 244
 QY 282 FLVY-----LVKDKAKESVYADALMWGITLTITIGYGDKPTLTWGR 325
 DB 245 TIVYSTELAQGIQDNGYGLIVPEGTNATFPTMAHSMWFTAVTVGVDIYPVALTK 304
 QY 326 LLSAGFALLGISFPALPAGILGSGFALKVQDQHRQKHEKRRNPAANLIQCVRSYADE 385
 DB 305 FLVGVLFGLFCTFOAANTQISVGLTLMMEENKQOTNRRLNLAATIQCWRYHLA-- 362
 QY 386 KSVSIATWKP---HLKALHTC-----SPTNOKLSFEKRYMASPRQOSIKSROAVGD 435
 DB 363 -----TNMKPRRYTYFVHCYKLYTEERINQNRVLAKILREKLEKRPICK--SLTH 415
 QY 436 RNSPSTIDITAEG---SPYVQKWSFND-----RTPR-----PSLRKSSOP 475
 DB 416 QNSVTAEILKFGKGMKPMLEKODSFDKERKISLTRRKYVFAEARNSSVETSMSSS 475
 QY 476 KPIVADTALGTDDVYDEKQCCQSVEDLPPPK--TVIRAIRIMKRVAKRKETLR 533
 DB 476 VDVSELETQETINFLQANDVLSKVEDLSILKIRPLNPFYVFMRFYNNKH---- 531
 QY 534 PYDVKDVIEQYSAGHLDL-----CRISLQTRVQDILGKQISDCKSRKRI 581
 DB 532 -----TORIAGQLIMEAIEAERENQNRQKKELEAILELGRKPTVSFDDSGQK- 582
 QY 582 TAEHETDLSMGRVYKVKQVQSTSKDCLDI 617
 DB 583 -----LSIIELECEKRMEDLERKTDALNEI 609

RESULT 22
 QY 09BOU5 PRELIMINARY; PRT; 399 AA.
 AC 09BOU5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2002 (Tremblrel. 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE BA261N1.6.2 (Potassium voltage-gated channel, KQT-like subfamily,
 DE member 2, isoform 2) (Fragment).
 GN KCNQ2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL121827; CAC36120.1; -
 DR InterPro: IPR003946; KCNQ1_channel.
 DR InterPro: IPR002965; P_rich_extensn.
 DR Pfam: PF03520; KCNQ1_channel; 1.
 DR PRINTS; PRO1217; PRICHEXTENS.
 FT NON_TER 1
 SQ SEQUENCE 399 AA; 43443 MW; ECC9545846F3B969 CRC64;

Query Match 9.0%; Score 424.5; DB 4; Length 399;
 Best Local Similarity 33.4%; Pred. No. 2e-22;
 Matches 130; Conservative 36; Mismatches 94; Indels 129; Gaps 15;


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Db 277 IFLESNKSVLOFQONVRRVOIFRIMRLIRILIKLARHSTGLQSLGFTLRSYNELGLTL 336
Qy 271 YIGFLVLIFFSEFLVYVEKDA-NKEESFYADALMNGTITLTIGYDKPTLWLGRLLSA 329
Db 337 FLAMGIMTFSS-LVFFAKEDDDTKFKSIPASFWMATITMTVGDIYKPLLGITVGG 395
Qy 330 GFALLGISFFALPGAGILSGFALKVQEQHROKHFEKRRNPANLIQCWRSTAADEKSYS 389
Db 396 LCCIAGLVIALPPIIYNNSEFYKBEKROEKAIKRR-----EALERAKRNGS 444
Qy 390 IATWKPRLKALHTCSPTNOKLSFEKERVN-----ASPROGSIKRSQASVDRSPSTDITA 445
Db 445 IVS-----NMKDAFARSYEMMDIYVEKNGENLAKKEKRVODNHNLSPNWKMT 491
Qy 446 EGSPTKVQKSWSFNDRTFRPSLRKSSQPKPYIDADALGDDVYDEKGCOCODSVEDL 505
Db 492 KRTISEYSSSKSFETKEGSEKARSSSPQHL-----NVQULEDMINKNA----- 537
Qy 506 TPPLKTVIRAIRIMKFNHAKRRKFTLRPYDKVIEOYSAGHLDMLCRKISLOTFRVDOI 565
Db 538 -----KTQSOPYLNTKKEAAOSKPKLELMESIPS-----PVAPLPRTTEGV 579
Qy 566 LGKGQITSDKKSREKITAHEHTTDDLMLGRVYVKEKOVOSTIESKLDCLLDIYOVLKRG 625
Db 580 I-----DMRS-----MSIDSFISCATDF----- 598
Qy 626 SASALALAPQIPPEFECQTSIDYOSPVDS-----KDLSSGANSQGLSRSSANISRLQPI 682
Db 599 -----PEATRPSHSPSLASLPKACGAPBELGMRG-ALGASGGRIVEAN 641
Qy 683 LTPNEFSNQTFVALSPTMHSOATQVPISQSDGSAVAATNTIANQITAPKPAFTLQIP 742
Db 642 PTPASHSGSGFTIESP-KSSMKTNNPLK-----LRALKVFMAGE-----GPIPLPVLGWH 692
Qy 743 PPL-----PAIKHLPRPELHPNPAGLOESISVPTTCLVASKENVOVAQSNLTKDRSM 795
Db 693 DPLRTGRGAAAV-----AGIL-ECATLLDKVVLSPESISITTAARTPPRSP 738
Qy 796 RK-----SFDMG-----GELLISYCPWPKDGLKSLSQNLIRSEELNIQL 837
Db 739 EKPAIINAFNFGVHQYIDATDDEGQLYSVDSPPKSLH----- 779
Qy 838 SGSSSSGSGSODFFPKWRRESKLTITDEVEGPEETETDTPDAPOPA-----REAAFASD 892
Db 780 GGAPKPKCIGAR-----SEKNHFSAPLPTSPKFLRQNCIYST 817
Qy 893 SLRTGRSSQSICKAGE--STDALSLP 918
Db 818 EGLTGKSLSGQEKCKLGNHISPDVRLP 845

RESULT 26
014193 PRELIMINARY: PRT: 858 AA.
ID 014193
AC 014193;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE H-DRK1 K(+) channel (DJ791K14.1) (Potassium voltage-gated channel,
SHAB-related subfamily, member 1).
GN H-DRK1 OR KCMB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_Taxid:9606;
RN [1]
RP MEDLINE=94363205; PubMed=8081723;
RA Albrecht B., Loria C., Stocker K., Pongs O.;
RT "Cloning and characterization of a human delayed rectifier potassium
channel gene.";
RL Recept. Channels 1:99-110(1993).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL (In) Civan M.M. (eds.);
RL The eye's aqueous humor - from secretion to glaucoma, pp 69-104,
RL Academic Press, San Diego (1998).
RN [3]
RN SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: X68302; CAA48374.1;
DR EMBL: AF026005; AAB88808.1;
DR EMBL: AL035685; CAB89417.1;
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K_channel_pore.
DR InterPro: IPR004350; K21channel.
DR InterPro: IPR004351; K22channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M_channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF03521; Kv2channel; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1514; KV21CHANNEL.
DR PRINTS: PRO1491; KVCHANNEL.
DR PRINTS: PRO1495; SHABCHANNEL.
DR SMART: SM00225; BTB; 1.
DR Ionic channel.
SQ SEQUENCE 858 AA; 95877 MW; C4B426174ED0DEE4 CRC64;

Query Match 6.2%; Score 291.5; DB 4; Length 858;
Best Local Similarity 20.2%; Pred. No. 2.8e-12;
Matches 176; Conservative 127; Mismatches 301; Indels 267; Gaps 33;

115 LYVLEPRGMA--FIYHAFVLLVFCGLISVSTPEHTKL-----ASSCLLIE 164
175 LMDLEKPNSSVAAKILAIISIMPLVSTIALST-NITPELOSLDEFGSTGNPOLAHYE 233
165 FVMIVTGLEPIIRIRMSAGCCRRYRQGRLEFARKPCVVIDTIVLNASIAVSAKTQGN 224
234 AVCIAMFTMEYLLRFLSP-----KKW-----KFKGPIAIDLLAILPYVY-----T 276
225 IFATSAIARSL-----RFLQILRWIRMDRRCGTWKLISVVAHAKEL-ITAW 270
277 IFLESNKSVLOFQONVRRVOIFRIMRLIRILIKLARHSTGLQSLGFTLRSYNELGLTL 336
271 YIGFLVLIFFSEFLVYVEKDA-NKEESFYADALMNGTITLTIGYDKPTLWLGRLLSA 329
337 FLAMGIMTFSS-LVFFAKEDDDTKFKSIPASFWMATITMTVGDIYKPLLGITVGG 395
330 GFALLGISFFALPGAGILSGFALKVQEQHROKHFEKRRNPANLIQCWRSTAADEKSYS 389
396 LCCIAGLVIALPPIIYNNSEFYKBEKROEKAIKRR-----EALERAKRNGS 444
390 IATWKPRLKALHTCSPTNOKLSFEKERVN-----ASPROGSIKRSQASVDRSPSTDITA 445
445 IVS-----NMKDAFARSYEMMDIYVEKNGENLAKKEKRVODNHNLSPNWKMT 491
446 EGSPTKVQKSWSFNDRTFRPSLRKSSQPKPYIDADALGDDVYDEKGCOCODSVEDL 505
492 KRTISEYSSSKSFETKEGSEKARSSSPQHL-----NVQULEDMINKNA----- 537
506 TPPLKTVIRAIRIMKFNHAKRRKFTLRPYDKVIEOYSAGHLDMLCRKISLOTFRVDOI 565
538 -----KTQSOPYLNTKKEAAOSKPKLELMESIPS-----PVAPLPRTTEGV 579
566 LGKGQITSDKKSREKITAHEHTTDDLMLGRVYVKEKOVOSTIESKLDCLLDIYOVLKRG 625
580 I-----DMRS-----MSIDSFISCATDF----- 598

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QY 626 SASALALASFOIPEECOTSDYQSPVDSKLSGAQNSGCLSRSTANISRGIOFILTP 685
D 606 HSPILSLPS-----KTGSTAP--EYGMWALGASG--GRFVANPS-----P 644
QY 686 NEFSQOTYALSP-----TWHSQATOVPIQSOD-----GSAAVA 719
D 645 DASOHSFFIEPSKSMKTNPLKLRALKYFMWEGDPSPLPVLMGYHDLPRNGSAANA 704
QY 720 T-----NTIANQINAPKPAFTLQIPPLPAIKHLPRETLHPN-----PALQESIS 769
D 705 VAGLECATLLDKAVISPESSITTTASAKTP-----PRSPKHTAIAFNEAGVHOYT- 756
QY 770 DVTTCVLAISKENVQAQSNMLTRDSMRKSGDMGFTLLSYCPWPKDLGKSLSYQNLIRS 829
D 757 DADT-----DDEGQLLYSVDSSPKSLPGSTSPK----- 785
QY 830 TEELNIQUSGSSSSSGSQDFFPKWRESKLFITDEVGPEETDTFDDAAPQAPAREAA 889
D 786 -----FSTGTGRSEKNHF-----ESSPLPTSPKFLRQNCI 814
QY 890 ASDSLTRGSRSSQISCKAGE--STDALSLP 918
D 815 YSTEALTRGKPSGQCKCKLENNHISPDVRYLP 845

RESULT 27
ID 018868 PRELIMINARY: PRT: 858 AA.
AC 018868:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Delayed rectifier potassium channel Kv2.1.
GN DRK1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026006; AAB8809.1; -.
DR HSSP: Q54397.1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR004350; Kv21channel.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF03521; Kv2channel; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PRO0169; KCHANNEL.
DR PRINTS: PRO1514; KV21CHANNEL.
DR PRINTS: PRO1491; KCHANNEL.
DR PRINTS: PRO1495; SHABCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel.
SQ SEQUENCE 858 AA; 96117 MW; A9E24C3ABE13B491 CRC64;

Query Match 6.1%; Score 287.5; DB 6; Length 858;
Best Local Similarity 19.8%; Pred. No. 5.4e-12;
Matches 173; Conservative 120; Mismatches 307; Indels 275; Gaps 31;

QY 115 LYNNLEPRGMA---FTYHAFVFLVYFCGLISVSTPEHNTKL-----ASSCLLIE 164
D 175 LMDLEKPNSSVAKIILAIISIMFTIVSTIALSL-NTLPELOSLDEFGQTTPNOLAHVE 233

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QY 165 FNVIVGELFETIRIWSAGCCCRYRGNGRLRPAKPCVVIDTYLIASIAVSAKTOGN 224
D 234 AVCIAMFTMYELFELSSP-----KMW---KFFEGPINALDILALIPVYV-----T 276
QY 225 IFATSAIRSL-----RFLQILRMVRMDRRCGTWKLGSVYAAHSEL-ITAM 270
D 277 IFETESKSYLQGNVRRVQYIFRIMILRLILKLAHSTGLOSLQFTLIRSTNELGLLL 336
QY 271 YIGFVLVLISSFLVYLVKKA-NKESTYADALMMGTITLTITGIGDKTPTLWIGRLISA 329
D 337 FLMGIMIESS-LVFEAKEDDDTKFKSIPASFMAATITMTTVGCDIYPKLLGKIYVG 395
QY 330 GFALLGISFPALDAGITSGSPALKVOOHRKHEKRRNPANLIQCWRSYAABEKSS 389
D 396 LCCIAGVLVIALPIITIVNNSSEFYKDKKROEKAIKR----- 433
QY 390 IATWPKHLKALHTCSPNTQKLSFEKERYMASPRGOSIKRQASVGRDRSPSTDTAE-- 446
D 434 -----EALBRARNGSIYSMMKKDAFPRSEIMMDIYVERKV 469
QY 447 ---GSPTKVO-----KSWGFNDTRFRPRLKSSQKPYVIDADTALGTDVYDEKCO 497
D 470 ENMGQDKYQDNHLSPKKWTWKRTLSETS--SKSSEFETK-----EGG-- 510
QY 498 CDVSVEDLPPLKTVIRAIRIMKFKRKFKETLRPDYKDYIEQYSAGHLMCLRIKS 557
D 511 -----SP-----EKARSSSPQHLNVOOLEDMTN-----KM 536
QY 558 LQTRVDOLLGQGITSDKRSREKITAEHETTDLSMLGRVYKV--EKQVOSIESRLDCLL 615
D 537 AKTOSQPIILNTRKSAQOSKPKKELEMEISPSVAPLFRTRGVIDMRMSIDSFSICAT 596
QY 616 DIYQVLRKGSABALALASFOIPEECQTSIDYQSPVDSKLSGAQNSGCLSRSTANI 675
D 597 DEPEAT--RFSHSPLA-----SLPSKSGSMAPEVWNG-ALGATG 634
QY 676 SNGIOLFILIPNESAQTFYALSPTHMSQATQVPIQSODGSVAATNTT-----ANOINT 729
D 635 GRFVEANPTPDASHHSTFTLESK-----SSMKTTPNKLALAKYFMWEG 679
QY 730 APRPAAPFTLQIPPLPAIKHLPRETLHPNPAQLOESIDVTC-----LVASKENVO 783
D 680 DESPLVPVLMGYHDP-----RNRGGAANAVALTECATLLDRVYLSPESSIT 726
QY 784 VAQSNLTKRSMK-----SFDMG-----GETLLSYCPWPKDLGKSLSYQ 825
D 727 TTASARTPPRSPKHTAIAFNEAGIHQYIDADTDDEGOVLYSVDSPPKSLHGSTSPK- 785
QY 826 LIRSTEELNIQUSGSSSGSQDFFPKWRESKLFITDEVGPEETDTFDDAAPQAPAR 885
D 786 -----FSIGTRSEKNHF-----ESSPLPTSPKFLR 810
QY 886 EAFASDSLTRGSRSSQISCKAGE--STDALSLP 918
D 811 QNCIYSTALTGKAPSGQCKCKLENNHISPDVRYLP 845

RESULT 28
ID 08WNO3 PRELIMINARY: PRT: 611 AA.
AC 08WNO3:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Potassium voltage-gated channel (Fragment).
GN KCNB2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

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DR InterPro: IPR004350; Kv21channel.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003968; Kv2channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR Pfam: PF00520; Ion_trans.1.
DR Pfam: PF03521; Kv2channel.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01514; KV2CHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR SMART: SM00225; BTB.1.
SQ SEQUENCE 857 AA; 95692 MW; 772F1C42C25EF3A5 CMC64;

Query Match 5.9%; Score 279; DB 11; Length 857;
Best Local Similarity 20.4%; Pred. No. 2.2e-11;
Matches 181; Conservative 124; Mismatches 280; Indels 304; Gaps 37;

QY 115 LYNVLERPRGMA---FIYHAFVLVFGCLISVFSTIPEHTKL-----ASSCLLLE 164
DB 175 LMDLEKPNSSVAAKIIAIIISIFIVISTALSL-NLPELQSDIEFGQSTDPQLAHE 233
QY 165 FVNIIVFGLFIIRIRISAGCCCRGRGMRLEFARKPCVDTIYLIASIAVSAKTOGN 224
DB 234 AVCIAMFTMYELRFLSSP-----KKV-----KFFKGPLNADLDLAILPYV-----T 276
QY 225 IFATSAIRSL-----RFLQILRMVRMDRGGTWKLGSVYVAHSKEL-TAW 270
DB 277 IFLESNKSVLOFQONVRVVOIFRIMRILRIKLAKHSTGLQSLGFTLRSYNELGLLIL 336
QY 271 YIGFIVIESSTFIYVLEKDA-NKEFSTYANALMGTTTLTGIGDKTPTLTKRLISA 329
DB 337 FLAMGIMIFSS-LVFEAKEDDDTKFKSIPASFWMTITTVGIDYPTLLKIKYVG 395
QY 330 GFALLGISFPALPAGIISGFALKVQOHRQKHEKRRNPANLIOCWRSYAADKSVS 389
DB 396 LCIIAGVLVALPIPIIVNNSEFYKCKRKOKAKIKRR-----EALERAKRNS 444
QY 390 IATWPKLALHCTSPNOKISFEKERVAM-----ASPRQSIKSROASVDRSPSTDITA 445
DB 445 IVS-----NNMKDAFARSIEMMDIIVEKEGVAKKKQVODNHLSPMKMKWT 491
QY 446 EGSPITKQKSMENDRIRFRSLKLSQPKRVIDADALGDDVYDEKGCOCDDSVEDL 505
DB 492 KRALSETSSSKSEFTKEQSGPEKARSSSPQHL-----NVQOLQDMYSK-----MAKTOS 541
QY 506 TPPLKTVIRAIRIMKPFVAKRFEKTELRYDVKDVIIEQYSAGHLMCLRIKSLQTRVDQI 565
DB 542 QPILNT-----KEMAPQSQPOELEMGS-----MPSVVALPRTREBV 579
QY 566 LKGQITSDKKSREKITAHEHTTDDLSMLGRVYKVEKOVOSTIESLDCLLDIYOVLKRG 625
DB 580 I-----DMKS-----MSSIDISFISCATDF----- 598
QY 626 SASALALASQIIPPECEQTSDYQSPYDCKLDSGAONS-----GCLSTSTANISR 677
DB 599 -----PEATRFSSPLAS--LSGKSGSTAEVGMWGLGASGR----- 636
QY 678 GLQFILPN--EFSAQTFYALSP-----TMHSAOTOVPISSQDSGSAVATNTIANO 726
DB 637 ---LMEINPIPEASRSGFVESPSSSMKTHNPKMLRALKVFLGSD----- 679
QY 727 INNAPKAAPPTLLOIPPLPAIKHLPRPETHPNP-----AGIQESISDVTTL 775
DB 680 -----PLPAL-----GLYHDLIRNNGGARAANAAGL-ECASLIDKPV 717
QY 776 VASKENVOAQSNTLKQSRMR-----SPDGM-----GELLASVCPMVKPL 817
DB 718 LSPSSITTTASARTPPRSPKHTAIANFAGVHOYIDTPTDDEQOLLYSDVSSLPKSL 777

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QY 818 GKSLVONLIRSTEELNQLSGSESSGSGSODFPKWRSKLETTDEWGEETETDTF 877
DB 778 HGSTSPK-----FSLGAR-----TEKNHF 796
QY 878 DAAPQPAR-----EAFASDSIRTRGSRSSQSIKRAGEST--DALSLP 918
DB 797 ESSPLTPSPKFLRPNVCYASECL-PGKGPAOEKCKLEHNTSPVHMLP 844

RESULT 32
Q98SV4 PRELIMINARY; PRT; 816 AA.
AC Q98SV4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Delayed rectifier potassium channel Kv2.
OS Ictalurus punctatus (channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAXILLARY BARBEL;
RX MEDLINE-21136584; Pubmed-11238731;
RA Kang J., Teeter J.H., Brazier S.P., Nguyen N.D., Chang C.C.,
RA Buchalski R.B.
RT "Molecular Cloning and Functional Characterization of a Novel Delayed
RT Rectifier Potassium Channel from Channel Catfish (Ictalurus
RT punctatus): Expression in Taste Buds."
RL J. Neurochem. 76:1465-1474(2001).
DR EMBL: AF319664; AK15623.1;
DR HSSP: Q54397; 1BL8.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003969; Kv6_channel.
DR InterPro: IPR003970; Kv8_channel.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR001313; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR InterPro: IPR003974; Shab_channel.
DR Pfam: PF00520; Ion_trans.1.
DR Pfam: PF03521; Kv2channel.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01492; KVCHANNEL.
DR PRINTS: PR01493; KVCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR PRINTS: PR01498; SHABCHANNEL.
DR SMART: SM00225; BTB.1.
KW Ionic channel.
SQ SEQUENCE 816 AA; 92092 MW; 0B9B22042CA297E CMC64;

Query Match 5.8%; Score 274.5; DB 13; Length 816;
Best Local Similarity 20.5%; Pred. No. 4.4e-11;
Matches 150; Conservative 100; Mismatches 225; Indels 255; Gaps 29;

QY 115 LYNVLERPRGMAFIYHAFVLVFGCLISV-----FSTIPE-----HFKLSS 158
DB 180 LMDLEKPNSSVAAKIIAIIISILF--IILSTIALSLNLPLOVYDEFGQANDPQLAH- 236
QY 159 CLILIEFVIIVFGLFIIRIRISAGCCCRGRGMRLEFARKPCVDTIYLIASIAVVS 218
DB 237 ---IEAVCIAMFTMYELRFLSS-----PKMKFFFGPLNVIDLAILPYV--- 280
QY 219 AKTOGINFATSAIRSL-----RFLQILRMVRMDRGGTWKLGSVYVAHSKE 265

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Db      281 -----TFLTESNKSVALQFQNVRRVQJFRIMKILILKLARKSTGLSGLGTLRSYNE 335
QY      266 L-ITAWYIGFVLVLFSSFLVYLVEKDAN-KERSTYADALMMGTITLTIGYDKTPTLWL 323
Db      336 LGLILFLAMIMIFSS-LVFEAEKDEDATKFTSIPASFWMATITMTVGYGDIYPOTLL 394
QY      324 GRLLSAGFALLGISFLLPAGILSGFALKVOEHROKHFEKRRNP-----AAN 372
Db      395 GKIYGGCLCCIAGVLYALPIPIIVNNFSEFYEQKQEKAKIKRREALERAKRNGSIYSMN 454
QY      373 LIQCVMSY-----AADEKSVSIATWKPHLKALH-----TCSPTNOKLSFKRRVR 417
Db      455 LKDAFARSMELIDVYVEKSEKPSFDNLSPSRMGIPKRASDASIRPFDRKVGSRCECFK 514
QY      418 MASPR-----GOSIKRSQASVGDGRSPSTDTITAEQSPTKYOKSMSPFDRTRFRP 466
Db      515 SSSSQHLNVOKLEEMYNOMSKARSLSDLDKN-----NASGPKLEOMNASKSGQRNR 566
QY      467 SLRLKSSQPKFVIDADTALGTDVYDEKGCQCQSVEDLTPPLKTVIRAIRIMKFHVAKR 526
Db      567 -----PVSDVPHMASTDSF----- 580
QY      527 KKEETLAPYDVKDIYEQVSAGHLDMLCRIKSIQTRVDQLGKQITSDKSKREKITAEHE 586
Db      581 -----GSCITDELREASKLTPSSK 598
QY      587 TTDDLMLGRVYKVEKQVOSIESKLDCLLDIYOVLRLKGSASALALASFOIPEECQOTS 646
Db      599 DDKRSYKNTTSLVES-SNPETPLD-----TQOISP-----EQRS 633
QY      647 DYQ-SPVDSKDLGSA-----QNSGLSRSTS-----ANISRGLOFLTPNEFSAQFYALSP 699
Db      634 QFYAP-----SGHVYNEDEECIVDNTFLIOSINPMRV-----NPLESTDVPLTP 683
QY      700 MHSQATQVPS--QSDGSAVATNTIANQINAPKPAATFIQIP-----PLPAIKH 750
Db      684 STSAGLSLSTLDDNS-----PROESTPPESVILAKIPROGLILSPLPV--- 732
QY      751 LPRPETLHPN 760
Db      733 -----GDFHPN 738

RESULT 33
Q95L11 PRELIMINARY; PRT; 911 AA.
AC 095L11;
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Voltage-gated potassium channel alpha subunit Kv2.2.
GN KCNB2.
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Malysz J., Farrugia G., Ou Y., Szurzewski J.H., Nehra A.,
RA Gibbons S.J.;
RT "The rabbit Kv2.2 alpha subunit contributes to delayed rectifier K
RT currents in freshly isolated cavernosal myocytes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY037947; AAK84954.1;
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR004351; Kv22channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF03521; Kv2channel; 1.
DR Pfam: PF02214; K_tetra; 1.
KW Ionic channel.

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SQ SEQUENCE 911 AA; 102278 MW; 69353D0664C5D689 CRC64;
Query Match 5.8%; Score 274.5; DB 6; Length 911;
Best Local Similarity 22.9%; Pred. No. 5.2e-11;
Matches 170; Conservative 114; Mismatches 308; Indels 151; Gaps 30;

QY 115 LVNVLERPRGWA---FLYNAFVELLVFGCILISVFSTIPE-----HTKLASSC 159
Db 179 LMDLEKPRSSVAKALAIYLSILFVISTALSL-NLPLEQEDDERQSPDNKRLAH-- 235
QY 160 LILFVMTLVVGLFTIRIWSAGCCCRYMGQRLPRAPKPFVIDTIVLIASIAVVA 219
Db 236 ---VEAVVICAMFMEYLRLRLS-----PKMKRFKGPLVIVDILALIPYVV--- 279
QY 220 KTOGNIFATSLRSL-----RFLQILRMVBMORGGTWTLLGSVVAHAKEL 266
Db 280 -----TFLTESNKSVALQFQNVRRVQJFRIMKILILKLARKSTGLSGLGTLRSYNE 335
QY 267 -ITAWYIGFVLVLFSSFLVYLVEKDAN-KERSTYADALMMGTITLTIGYDKTPTLWL 324
Db 336 LGLILFLAMIMIFSS-LVFEAEKDEDATKFTSIPASFWMATITMTVGYGDIYPOTLL 394
QY 325 RLLSAGFALLGISFLLPAGILSGFALKVOEHROKHFEKRRNP-----AANL 373
Db 395 KIVGGCLCCIAGVLYALPIPIIVNNFSEFYEQKQEKAKIKRREALERAKRNGSIYSMN 454
QY 374 IQCVMSY-----AADEKSVSIATWKPHLKALHSCSPNOKLSFKEVRVMA SPRGOSTISR 429
Db 455 KDAFARSMELIDVYVAKAGETANTKOSADNH--LSPSRWKWARKALSESSNKSSTENKYO 513
QY 430 QASVDRSPSTDTITAEGRP--TKYOK-SWSFNDTRFRP-SLRLKSSQPKFVIDADTAL 485
Db 514 EYSQKDSHQNLNN-TSSSPQHLQAQLEMLVNEITKQPHSHQAPQOQEP--ERPSAY 570
QY 486 GTDDVYDEKGC---QCDVSEVEDLTPPLKTVIRAIRIMKFHVAKKFEETLAPYDVK 542
Db 571 EEIEMEVEVVCQEOQLAVAOEYIVDMKS---TSSIDSFSCATDIFETER---SPL 622
QY 543 QYSAGHLDMLCRIKSIQTRVDQ-ILGKQITSPKSKREKITAEHETDDLMLGRVYV- 600
Db 623 PPSASHLNMKFTDPFGTEHEHQARARPPFLT---LIREKPARREGALESPDITVYND 679
QY 601 -----EKOVOSIESKLDCLLDIYOQVLR-----KGSASALALASFOIPEF 640
Db 680 AGSSQCGLHGPLQOSATSPKSLKGNPLKRSIKLVNFKENKNGSAP-----QRP- 731
QY 641 ECEORTSDVQSPVDSKDLGS-----AQNSGLSRSTSANISRGLOFILTLPN 686
Db 732 -----STARPLVTTADFSLSTPOHISTILLESPPAOGDRLLDLDELPAQCQGLAKGLSP- 786
QY 687 EFSAQTFYALSPTMHSAQTVPI-----SOSDGSAAVATNTIANQINAPKPA 735
Db 787 RFPKQKLFASFSSRRERSRFTIEDTGEDFLELGARADKQADSSPNFAEKPSDARRPLS 846
QY 736 PTTIOLIPPLPAIKHLPRPETLH 758
Db 847 EEGCGSSSPPTGNCRQDSFH 869

RESULT 34
Q97045 PRELIMINARY; PRT; 959 AA.
AC 097045;
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Kv2 channel alpha-subunit.
GN TUKV2.
OC Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyrosidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]

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QY 390 IATWPKHALHTCSEPTNOKLSFEKERV-----ASPRGOSIKSHQASVGDRRSP----- 439
 DB 445 IVS-----MNMKDAFARSIEMMDIYERKGEISAKDXQDNLSPKMKMKWT 491
 QY 440 -----STDTAESSPTVKQS-----WSFNDRTRFRPSRLK--- 471
 DB 492 KRALSETSSKSFETKEGSPKARSSSPQHLNVQOILEDYMSKMAKTOSQPIINTKEMA 551
 QY 472 -----SSQPKV 478
 DB 552 POSKPPPELEMSMSPV 569

RESULT 36
 ID P91784 PRELIMINARY; PRT; 478 AA.
 AC P91784;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Potassium channel alpha subunit.
 GN JSHAL-ALPHA-1.
 OS Polyorchis penicillatus (Hydromedusa).
 OC Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydrozoa; Anthomedusae;
 OC Polyorchidae; Polyorchis.
 OX NCBI_TaxID=6091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jegla T., Saloff L.;
 RT "A Novel Subunit for Shal Potassium Channels Radically Alters
 Activation and Inactivation.";
 RL J. Neurosci. 0:0-0(1996).
 DR EMBL: U78642; AAB39750.1; -;
 DR InterPro: IPR000210; BTB_Po2.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF02214; K_tetra. 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01491; KVCCHANNEL.
 DR SMART: SM00225; BTB. 1.
 SO SEQUENCE 478 AA; 54714 MW; 1898FE75089280F5 CRC64;

Query Match 5.5%; Score 260.5; DB 5; Length 478;
 Best Local Similarity 27.4%; Pred. No. 2e-10;
 Matches 78; Conservative 63; Mismatches 101; Indels 43; Gaps 11;
 QY 105 NVKRYRVONYLVNLEERPGRGAFIYHAFVLFVFGCLLSVFSPIREHT-----KL 155
 DB 178 NHQAKNEOKYHGLEENPQS-TFLARILYITGF-FIYVSGSTIETIDCSANRPGCV 235
 QY 156 ASSCLLLEFVWIVVGFEEIIRIMSAGCCCRYRGWQRLRFARKPCVIDTIVLIA-SI 214
 DB 236 YNKLFENIEAVCVVETLEYLARLSAPC-----RFRHARISLSIIDVIALDPYI 286
 QY 215 AVSAKKTQGNIFATLSALSRLOILRMVMDRGGTWKLGSVYVAHSEKELITAWYIGF 274
 DB 287 GIAMTKTS-----ISGAFVSLRFRVFRIRKFSHSGRLIGSTLTSASCASEL-----GF 336
 QY 275 L-----VLIFSSPLVYLVKEDAN-KERSTYADALMWGITLTIGYGDKPTLWIGRL 326
 DB 337 LIFSISMAIILFAT-VVFVEVDVNDSDTSTIPASTWYITVITWTTIGYGDMPKTIPOKL 395
 QY 327 LSAGFALGISEFALPAGILGSGFA--LKVOEQRHOKHFEKRRRN 368
 DB 396 VGSICSLGVLIALPVPYIVSNFSRIYLQNGRADKRRANQKLRN 440

Q26094
 ID 026094 PRELIMINARY; PRT; 487 AA.
 AC 026094;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Potassium channel homolog.
 GN JSHAK1.
 OS Polyorchis penicillatus (Hydromedusa).
 OC Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydrozoa; Anthomedusae;
 OC Polyorchidae; Polyorchis.
 OX NCBI_TaxID=6091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jegla T., Grigoriev N., Gallin W.J., Saloff L., Spencer A.N.;
 RT "Multiple Shaker potassium channels in a primitive metazoan.";
 RL J. Neurosci. 15:7989-7999(1995).
 DR EMBL: U32922; AAB02603.1; -;
 DR HSSP: Q54397; IBL8.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF00520; Ion_trans. 1.
 DR Pfam: PF02214; K_tetra. 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01491; KVCCHANNEL.
 SO SEQUENCE 487 AA; 56125 MW; 731AD03B1C30A331 CRC64;

Query Match 5.5%; Score 260.5; DB 5; Length 487;
 Best Local Similarity 23.7%; Pred. No. 2.1e-10;
 Matches 83; Conservative 75; Mismatches 129; Indels 63; Gaps 11;
 QY 113 NV-----LYNVLEBP--RGNAFIYHAFVLLVFGCLLSVFSPIR----- 150
 DB 153 NYEPFKALMOFLBNPDSSNAKIFALISVLIIVSLIMFVETLETPVFAFKELLTNGRTY 212
 QY 151 -----EHTKLASSCLLLEFVWIVVGFEEIIRIMSAGCCCRYRGWQRLRFARKPCVI 205
 DB 213 KTVYSEH---AWMFVNTAVICWFTTEFLRL---TCC---PKIKFELTNGTII 259
 QY 206 DTIVL---ASIVWSAKTOGNIFATLSALSRLOILRMVMDRGGTWKLGSVYVAH 262
 DB 260 DFLSLPYLSIVLVSS-----SKGSFSLRYIRVLRVRLKLSHSGLOLTGWTIKRS 312
 QY 263 SKEL-ITAWYIGFVLVLFSSFLVYLVKEDANKFSTYADALMWGITLTIGYGDKPTLT 321
 DB 313 FNEMLMLAFPLFWIILIFGSCVYVAEYKEPSTKFTISPSFWMAIVTWTGYGDMHPVT 372
 QY 322 WIGRLSAGALLGISFALPAGILGSGFA-LKVOEQRHOKHFEKRRRNPAALIQCVNR- 379
 DB 373 FWQIVGSMVAVGVLTIALPVPVYVSNFVEYFTEKRRRRTTEARKQDANSKQEMVSR 432
 QY 380 -----SYADEKSVSIATWKPHLKALHTCSPYQKLSFEKRVMA 419
 DB 433 NVNFKIVLKNYAKSIKHSSTKRSRNRRECKTQYSPVSLNLDKRDQTA 482

RESULT 38
 ID 09H1V7 PRELIMINARY; PRT; 582 AA.
 AC 09H1V7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE DJ1003J3.3.1 (potassium voltage-gated channel, Shaw-related subfamily, member 4).
 GN KCNC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RESULT 37

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Graves T.;
 RT "The sequence of *C. elegans* cosmid Y73B6B.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084197; AAF68591.1; -
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003131; K_tetra.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR Hypothetical protein
 KW SEQUENCE 609 AA; 70370 MW; 707C39BE115821A CRC64;

Query Match 5.2%; Score 246; DB 5; Length 609;
 Best Local Similarity 24.2%; Pred. No. 3.3e-09;
 Matches 72; Conservative 64; Mismatches 106; Indels 56; Gaps 11;

QY 103 RRVKRYRNVLYNLE---RPRGMAFYH-----AFVLLVGCGL-----LSVST 148
 DB 150 QERLOEERVENADSTLKLSEKMMAFENPHSTSLVFEYVIGFIAVSVMCNIVET 209
 QY 149 IP--EHKRLASSC-----LLLEFVIVVGFLEFIRMSAGCCCRMGRLRFR 199
 DB 210 IPCGIEDNVSTGCEATGEQFVIDTACVITFTIEYFLRLSA-----PDRIKFR 260
 QY 200 KPCVIDTIVL---ASIAVVSARTQGNIFATSLRSLRFLQILRMVDRRGCTWKL 256
 DB 261 SIMSVTDVIAIMPYVSLVLTNDKDVSGLFVT---LRVFRFLFKFSRHSQGLRI 315
 QY 257 SVVYAHSEKELITANYIGLV-----LIFSSFLVLYVEKANKFSTYADLWGTITL 309
 DB 316 YTLKSCASEL-----GFLVFSLAMALITIMYAEKKVDATRFTSPSAFWYITVL 369
 QY 310 TTIGYGKPTLWGLRSLASGAFALGIFLAPAGILGSGFALKVOEHRKHFEKRR 367
 DB 370 TTIGYGMVSTIMGKIVGCVSLGVIVIALPVPVIVSNFS---RIYHONRADKRR 424

RESULT 43

Q26344 PRELIMINARY; PRT; 905 AA.
 AC Q26344;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Action potential broadening potassium channel.
 GN SHAB.
 OS *Aplysia* sp. (Sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_Taxid=6504;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94121918; PubMed=8292361;
 RA Quatrocki E.A., Marshall J., Kaczmarek L.K.;
 RT "A Shab potassium channel contributes to action potential broadening
 RT in peptidergic neurons.";

RL Neuron 12:73-86(1994).
 DR EMBL: S68356; AAC60504.2; -
 DR HSSP: Q54397; 1BL8
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003968; Kv_channel.
 DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003973; Shab_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PRINTS: PR01491; KVCHANNEL.
 DR PRINTS: PR01495; SHABCHANNEL.
 DR SMART: SM00225; BTB; 1.
 KW Ionic channel.
 KW SEQUENCE 905 AA; 100050 MW; 2437F102167E6451 CRC64;

Query Match 5.2%; Score 245.5; DB 5; Length 905;
 Best Local Similarity 27.6%; Pred. No. 6.5e-09;
 Matches 76; Conservative 53; Mismatches 107; Indels 37; Gaps 9;

QY 115 LYNVLEP-----RGMAFYHAFVFLVFGCLLSVFSTIPERTKLA-----SSCLL 161
 DB 301 VMDLEKPTSMARVVAIISLFIYL-----STALTLNTIPALQDRADPSLQNDMDIA 356
 QY 162 ILFVWIVVGLFEFIIWISAGCCCRMGRLRFRAPKPCVIDTIVLISIAVVSART 221
 DB 357 VVEAVICGMPTLEIARFMAS-----PNKKRFFRGPLNVLD-LIIMPYFISLGLT 406
 QY 222 QGNIFATSLRSL-----RFLQILRMVDRRGCTWKLGSVYVYASKEK-TYAWYIG 273
 DB 407 ETKKSTTEQONVRRVVOIRIMRILILIKARSTGLQSLCYTLQRSYKELGMLMTLA 466
 QY 274 FLVLISSFLVLYVEK-ANKFSTYADALWGTITLTIGYDKPTLWGLRSLASGFA 332
 DB 467 IFLLFSS-LAYFAEKDEPEKYSIDPETFWMAITMTVVGDIYPTVLGVKVGVC 525
 QY 333 LIGISFPALPAGILGSGFALKVQEOHRKHFEKRR 367
 DB 526 ICGVLVIALPIPIIVNFAEYKQDMREKAKFR 560

RESULT 44

Q22012 PRELIMINARY; PRT; 484 AA.
 AC Q22012;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE R186.5 protein.
 GN R186.5.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z78016; CAB01442.1; -
 DR HSSP: Q54397; 1BL8.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003968; Kv_channel.

DR InterPro: IPR003091; K_channel.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR InterPro: IPR003974; Shaw_channel.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF02214; K_tetra.1.
 DR PRINTS: PR01491; KCHANNEL.
 DR PRINTS: PR01491; KCHANNEL.
 DR PRINTS: PR01498; SHAWCHANNEL.
 DR SMART: SM00225; BTB.1.
 SO SEQUENCE 484 AA; 55471 MW; 39F02D8F26705609 CRC64;

Query Match 5.2%; Score 245; DB 5; Length 484;
 Best Local Similarity 24.2%; Pred. No. 2.7e-09;
 Matches 72; Conservative 59; Mismatches 117; Indels 50; Gaps 8;

DB 108 YRNVNYLYNVLERP---RGMAFIYHAFVFLVFGCLL-----LSVFSTIPE 151
 148 WQIKRPRWRLFDEPNSSRQAQFIATISVFELTATIVFCIKTHPGLRIPBLAFPGNFSR 207
 QY 152 HTKLASS-----CLLLEFYMTVFGLEFIRIMSGCCCRFGMG 193
 DB 208 NHRSSSHHPAQINIDKANSRPHPTFMVETICNTWTEIL-----AFSSGPS 258
 QY 194 RLRRARKPCVDTVYLASIAVSAKTOGINFATSLRSLRQLLRVMDRRGGTWK 253
 DB 259 RFEYLRAPVNIID---IVATLTFYIDLSSMGATADLEFFSIRIRMLFKLTHHNSGLK 315
 QY 254 LLGSVVAHAKSL-ITAWYIGFLVLFSSFLVYL--VEKANKFSTYADALMMGTTLT 310
 DB 316 LLMHTFRSAKSLMLVFFLVGVVVFASLVYAERESNEDNOFVSIPGLMVAIVMT 375
 QY 311 TIGYGDKPLPLTWLGRLLSAGFALGISFPALPGIISGFGALKVQE--QHRQKHEKRR 367
 DB 376 TIGYGDITPHYTLGRLLSICALAGVLTALTALPVPVIVSNAMFYSHIQASKMKRRK 433

RESULT 45

Q9NSA2 PRELIMINARY; PRT; 647 AA.
 AC Q9NSA2;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE SHA1-type potassium channel (Kv4.1).
 GN KCND1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Makita N., Shira N., Sawa H., Sasaki K., Nagashima K., Yoshida M.C.,
 RA Kitabatake A.;
 RT "Homo sapiens mRNA for sha1-type potassium channel KCND1 (Kv4.1).";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB021865; BAA96454.1; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel.pore.
 DR InterPro: IPR004054; KVALchannel.
 DR InterPro: IPR003091; KCHANNEL.
 DR InterPro: IPR003131; K_tetra.
 DR InterPro: IPR000636; M+channel_nlg.
 DR Pfam: PF00520; Ion_trans.1.
 DR Pfam: PF02214; K_tetra.1.
 DR PRINTS: PR01491; KCHANNEL.
 DR PRINTS: PR01491; KCHANNEL.
 DR SMART: SM00225; BTB.1.
 KW Ionic channel.
 SO SEQUENCE 647 AA; 71371 MW; 4643263D8398CC3A CRC64;

Query Match 5.2%; Score 245; DB 4; Length 647;

Best Local Similarity 22.7%; Pred. No. 4.2e-09;
 Matches 108; Conservative 79; Mismatches 171; Indels 118; Gaps 22;

QY 115 LYNVLEPR---GMATYHAFVFLVFGCLLSVFSITP-----EHTL 155
 DB 172 LMRAPENPHSTALVFFVYVTFEIV--SVIANVETIPCGSARRSSRPPCGRRPO 229
 QY 156 ASSCLLLEFVMTVFGLEFIRIMSGCCCRFGMGRLRPARAPFCVDTIVLA-SI 214
 DB 230 AFEC---MDRACVILTFGEYLLRLEFA-----PBCRFLRSVMSLIDVAILPYTI 277
 QY 215 AVASANTQGINFATSLRSLRQLLRVMDRRGGTWKLLGSVVAHAKSLITAWYIGF 274
 DB 278 GLLVPR---MDVSGAFVTLVFFVRFYRFRFSRHSGRLIGYTLKSCASEL-----GF 328
 QY 275 L-----VLFSSFLVYLVENKANK--EFTSYADALMMGTTLTITIGYDGPPLWGL 326
 DB 329 LFLSLTMAIIFIVMVEY--AEKGTNKTFTNIPAFWYTIYMTLIGYDWPSTIAGKI 387
 QY 327 LSAGFALLGISFPALPGIISGFGALKVQEORQKHEKRRRPAANLIQC----- 376
 DB 388 FGSCISLGVVIALPPIIVSNFS---RIYHQRADKRR--AQCKRLAIRLAKSGT 442
 QY 377 -----VWRSTADEKSVSI---ATWRPHLALH-----TCSPTNOKLSFKER 415
 DB 443 TNAFLQKONGCEDSGSGEQLCVNRSAFEOQHHLHLEKTKCHEFTDELTFSSBA 502
 QY 416 VRMAFPGOSIKSRQAS---VG-----DRSPSDITAEQSPYQKMSRNDKRR 463
 DB 503 LGAVSPGGRTSRSTSVSOPGSLSSCCPRARRAIRLANSTASVRS-SQOELDM 561
 QY 464 FRPSLRKSSOPPVIDADTALGTDVYDEKGCOC-----VSVEDLPPLTK 511
 DB 562 LAGLRSHAPQSSSLNAKP-----HDSLDLNCDSDFYALISIP--TPRANT 608

RESULT 46

Q75671 PRELIMINARY; PRT; 647 AA.
 AC Q75671;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE SHA1-type potassium channel (Voltage-gated potassium channel Kv4.1).
 GN KCND1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN;
 RA Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
 RA Weindel A.;
 RT "Transcription map in Xp11.23";
 RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA, AND KIDNEY;
 RX MEDLINE=20193625; Pubmed=10729221;
 RA Isbrandt D., Leichter T., Waldschutz R., Zhu X., Luhmann U., Michel U.,
 RA Sauter K., Pongs O.;
 RT "Gene structures and expression profiles of three human KCND (Kv4) potassium channels mediating A-type currents (IT0) and (ISA).";
 RL Genomics 64:144-154(2000).
 DR EMBL; AJ005898; CA06755.1; -
 DR EMBL; AF166006; AAF65617.1; -
 DR EMBL; AF166004; AAF65617.1; JOINED.
 DR EMBL; AF166005; AAF65617.1; JOINED.
 DR EMBL; AF166003; AAF65616.1; -
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR001622; K+channel.pore.


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QY 123 -RGNAFIYHAEVFLVFG-----CL-----ILSVSTIPEHTKLASSCLLI 162
DB 225 SRAAFIFAFSLFFLIVSTTTTCLERHEAFNIYKNTKEPIYNGSVLQYIEIDPALTY 284
QY 163 LEFVMIIVFGLFEIIRIMSAGCCCRRYRGMOGRLEFARKPCVIDTIVLI-----ASIAV 217
DB 285 VEGVCVWFTEFEFLVIVFS-----PNKLEFIKNLNIIDFVALIPFLYEVGLSGL 335
QY 218 SAKTOGNIFATSLRPILOTILRMVMDRGGTAKLLGSVVAHSE-LITAVYIGFLV 276
DB 336 SSKAKADVL--GELKVVFRFRLIRLFKLRHVEGLRVLGHTRASTNEFLLLITFLALGV 393
QY 277 LIFSSFLVLYVER-----DANKFSTYADALMWGTTITLTIGGDKTPTLWGLRL 326
DB 394 LIFAT-MIYYAERVGAOPNDPSASEHTQFNKIPIGFWMAVYMTLTIGGDMYPTQWSGL 452
QY 327 LSGFALLIGISFPALPAGIL-----GSGFALKVOEQ-----HROKH 362
DB 453 VGCALCAGVLTITAMPVPVIVNNFGMYSLAMAKOKLPRKRKH 496

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RESULT 49

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Q96PRL PRELIMINARY; PRT; 638 AA.
AC 096PRL;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Voltage gated potassium channel Kv3.2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Vega-Saenz de Miera E.C., Lau D.H.P., Mathew S., Miller A.C.,
RA Kucherlapati R., Rudy B.;
RT "Localization of the Voltage-Gated Potassium Channel Gene KCNC2 to
RT Human Chromosome 12q21 and Cloning of Two of Its Alternatively-Spliced
RT Transcripts, Kv3.2a and Kv3.2b."
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF268896; AAL27272.1; -
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR01581; KV3CHANNEL.
DR Ionic channel.
KW SEQUENCE 638 AA; 70225 MW; 211CAF8395A58C5D CRC64;
SQ

```

Query Match 5.1%; Score 243; DB 4; Length 638;

Best Local Similarity 23.8%; Pred. No. 5.8e-09; Mismatches 109; Indels 88; Gaps 13;

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DB 82; Conservative 65; Mismatches 109; Indels 88; Gaps 13;
QY 65 AATLGGGGGGRNRGRKQAGKMSLLGKPLSTYSQSCRRNRYRYRYONYLVNLRP-- 122
DB 195 AAGGCGPD-----GKSG-----RMRRLOQPMWMLFDEPYS 224
QY 123 -RGNAFIYHAEVFLVFG-----CL-----ILSVSTIPEHTKLASSCLLI 162
DB 225 SRAAFIFAFSLFFLIVSTTTTCLERHEAFNIYKNTKEPIYNGSVLQYIEIDPALTY 284
QY 163 LEFVMIIVFGLFEIIRIMSAGCCCRRYRGMOGRLEFARKPCVIDTIVLI-----ASIAV 217
DB 285 VEGVCVWFTEFEFLVIVFS-----PNKLEFIKNLNIIDFVALIPFLYEVGLSGL 335
QY 218 SAKTOGNIFATSLRPILOTILRMVMDRGGTAKLLGSVVAHSE-LITAVYIGFLV 276
DB 336 SSKAKADVL--GELKVVFRFRLIRLFKLRHVEGLRVLGHTRASTNEFLLLITFLALGV 393
QY 327 LIFSSFLVLYVER-----DANKFSTYADALMWGTTITLTIGGDKTPTLWGLRL 326

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DB 394 LIFAT-MIYYAERVGAOPNDPSASEHTQFNKIPIGFWMAVYMTLTIGGDMYPTQWSGL 452
QY 327 LSGFALLIGISFPALPAGIL-----GSGFALKVOEQ-----HROKH 362
DB 453 VGCALCAGVLTITAMPVPVIVNNFGMYSLAMAKOKLPRKRKH 496

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RESULT 50

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Q9XXD1 PRELIMINARY; PRT; 490 AA.
AC 09XXD1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Y48A6B.6 protein.
GN Y48A6B.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
[2]
RP SEQUENCE FROM N.A.
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
RL EMBL; AL023844; CAI19530.1; -.
DR HSSP; 054397; 1BL8.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF02214; K_tetra_1.
DR PRINTS; PR00169; KCHANNEL.
KW SEQUENCE 490 AA; 55361 MW; 7DFAE90EED58C261 CRC64;
SQ

```

Query Match 5.1%; Score 242.5; DB 5; Length 490;

Best Local Similarity 27.1%; Pred. No. 4.2e-09; Mismatches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

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QY 104 RNKRYRYONYLVNLRP-----RGNAFIYHAEVFLV-FGLISVSTIPEHTKLASS 158
DB 192 KTLRFGEIRRCVWNIIEEPASSGKAQFAVCSVYFVLISGLVGLSLELOVATKORNN 251
QY 159 -----CLILFEVMIIVFGLFEIIRIMSAGCCCRRYRGMOGRLEFARKP 201
DB 252 LIGGEFTEPMPIILGIEYICVIMFMEGLKMLVS--AKRSTFROLNIIDILALIP 309
QY 202 PCVIDTIVLIASIAVYSAKTQGNIFATSLRPILOTILRMVMDRGGTAKLLGSVYA 261
DB 310 F-IIEMLLIFIGSTQLRLDKGAFV--VIRILVLRVIRVCLKIGRYSGLQMFKTLKA 366
QY 262 HSKELITANYIGLVLFSSFLVLYVERKD--ANKFSTYADALMWGTTITLTIGGDKTP 319
DB 367 SFRQLQMMAMVWVATGVIFSTLVYFEKDEPAK-FHSIPAAQWCIVTMTTVGVDLTP 425
QY 320 LFWLRLSAGFALLIGISFPALPAGILGSGFALKVOEQHR 359
DB 426 VTPPGKLVATGALACGVLTALPITTTIVDNF-MKVAETER 464

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Search completed: June 14, 2003, 17:44:21

Job time : 111 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2003, 17:44:26 ; Search time 54 seconds
(without alignments)
1827,466 Million cell updates/sec

Title: US-09-825-147-2
Perfect score: 4733
Sequence: 1 MPRHAGGEGGAAGWWS.....SICKAGESTDALSPHWK 923

Scoring table: BIOSUM62
Gap 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4733	100.0	923	10	US-09-825-147-2
2	4713.5	99.6	932	10	US-09-813-148-2
3	4547	96.1	888	10	US-09-810-796-5
4	4527.5	95.7	897	10	US-09-810-796-4
5	1991	42.1	695	10	US-09-810-796-15
6	1991	42.1	696	10	US-09-813-148-6
7	1793	37.9	844	10	US-09-813-148-4
8	1793	37.9	844	10	US-09-810-796-14
9	1792.5	37.9	722	9	US-10-128-870-23
10	1792.5	37.9	722	9	US-10-131-685-23
11	1788.5	37.8	871	9	US-10-128-870-20
12	1788.5	37.8	871	9	US-10-131-685-20
13	1620.5	33.2	872	10	US-09-813-148-5
14	1603.5	33.9	854	9	US-10-128-870-27
15	1603.5	33.9	854	9	US-10-131-685-27
16	1207.5	25.5	300	9	US-10-128-870-4
17	1207.5	25.5	300	9	US-10-128-870-6
18	1207.5	25.5	300	9	US-10-131-685-4
19	1207.5	25.5	300	9	US-10-131-685-6

20	1102	23.3	676	9	US-10-138-316-2	Sequence 2, Appl1
21	1102	23.3	676	10	US-09-840-125-2	Sequence 2, Appl1
22	1102	23.3	676	10	US-09-813-148-3	Sequence 3, Appl1
23	1100.5	23.3	605	9	US-10-128-870-24	Sequence 24, Appl1
24	1100.5	23.3	605	9	US-10-131-685-24	Sequence 24, Appl1
25	1085	22.9	310	9	US-10-128-870-18	Sequence 18, Appl1
26	1085	22.9	310	9	US-10-131-685-18	Sequence 18, Appl1
27	1081.5	22.9	570	9	US-10-138-316-114	Sequence 114, App
28	993.5	21.0	245	9	US-10-128-870-8	Sequence 8, Appl1
29	993.5	21.0	245	9	US-10-131-685-8	Sequence 8, Appl1
30	957	20.2	298	9	US-10-128-870-2	Sequence 2, Appl1
31	957	20.2	298	9	US-10-131-685-2	Sequence 2, Appl1
32	905.5	19.1	430	9	US-10-128-870-21	Sequence 21, Appl1
33	905.5	19.1	430	9	US-10-131-685-21	Sequence 21, Appl1
34	898.5	19.0	376	9	US-10-138-316-113	Sequence 113, App
35	485.5	10.3	137	9	US-10-128-870-109	Sequence 109, App
36	255	5.4	446	10	US-09-864-761-37011	Sequence 37011, A
37	250	5.3	539	9	US-10-325-891-13	Sequence 13, Appl1
38	245	5.2	646	9	US-10-121-746-10	Sequence 10, Appl1
39	243	5.1	601	9	US-10-121-746-4	Sequence 4, Appl1
40	243	5.1	638	9	US-10-024-623-11	Sequence 11, Appl1
41	242	5.1	638	9	US-10-024-623-33	Sequence 33, Appl1
42	232.5	4.9	635	12	US-10-062-879-2	Sequence 2, Appl1
43	230	4.9	511	9	US-10-192-116A-7	Sequence 7, Appl1
44	229	4.8	636	12	US-10-062-879-4	Sequence 4, Appl1
45	224	4.7	477	9	US-10-121-746-18	Sequence 18, Appl1
46	223	4.7	499	9	US-10-121-746-8	Sequence 8, Appl1
47	223	4.7	500	9	US-09-999-220B-5	Sequence 5, Appl1
48	206.5	4.4	494	9	US-10-325-891-4	Sequence 4, Appl1
49	206.5	4.4	494	12	US-10-143-002-4	Sequence 4, Appl1
50	206.5	4.4	532	9	US-09-875-321-13	Sequence 13, Appl1
51	206.5	4.4	532	9	US-10-162-012-13	Sequence 13, Appl1
52	206.5	4.4	532	10	US-09-993-811-6	Sequence 6, Appl1
53	204.5	4.3	456	10	US-09-974-712-2	Sequence 2, Appl1
54	204.5	4.3	490	9	US-10-121-746-6	Sequence 6, Appl1
55	204.5	4.3	491	9	US-09-999-220B-3	Sequence 3, Appl1
56	203.5	4.3	446	9	US-09-875-321-8	Sequence 8, Appl1
57	203.5	4.3	446	9	US-10-162-012-8	Sequence 8, Appl1
58	201.5	4.3	454	10	US-09-993-811-12	Sequence 12, Appl1
59	201.5	4.3	456	9	US-09-989-920-175	Sequence 175, App
60	201.5	4.3	456	10	US-09-993-811-2	Sequence 2, Appl1
61	199.5	4.2	513	9	US-10-325-891-2	Sequence 2, Appl1
62	199.5	4.2	513	12	US-10-143-002-2	Sequence 2, Appl1
63	198.5	4.2	579	9	US-09-922-364A-19	Sequence 19, Appl1
64	198.5	4.2	579	9	US-09-254-590-19	Sequence 19, Appl1
65	198.5	4.2	579	9	US-10-115-695-19	Sequence 19, Appl1
66	198.5	4.2	579	9	US-10-116-561-19	Sequence 19, Appl1
67	198.5	4.2	579	9	US-10-115-671-19	Sequence 19, Appl1
68	198.5	4.2	579	9	US-10-115-415-19	Sequence 19, Appl1
69	198.5	4.2	579	9	US-10-116-260-19	Sequence 19, Appl1
70	198.5	4.2	579	9	US-10-115-688-19	Sequence 19, Appl1
71	198.5	4.2	847	9	US-09-875-321-2	Sequence 2, Appl1
72	198.5	4.2	847	9	US-10-162-012-2	Sequence 2, Appl1
73	193	4.1	491	9	US-09-999-220B-4	Sequence 4, Appl1
74	192.5	4.1	580	9	US-09-922-364A-2	Sequence 2, Appl1
75	192.5	4.1	580	9	US-09-254-590-2	Sequence 2, Appl1
76	192.5	4.1	580	9	US-10-115-695-2	Sequence 2, Appl1
77	192.5	4.1	580	9	US-10-116-561-2	Sequence 2, Appl1
78	192.5	4.1	580	9	US-10-115-671-2	Sequence 2, Appl1
79	192.5	4.1	580	9	US-10-115-415-2	Sequence 2, Appl1
80	192.5	4.1	580	9	US-10-116-260-2	Sequence 2, Appl1
81	192.5	4.1	580	9	US-10-115-688-2	Sequence 2, Appl1
82	188	4.0	115	10	US-09-925-297-612	Sequence 612, App
83	186	3.9	425	9	US-10-016-647-2	Sequence 2, Appl1
84	174	3.7	61	9	US-10-138-316-108	Sequence 108, App
85	174	3.7	545	9	US-09-999-220B-2	Sequence 2, Appl1
86	174	3.7	545	9	US-09-999-220B-34	Sequence 34, Appl1
87	174	3.7	545	9	US-09-999-220B-36	Sequence 36, Appl1
88	174	3.7	545	9	US-09-999-220B-116	Sequence 116, App
89	174	3.7	545	9	US-09-999-220B-118	Sequence 118, App
90	174	3.7	545	9	US-09-999-220B-120	Sequence 120, App
91	174	3.7	561	9	US-09-922-364A-1	Sequence 1, Appl1
92	174	3.7	561	9	US-09-254-590-1	Sequence 1, Appl1

93	174	3.7	561	9	US-10-115-695-1	Sequence 1, Appl1
94	174	3.7	561	9	US-10-115-661-1	Sequence 1, Appl1
95	174	3.7	561	9	US-10-115-671-1	Sequence 1, Appl1
96	174	3.7	561	9	US-10-115-415-1	Sequence 1, Appl1
97	174	3.7	561	9	US-10-116-260-1	Sequence 1, Appl1
98	174	3.7	561	9	US-10-115-688-1	Sequence 1, Appl1
99	166.5	3.5	215	9	US-10-255-532-4	Sequence 4, Appl1
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101	163.5	3.5	223	9	US-10-162-012-9	Sequence 9, Appl1
102	163.5	3.5	557	9	US-09-922-364A-20	Sequence 20, Appl1
103	163.5	3.5	557	9	US-09-254-590-20	Sequence 20, Appl1
104	163.5	3.5	557	9	US-10-115-695-20	Sequence 20, Appl1
105	163.5	3.5	557	9	US-10-116-561-20	Sequence 20, Appl1
106	163.5	3.5	557	9	US-10-115-671-20	Sequence 20, Appl1
107	163.5	3.5	557	9	US-10-115-415-20	Sequence 20, Appl1
108	163.5	3.5	557	9	US-10-116-260-20	Sequence 20, Appl1
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110	163.5	3.5	736	9	US-09-922-364A-47	Sequence 47, Appl1
111	163.5	3.5	736	9	US-09-254-590-47	Sequence 47, Appl1
112	163.5	3.5	736	9	US-10-115-695-47	Sequence 47, Appl1
113	163.5	3.5	736	9	US-10-116-561-47	Sequence 47, Appl1
114	163.5	3.5	736	9	US-10-115-671-47	Sequence 47, Appl1
115	163.5	3.5	736	9	US-10-115-415-47	Sequence 47, Appl1
116	163.5	3.5	736	9	US-10-116-260-47	Sequence 47, Appl1
117	163.5	3.5	736	9	US-10-115-688-47	Sequence 47, Appl1
118	160.5	3.4	458	9	US-09-922-364A-4	Sequence 4, Appl1
119	160.5	3.4	458	9	US-09-254-590-4	Sequence 4, Appl1
120	160.5	3.4	458	9	US-10-115-695-4	Sequence 4, Appl1
121	160.5	3.4	458	9	US-10-116-561-4	Sequence 4, Appl1
122	160.5	3.4	458	9	US-10-115-671-4	Sequence 4, Appl1
123	160.5	3.4	458	9	US-10-115-415-4	Sequence 4, Appl1
124	160.5	3.4	458	9	US-10-116-260-4	Sequence 4, Appl1
125	160.5	3.4	458	9	US-10-115-688-4	Sequence 4, Appl1
126	159.5	3.4	553	9	US-09-922-364A-3	Sequence 3, Appl1
127	159.5	3.4	553	9	US-09-254-590-3	Sequence 3, Appl1
128	159.5	3.4	553	9	US-10-115-695-3	Sequence 3, Appl1
129	159.5	3.4	553	9	US-10-116-561-3	Sequence 3, Appl1
130	159.5	3.4	553	9	US-10-115-671-3	Sequence 3, Appl1
131	159.5	3.4	553	9	US-10-115-415-3	Sequence 3, Appl1
132	159.5	3.4	553	9	US-10-116-260-3	Sequence 3, Appl1
133	159.5	3.4	553	9	US-10-115-688-3	Sequence 3, Appl1
134	159.5	3.4	732	9	US-09-922-364A-43	Sequence 43, Appl1
135	159.5	3.4	732	9	US-09-254-590-43	Sequence 43, Appl1
136	159.5	3.4	732	9	US-10-115-695-43	Sequence 43, Appl1
137	159.5	3.4	732	9	US-10-116-561-43	Sequence 43, Appl1
138	159.5	3.4	732	9	US-10-115-671-43	Sequence 43, Appl1
139	159.5	3.4	732	9	US-10-115-415-43	Sequence 43, Appl1
140	159.5	3.4	732	9	US-10-116-260-43	Sequence 43, Appl1
141	159.5	3.4	732	9	US-10-115-688-43	Sequence 43, Appl1
142	158.5	3.3	244	10	US-09-815-24-12713	Sequence 12713, Appl1
143	153	3.2	120	9	US-10-128-870-28	Sequence 28, Appl1
144	153	3.2	120	9	US-10-131-685-28	Sequence 28, Appl1
145	151	3.2	890	9	US-10-158-684-4	Sequence 4, Appl1
146	151	3.2	890	9	US-10-158-711-4	Sequence 4, Appl1
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QY 841 ESSGSRGSDQDFPKWRESKLFITDEVEGPETETDTPDAPOPARAAAFASDLSRTGRS 900
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Db 841 ESSGSRGSDQDFPKWRESKLFITDEVEGPETETDTPDAPOPARAAAFASDLSRTGRS 900
QY 901 SSOSICKAGESTDALSLPHVKLK 923
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Db 901 SSOSICKAGESTDALSLPHVKLK 923

RESULT 2

US-09-813-148-2
Sequence 2, Application US/09813148
Patent No. US20020076809A1
GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHE, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEBOHM, Guiscard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 932
TYPE: PRT
ORGANISM: Homo sapiens
US-09-813-148-2

Query Match 99.6%; Score 4713.5; DB 10; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 922; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
QY 1 MPRHAGGEEGGAALMWKSGAAAAAGGGRGSGMKDVESEGRVLLNSAARGGILL 60
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Db 1 MPRHAGGEEGGAALMWKSGAAAAAGGGRGSGMKDVESEGRVLLNSAARGGILL 60
QY 61 LGTRATATGGGGGGLRESRGRKOGARMSLLGKPLSTSSQSCRNNKYRRVQVLYNVLE 120
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Db 61 LGTRATATGGGGGGLRESRGRKOGARMSLLGKPLSTSSQSCRNNKYRRVQVLYNVLE 120
QY 121 RPRGMAFYHAFVFLVFGCLLSVFTIPEHTKLASSCLLLEFVMAIVVGELEFIIRIW 180
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QY 181 SAGCCCRRRGNGRLRPAKPCVDTIVLIASIAVSAKQGNITATSLRSLRQTL 240
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Db 181 SAGCCCRRRGNGRLRPAKPCVDTIVLIASIAVSAKQGNITATSLRSLRQTL 240
QY 241 RMVRDRRGGTWKLGLSVYVAHSHKELITAMVIGFLVLISSEFVYVVEKANKNEFTYAD 300
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Db 241 RMVRDRRGGTWKLGLSVYVAHSHKELITAMVIGFLVLISSEFVYVVEKANKNEFTYAD 300
QY 301 ALMWGTITLTITIGYDQKPTLWLGRLLSAGFALLGISFPALPAGILGSGFALKVQEOHRQ 360
|||||
Db 301 ALMWGTITLTITIGYDQKPTLWLGRLLSAGFALLGISFPALPAGILGSGFALKVQEOHRQ 360
QY 361 KHEERBRNANALICVMSRYAADEKSVSIATWKPPLKALHTCSPT-----NOKLS 411
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Db 361 KHEERBRNANALICVMSRYAADEKSVSIATWKPPLKALHTCSPT-----NOKLS 411
QY 412 FKERVMAASPRGOSIKRSQASVGDRRSPSTDTITAECSPTVKQKSWSFNDTRFRPSLRK 471

Db 421 FKERVMAASPRGOSIKRSQASVGDRRSPSTDTITAECSPTVKQKSWSFNDTRFRPSLRK 480
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Db 481 SSQPKPIYDADPALTGDVYDEKGCQCVSVEDLTPPLKTYIRAIRIKKFNHAKRKRET 540
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Db 541 LRPYDADVIEQYAGHDMCLCRISLQTRPDQILGKQITSDKSKREKTFAEHETDOL 600
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Db 601 SMLGRVYKVEKQVSIKSLDCLDIYQVLRKGSASALALASFQIPPECEQTSIDYOSP 660
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Db 661 VDSKDLGSAQNSGCLSRSTANISRGLOFILTPEFSAQTFYALSPMHSAQATVPISQ 720
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QY 892 DSLRTGRSRSSOSICKAGESTDALSLPHVKLK 923
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Db 901 DSLRTGRSRSSOSICKAGESTDALSLPHVKLK 932

RESULT 3

US-09-810-796-5
Sequence 5, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jegla, Timothy James
APPLICANT: ICAGEN, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 888
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-2
US-09-810-796-5

Query Match 96.1%; Score 4547; DB 10; Length 888;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 MKDVESEGRVLLNSAARGDGLLIGTRATLGGGGGLRSRGRKOGARMSLLGKPLS 95
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Db 61 YTSQSCRRNNKYRRVQVLYNVLEPRGMAFYHAFVFLVFGCLLSVFTIPEHTKL 120
QY 156 ASSCLLLEFVMAIVVGELEFIIRISAGCCCRYRGMQRLRPAKPCVDTIVLIASIA 215

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Db 121 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRYGMOGRLEFARKPFCVIDITVILASIA 180
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Db 181 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTKLLGSVYVAHSELITANYIGFL 240
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Db 241 VLISSFLVYLVEKDANKKESTYADALMMGTITLTIGYDGTPLTWLGRLLSAGFALLG 300
QY 336 ISEFALPAGILGSGFALKVOEHRKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 395
Db 301 ISEFALPAGILGSGFALKVOEHRKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 360
QY 396 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAGSPKVKOKS 455
Db 361 HLKALHTCSPTNOKLSFKERVRMA SPRGOSIKSRQASVGD RSPSTDTITAGSPKVKOKS 420
QY 456 WSFNDRTFRPSLRKSSQPKPVYIDADTALGTDVYDEKGCQCDVSEDLTPPLKTIVIRA 515
Db 421 WSFNDRTFRPSLRKSSQPKPVYIDADTALGTDVYDEKGCQCDVSEDLTPPLKTIVIRA 480
QY 516 IRIMKEHVAKRKFKETLRPYDKVDYIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 575
Db 481 IRIMKEHVAKRKFKETLRPYDKVDYIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 540
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QY 636 QIPPECCQTSYQSPVDSKDLSGSAQNSGCLSRSTSANISRGLOFTLTPNEFSAQTFYA 695
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QY 816 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDPYPKWRRESKLFITDEBVGPEETED 875
Db 781 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDPYPKWRRESKLFITDEBVGPEETED 840
QY 876 TFDAAPAPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 923
Db 841 TFDAAPAPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 888

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RESULT 4
US-09-810-796-4
; Sequence 4, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegaia, Timothy James
; APPLICANT: ICAGEN, INC.
; TITLE OF INVENTION: KCNO5, A NO. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated

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; OTHER INFORMATION: potassium channel KCNO5-1
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(640)
; OTHER INFORMATION: conserved region of KCNO5-1
US-09-810-796-4

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Query Match 95.7%; Score 4527.5; DB 10; Length 897;
Best Local Similarity 98.9%; Pred. No. 1.8e-318;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

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QY 96 YTSQSCRNVKTRVONLYLVLEPRGMAFIYHAFVLVFGCLLSVESTIEPHTL 155
Db 61 YTSQSCRNVKTRVONLYLVLEPRGMAFIYHAFVLVFGCLLSVESTIEPHTL 120
QY 156 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRYGMOGRLEFARKPFCVIDITVILASIA 215
Db 121 ASSCLLIEFVMIYVFGLEFIIRIWSAGCCCRYGMOGRLEFARKPFCVIDITVILASIA 180
QY 216 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTKLLGSVYVAHSELITANYIGFL 275
Db 181 VVSATOGNIFATSAIRSLRFLQILRMVRMDRGGTKLLGSVYVAHSELITANYIGFL 240
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Db 301 ISEFALPAGILGSGFALKVOEHRKHFEKRRNPANLIOCVMRSYADEKSVSIATWKP 360
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Db 421 WSFNDRTFRPSLRKSSQPKPVYIDADTALGTDVYDEKGCQCDVSEDLTPPLKTIVIRA 480
QY 516 IRIMKEHVAKRKFKETLRPYDKVDYIEQYSAGHLMICRIKSLQTRVDQILGKQITSDK 575
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QY 576 KSREKITAEHETDLSMLGRVYKVEKQVOSIESKLDCLDIYOQVLRKGSASALATASF 635
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QY 696 LSPTHMSOATQVPIQSODGSAVAATNTIANQINTAPKPAPTLQIPPLPAIHLRPE 755
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QY 756 TLHPNPAGLQESISDVTTCVLVASKENVQVAAQSNLTKDRSMKSFDMGGETLLSYCPMPVK 815
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QY 816 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDPYPKWRRESKLFITDEBVGPEETED 875
Db 781 DLGSLSYQNLIRSTEELNIOLSGSESSGSRGSDPYPKWRRESKLFITDEBVGPEETED 840
QY 876 TFDAAPAPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 923
Db 841 TFDAAPAPAREAAFAFASDSLRTGRSRSSOSICKRAGESTDALSLPHVKLK 888

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RESULT 5
US-09-810-796-15

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; Sequence 15, Application US/09810796
; Patent NO. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeggia, Timothy James
; APPLICANT: IChogen, INC.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNO4
; US-09-810-796-15

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Query Match 42.1%; Score 1991; DB 10; Length 695;

Best Local Similarity 57.8%; Pred. No. 1,7e-135;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

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DB 2 AEAPRRRLGLGPPGDARAEVAVTAVOSEG-----EAGGGSPR----- 43
QY 85 ARMSLKGKPL-----SYSSQSCRNRVKKRVONYLYNVLERPGMAFIYH 130
DB 44 -RLGLLSPPLPGAPLPDPGSGSGSAGCGRSSAAKRRYRLQNMVYLVLERPGMAFIYH 102
QY 131 AFVFLVFGCLLVSFTIPEHTKLASSCLLLEFVMIVFGLFETIRIRMSGCCRRYG 190
DB 103 VFILVFLVSCVLSVSTIOHQELANECCLLLEFVMIVFGLFETIRIRMSGCCRRYG 162
QY 191 WQGRLEFARKPCVYIDTVILASIAVSAKTQGNIFATSAKLSRLPQLILRVYRMDRGG 250
DB 163 WQGRLEFARKPCVYIDTVILASIAVSAKTQGNIFATSAKLSRLPQLILRVYRMDRGG 222
QY 251 TWKLLGSVYVAHSEKELITAWYIGFLVLIFFSFLVYLVEKDANKESTYADALMWGTTTLT 310
DB 223 TWKLLGSVYVAHSEKELITAWYIGFLVLIFFSFLVYLVEKDANKESTYADALMWGTTTLT 282
QY 311 TIGYGDKPLTWLGLVLSAGFALLGISFPALPAGILGSGFALKVQEHQKHKKRRMPA 370
DB 283 TIGYGDKPLTWLGLVLSAGFALLGISFPALPAGILGSGFALKVQEHQKHKKRRMPA 342
QY 371 ANLIQCVWRSTYAAD-EKSVSIATW----- 393
DB 343 ANLIQCVWRSTYAAD-EKSVSIATW----- 393
QY 394 -----KPKLALHT-----CSPINOKLSFEKERVMAASPRGOSIKSRQ--ASVGR 436
DB 403 PVDPGAPSRYPVAVATCHPFGSTSPCGESSRGMGIDRIMGSSQRTGTGSKQOLAPPTMP 462
QY 437 RSPSTDIATAG-SPTKVOKSMGFNDRTFRPRLRLKSSQPKPVYIDADTLGTDVYDEKG 495
DB 463 TSPSEQVGEATSPTKVOKSMGFNDRTFRPRLRLKSSQPKPVYIDADTLGTDVYDEKG 516
QY 496 CQCDVSVEDLTPPLKTVIRAIRIMKFKVAKRKFKETLRPYDVYKDVIEQYSAGHLMDCRI 555
DB 517 YQCELTVDIMPAVYATVIRISIRILKFLVAKRKFKETLRPYDVYKDVIEQYSAGHLMDCRI 576
QY 556 KSLQTRVQVQILGKQITSDKRSR--KITAEHTTDDLSMGRVYKVEQVOVSIESKLD 612
DB 577 KSLQTRVQVQILGKQITSDKRSR--KITAEHTTDDLSMGRVYKVEQVOVSIESKLD 634
QY 613 CLLDYVOOVLRKGSALALASFOJPEPECQTSQVQVDSKDLGSAQNSCLSRSTS 672
DB 635 LILGYSKCLMSGSTA--SLGAVQVPLFPDITSDIHSFVDDHEDIVSAQTLT--ISRSVS 691

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QY 673 ANI 675
DB 692 TMM 694

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RESULT 6
US-09-813-148-6

; Sequence 6, Application US/09813148

; Patent NO. US20020076809A1

; GENERAL INFORMATION:

; APPLICANT: STEINMEYER, Klaus

; APPLICANT: LERCHER, Christian

; APPLICANT: SCHERER, Constanze

; APPLICANT: SEBOHM, Gulschard

; APPLICANT: BUSCH, Andreas E.

; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF

; FILE REFERENCE: 38005-119

; CURRENT APPLICATION NUMBER: US/09/813,148

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: DE 100 13 732.6

; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 696

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-813-148-6

Query Match 42.1%; Score 1991; DB 10; Length 696;

Best Local Similarity 57.8%; Pred. No. 1,7e-135;

Matches 418; Conservative 81; Mismatches 122; Indels 102; Gaps 14;

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QY 25 AAAGGRLSGMKVDSGRGVLLNSAARGDGLLLGTRAAVLGGGGGLRESRRKG 84
DB 2 AEAPRRRLGLGPPGDARAEVAVTAVOSEG-----EAGGGSPR----- 43
QY 85 ARMSLKGKPL-----SYSSQSCRNRVKKRVONYLYNVLERPGMAFIYH 130
DB 44 -RLGLLSPPLPGAPLPDPGSGSGSAGCGRSSAAKRRYRLQNMVYLVLERPGMAFIYH 102
QY 131 AFVFLVFGCLLVSFTIPEHTKLASSCLLLEFVMIVFGLFETIRIRMSGCCRRYG 190
DB 103 VFILVFLVSCVLSVSTIOHQELANECCLLLEFVMIVFGLFETIRIRMSGCCRRYG 162
QY 191 WQGRLEFARKPCVYIDTVILASIAVSAKTQGNIFATSAKLSRLPQLILRVYRMDRGG 250
DB 163 WQGRLEFARKPCVYIDTVILASIAVSAKTQGNIFATSAKLSRLPQLILRVYRMDRGG 222
QY 251 TWKLLGSVYVAHSEKELITAWYIGFLVLIFFSFLVYLVEKDANKESTYADALMWGTTTLT 310
DB 223 TWKLLGSVYVAHSEKELITAWYIGFLVLIFFSFLVYLVEKDANKESTYADALMWGTTTLT 282
QY 311 TIGYGDKPLTWLGLVLSAGFALLGISFPALPAGILGSGFALKVQEHQKHKKRRMPA 370
DB 283 TIGYGDKPLTWLGLVLSAGFALLGISFPALPAGILGSGFALKVQEHQKHKKRRMPA 342
QY 371 ANLIQCVWRSTYAAD-EKSVSIATW----- 393
DB 343 ANLIQCVWRSTYAAD-EKSVSIATW----- 393
QY 394 -----KPKLALHT-----CSPINOKLSFEKERVMAASPRGOSIKSRQ--ASVGR 436
DB 403 PVDPGAPSRYPVAVATCHPFGSTSPCGESSRGMGIDRIMGSSQRTGTGSKQOLAPPTMP 462
QY 437 RSPSTDIATAG-SPTKVOKSMGFNDRTFRPRLRLKSSQPKPVYIDADTLGTDVYDEKG 495
DB 463 TSPSEQVGEATSPTKVOKSMGFNDRTFRPRLRLKSSQPKPVYIDADTLGTDVYDEKG 516
QY 496 CQCDVSVEDLTPPLKTVIRAIRIMKFKVAKRKFKETLRPYDVYKDVIEQYSAGHLMDCRI 555

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QY 201 PFCVIDITVLIASTAVYSAKTQGNIFATLSRLFLQILRMVDRMGRTKLLGSVY 260
DB 167 PFCVIDITVLIASTAVYSAKTQGNIFATLSRLFLQILRMVDRMGRTKLLGSVY 226
QY 261 AHSKELITAMWIGFLVLIFFSFLVLYVEKDANKKESTFADALMWTITLTITGCGDKPPL 320
DB 227 AHSKELITAMWIGFLVLIFFSFLVLYVEKDANKKESTFADALMWTITLTITGCGDKPPL 286
QY 321 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEHOHROKHFEKRRNPANLIQCWRS 380
DB 287 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEHOHROKHFEKRRNPANLIQCWRS 346
QY 381 YAAD-----EKSYSIATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSRTDLHSTMOYERYVTVPYRLPLPLNQLLELNKSKSGLAFFKRPPEPPSP- 405
QY 407 NOKLSFERVMAASPRGOSIKSROASVGD--RRSPSTDTAEGSPTKYOKSMSEFDRTRF 464
DB 406 SOKVSLKDRV-FSSPRGVAAGKGSPOAQYVARSADQSLDSDSPSKVMSFGDRSRA 464
QY 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVEDLTPPLKTVIRAIRIMKFNVA 524
DB 465 RQAFRIKGAASRONSE-EASLPGEIDYDCKSCPEFVETLTPGLKVSIRAVCMFRLVS 523
QY 525 KRKFETLRPYDVADVYEQYSAQHDMLCRIKSLQTRVDQILGKQOITSDKRSREKRTAE 584
DB 524 KRKFETLRPYDVADVYEQYSAQHDMLCRIKSLQTRVDQILGKQOITSDKRSREKRTAE 582
QY 585 HETTDLSMLGRVYVKEKOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPREC-- 642
DB 583 AELPEDESMGRIGLVEKOVLSMEKKDLFLVNIYMO--RMG-----IPPEFTEA 629
QY 643 -----EOTSIDYOSPVDSKDLSSAONSGCLSRSTANISRGLOPILTPNESAQTFVA 655
DB 630 YFGAKEPPAPPYHSPEDSRD---HYDRHGCTIVKIVRSSSTG-----QKNSSAPR-A 678
QY 696 LSPMHQSQTQVPIISOS-----DGSVAANTNTIANTOINPAKPAAPLTIQI----- 741
DB 679 APP-----VOCPESTSMQPSHPROGHGTSVYDGHSLVIRPPRAHERSLAYSAGNR 732
QY 742 -----PP-----PLPAIKHLPRPETLHPNAGLOESISDVTTCL 775
DB 733 ASMEFLROEDTPGCRPEPGLTLDSDTSLISIPSVH---EELERSPSGF--SISQ----- 781
QY 776 VASKENVOYAO 787
DB 782 --SKENIDLANS 791

RESULT 9
; Sequence 23, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauser, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DCS8ADIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

```

```

; LENGTH: 722
; TYPE: PRT
; ORGANISM: MOUSE
US-10-128-870-23
Query Match 37.9% Score 1792.5; DB 9; Length 722;
Best Local Similarity 53.4%; Pred. No. 4,1e-121;
Matches 395; Conservative 76; Mismatches 162; Indels 107; Gaps 19;

QY 21 GAAAAAAGCGRLSGMKDVESEGRVULNSAAAGDGLLLGTRATITGGGGGGLRESR 80
DB 9 GVPYGTSGEKKLKKGFVGLDPGA-----PDSTRGALLIAGSEAPK---RGSVLSKPT 59
QY 81 GKOGARSLGKPLSTYSSOSCRNRVYRRONYLYNLEPRRGAFIYHAFVFLVFGC 140
DB 60 GGAGA-----GKP-----PKRNAPFRKQNLNPLYNLEPRRGAFIYHAFVFLVSC 106
QY 141 LLSVFSTIPEHTKLASSCLLILFVMIIVFGLFETIRIMSAGCCCRYRGWQRLPARK 200
DB 107 LVLSVFSTIPEHTKLASSCLLILFVMIIVFGLFETIRIMSAGCCCRYRGWQRLPARK 166
QY 201 PFCVIDITVLIASTAVYSAKTQGNIFATLSRLFLQILRMVDRMGRTKLLGSVY 260
DB 167 PFCVIDITVLIASTAVYSAKTQGNIFATLSRLFLQILRMVDRMGRTKLLGSVY 226
QY 261 AHSKELITAMWIGFLVLIFFSFLVLYVEKDANKKESTFADALMWTITLTITGCGDKPPL 320
DB 227 AHSKELITAMWIGFLVLIFFSFLVLYVEKDANKKESTFADALMWTITLTITGCGDKPPL 286
QY 321 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEHOHROKHFEKRRNPANLIQCWRS 380
DB 287 TWIGRLLSAGFALLIGISFFALPAGILSGFALKVOEHOHROKHFEKRRNPANLIQCWRS 346
QY 381 YAAD-----EKSYSIATWK--PHLKALHTC-----SPT 406
DB 347 YATNLSRTDLHSTMOYERYVTVPYRLPLPLNQLLELNKSKSGLAFFKRPPEPPSP- 405
QY 407 NOKLSFERVMAASPRGOSIKSROASVGD--RRSPSTDTAEGSPTKYOKSMSEFDRTRF 464
DB 406 SOKVSLKDRV-FSSPRGVAAGKGSPOAQYVARSADQSLDSDSPSKVMSFGDRSRA 464
QY 465 RPSRLKSSOPKPYIDADTALGTDVYDEKGCQCVSVEDLTPPLKTVIRAIRIMKFNVA 524
DB 465 RQAFRIKGAASRONSEALP--GEDIVEDNKSCEVETLTPGLKVSIRAVCMFRLVS 523
QY 525 KRKFETLRPYDVADVYEQYSAQHDMLCRIKSLQTRVDQILGKQOITSDKRSREKRTAE 584
DB 524 KRKFETLRPYDVADVYEQYSAQHDMLCRIKSLQTRVDQILGKQOITSDKRSREKRTAE 582
QY 585 HETTDLSMLGRVYVKEKOVOSIESKLDCLDIYOQVLRKGSASALALASFOIIPREC-- 642
DB 583 TELPEDESMGRIGLVEKOVLSMEKKDLFLVNIYMO--RMG-----IPPEFTEA 629
QY 643 -----EOTSIDYOSPVDSKDLSSAONSGCLSRSTANISRGLOPILTPNESAQTFVA 655
DB 630 YFGAKEPPAPPYHSPEDSRD---HADKHGCTIKIVRSTSS-----TGQR 671
QY 693 FYALSPTMHQSQTQVPIISOS 712
DB 672 NYAAPPAL--PPAQCPSTSS 689

RESULT 10
; Sequence 23, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blannar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauser, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

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? FILE REFERENCE: DC58aCON
? CURRENT APPLICATION NUMBER: US/10/131,685
? CURRENT FILING DATE: 2002-07-23
? PRIOR APPLICATION NUMBER: US 09/105,058
? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: US 60/055,599
? PRIOR FILING DATE: 1997-08-12
? NUMBER OF SEO ID NOS: 28
? SOFTWARE: PatentIn Ver. 2.1
? SEO ID NO 23
? LENGTH: 722
? TYPE: PRF
? ORGANISM: MOUSE
? SS-10-131-685-23

```

Query Match	37.9%	Score 1792.5	DB 9	Length 722
Best Local Similarity	53.4%	Pred. No. 4.1e-121		
Matches 395	Conservative 76	Mismatches 162	Indels 107	Gaps 19

QY	21	GAANAAGGRGLSGMKDVESSGRGRVLLNSAARGDGLLLGTRAAVTGGGGGGLRESRR	80
Db	9	GVTGPTSGEKKLKGVGLDPGA-----PDSRBDGALLINGSSEAPK---RGSVLSKRT	59
QY	81	GKGARMSLLGKPLSTYSSOSCRRNNKTKRRQNTLYNLVLEPRGMATFYAAFFVLLVFGC	140
Db	60	GGAGA-----GKP-----PKRNAEYRKQLNPLNYLNEPRGMATFYAAHYVFLVESC	106
QY	141	LIISVFSTIEPHTKLASSCLLIEFWMLVNGLEFFITRIMWAGCCCRGMGRLEFRK	200
Db	107	LVLSVFSTIEKEKSSGALYITIEVITVYVGVETPKRIMWAGCCCRGMGRLEFRK	166
QY	201	PGCVIDTVLIASIAVYSAKTQGNIFATSAISSLRLFLQILMVRNDRGRGTMKLGSVY	260
Db	167	PGCVIDTVMIASIAVLAAGSQGNVATSAISSLRLFLQILMVRNDRGRGTMKLGSVY	226
QY	261	AHSEKELTAVYIGFLVLIIFSSFLYYLYEKBANKFSTYAADLMNGTTLTITIGYDKTPL	320
Db	227	AHSEKELTAVYIGFLCLILIASFLYLLAEKGNDFHDYADALMGLTTLTITIGYDKYDQ	286
QY	321	TWIGRLISAGFALIGISFALPAGILISGFALTKQEOBHRKHFKRRRNPANLQCVRS	380
Db	287	TWNGRLLAAFTLIGVSFFALPAGILISGFALTKQEOBHRKHFKRRRNPAGLIQSAWRF	346
QY	381	YAAD-----EKSVSIATWK--PILKALHTC-----SPT	406
Db	347	YATNLSTDLHSTWQYERTVTPMYRLPLPLNQLLELLRNLSKSGLTFRKEQPPEPSP	405
QY	407	NOKLSFERERYRMASSPRQGSIKSQAASGD--RSPSPDITAEQSPTYQKWSNRDTRF	464
Db	406	SQKVSLSKDRY-FSSPRGMAAKGSGPOAQTVRRSPSADQSLDDSPSKPKWSGDRSRT	464
QY	465	RPLRLKSSQPKVVIDADTALGTDDVYDEKGCOCDAVEDITPLPKNYIRAIRLMMKFFVA	524
Db	465	ROAFRLKGAASRONSEASLP-GEDYVDNKSCEPEYTEDITPLKASIRAVCVWRFLVS	523
QY	525	KRFKEKTLREYDVKVDIEQYSAGHLDMLCRKISLQTRVDDILGKQITSDKKSREKITAE	584
Db	524	KRFKEKTLREYDVMDVIEQYSAGHLDMLSRKISLQSVADQVGVGPIITD-KDITKGAE	582
QY	585	HEITDLSMLGRVYKYEKQYOSIESKLDLIDYIQVYLKRGASALALASFOIDPEFC--	642
Db	583	TELPEDPSMWGRIGKYEKOVLISMEEKLDLIVSIYTO--RMG-----IIPAETEA	629
QY	643	-----EQSDVQSPVDSKDLGSAQNQSC---LSRSTANISRGQILITPREFSAQT	692
Db	630	YEGAKEPEPAPRYHSPEDSRD---HADKHCCLIKYVSTSS-----TGOR	671
QY	693	FVALSPTMHSQATOVPIQS	712
Db	672	NYAAPPAI--PRAQCPPTS	689

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US-10-128-870-20
? Sequence 20, Application US/10128870
? Patent No. US20020168724A1
?
? GENERAL INFORMATION:
? APPLICANT: Bliana, Michael A.
? APPLICANT: Dworetzky, Steven
? APPLICANT: Gridkoff, Valentin K.
? APPLICANT: Levesque, Paul C.
? APPLICANT: Little, Wayne A.
? APPLICANT: Neubauer, Michael G.
? APPLICANT: Yang, Wen-Pin
? TITLE OF INVENTION: KCMO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
? FILE REFERENCE: DC58adv
? CURRENT APPLICATION NUMBER: US/10/128,870
? CURRENT FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 09/105,058
? PRIOR FILING DATE: June 26, 1998
? PRIOR APPLICATION NUMBER: 60/055,599
? PRIOR FILING DATE: August 12, 1997
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 20:
? LENGTH: 871
? TYPE: prt
? ORGANISM: Homo sapiens
US-10-128-870-20

```

	Score	DB	Length
Query Match	37.8%	1788.5	871
Best Local Similarity	46.8%	pred. No. 1e-120	
Matches 411; Conservative	93	Mismatches 194	Indels 181; Gaps 25

QY	21	GAAMAAAGGRLGSGMKDYESGRVLLNSAAARGDGLLGTAAATLGGGGGLRESRR	80
Db	9	GVPYGPSEGEKRLKXVFGVGLDPGA-----PDSTRDQALLIAGSEAP---RGSILSKPRA	59
QY	81	GKOGARMSLLGGPLSYTSQSCRMMVKRYRQVNIYNVLERPBGMAFIYAPELLVFGC	140
Db	60	GGAGA-----GKP-----PKRNAFYKQLONEFLNVLERPBGMAFIYAIFYFLVESC	106
QY	141	LILVSFTIPEHTKLASSCLLILEFVMIVVFGLEFIIRIWSAGCCCRYRGOGRLREARK	200
Db	107	LVLVSFTIKEYEKSESEGALYILEIVTVIVFGEYEFVRIWMAAGCCCRYRMBRRLKEARK	166
QY	201	PFVVIDFTVLIASIIVSAKTOGNIENFATSLRSLRLOILRMVBMROGSTWMLLSVYV	266
Db	167	PFVVIDHVLVLASIAIVLAAGSOGNENFATSLRSLRLOILRMVBMROGSTWMLLSVYV	226
QY	261	AHSEKELIYATIGELVLIFFSFLVLYLVEKDANKESTYVDALMWGTTILTTIGYDKTPL	320
Db	227	AHSEKELIYATWYIGELVLIFFSFLVLYLVEKGEHDHFTYADALMWGTTILTTIGYDKYPO	286
QY	321	TWLRRLSAGFALLGISFFALPAGILGSGFALKVODQHOHKEKRRNPANLIGCWRS	380
Db	287	TWNRRLAATITLLICVSFFALPAGILGSGFALKVODQHOHKEKRRNPANLIGQSMRF	346
QY	381	YAAD-----EKSYSIATWK-----PHLKALHT-----	4020
Db	347	YATMLSRDLHSTWOYERTVYVPMKSSOTQTYGASRLIPPLQIOLLELNLKSKSLAFR	4067
QY	403	-----CSP-----TNOKLSEKFEVRNAPSPOSIGISKSOAVGDO--RR	437
Db	407	KDPPPEPSPKSGPCRGPLCGCCPCPSSQKVLKDRV--FSSPRGVAAKKGSQAOATYRR	4655
QY	438	SPSTDTIAEGSPYKQKSWSFENDRTFRFRLSLKSSQKPAVIDADATLGTDDVYDEKGCQ	497
Db	466	SPSADOSTLESPPSKYKPSGSEFGDRSARAQAFIKKAASRO--NSEASLEGEIDIVDDKSCP	523
QY	498	CDVSEVEDLTPKLYIVIRALIRLMKKFVARKRKFEETLRPYVQVNYIEOYSAGHIDMLCRKS	555
Db	524	CEFTYEDTLTRELKYSIRAVCYMRFLYSKRKFKFESLRPYVDVYIEOYSAGHIDMLSRKS	563
QY	558	LQTRVODIILGQGLTSDDKSRREKLTAEHETTDLSMLGNVYRVEKQVOSIESKLDCLDLDI	617

Db 584 LOSRVDOIVGPAITD-KDRTKGPAEALPEPDSMGRGLGVEKOVLSMEKKLDELVNI 642
 Qy 618 YOQVLRKGSASALALASFOIPPEFC-----EOTSDYOSPVDSKDLGSAONSGCLS 668
 Db 643 YMO--RNG-----IPTEEAIFGAKEPEPAPYPHSPEDSRE---HYDRGCIY 686
 Qy 669 RSTSANISRGLOFTLPNEFSAOTFYALSPTMHSQATOVPIQS-----DGSVAAT 720
 Db 687 KIVSSSSSTG-----QKNFSAP--AAP-----VOCPPSTSMQOSHPRQHGTSIPV 732
 Qy 721 NTIANQINTAPKPAFTLQI-----PP-----PLPAI 748
 Db 733 GDHGSILVRIPPPAHERSLAYGGGNRASMEFLROEDTPGCRPPETGLRDSITSISIPV 792
 Qy 749 KHLRPELHPNPAQLQESISDVTTCLVASKENVOAOS 787
 Db 793 DH----BELERSFSGF--SISO-----SKENLALNS 818

RESULT 12

US-10-131-685-20
 ; Sequence 20, Application US/10131685
 ; Publication No. US20030044912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blanaer, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubaer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ACON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; PRIOR FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-131-685-20

Query Match 37.8%; Score 1788.5; DB 9; Length 871;

Best Local Similarity 46.8%; Pred. No. 1e-120;

Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

Qy 21 GAAAAAGGRLGSGMKDVEGSRGVLLNSAARGDGLLGTTRATLGGGGGLRESRR 80
 Db 9 GVGPGSEKKLKVGVLDPCA-----PDSTRGALLIASSEAK---RGSILKPR 59
 Qy 81 GKGARMSLCKPLSTYSOSCRNVKRYVONYLVNLEPRGMAFIYHAEVLLVFGC 140
 Db 60 GGAGA-----GKP-----PKRNAFYKLIQNFVLYNLEPRGMAFIYHAEVLLVFGC 106
 Qy 141 LLSVFTIPHTKLIASSCLLLEFVMIVVFCLEFIRIWSAGCCCRVGMQRLFAK 200
 Db 107 LVLSVFSTIKYEKSESGALYLETIVTVFVEYFVRIMAGCCCRVGMQRLFAK 166
 Qy 201 PFCVIDTIVLALIVSAKTOGNIFATSALSLRFLQILIRVMDRGRGTWKLGSVY 260
 Db 167 PFCVIDIVLALIVSAKTOGNIFATSALSLRFLQILIRVMDRGRGTWKLGSVY 226
 Qy 261 AHSKELTAMWYIGFLVLFSSFLVLEKDKNEPSTYADALMWGITLTITIGYDXTPL 320
 Db 227 AHSKELTAMWYIGFLVLFSSFLVLEKDKNEPSTYADALMWGITLTITIGYDXTPL 286
 Qy 321 TWLGLSAGFALLISFALPAGLIGSGFALKVOQHOKHFKRRNPAANLIOCVMRS 380
 Db 287 TWNGKLAAATYTLTIGVSPFALPAGLIGSGFALKVOQHOKHFKRRNPAAGLIGSAMRF 346

Qy 381 YAAD-----EKSVIATWK-----PHIKALHT----- 402
 Db 347 YATNLSRSTDLHSTWQYERVTYVPMYSSQOTQYCASRLIPLNQLLELRLNLSKSGLAER 406
 Qy 403 -----CSP--TWOKLSFKERYVMAAPRSGISRSQASVD--RR 437
 Db 407 KDPPEPSPKSGPCRGELCGCCGRRSSQKVSLLDRV-FSSRGVAAKGGSPQAQTVAR 465
 Qy 438 SPSTDIATGEGSPTVOKMSFNDRTFRPSPRLKSSQPKVYADATLGTDDVDEKGO 497
 Db 466 SPADQSLIEDSPSVKPSKWSFGDSRAQARIKAAARQ--NSASLPGEDIYVDKSP 523
 Qy 498 CDVSEDLTPPLKTVIRAIRMKFHVAKRKEETLPRYDVKDVIQYSGHLDMLCRKS 557
 Db 524 CEVYTEDLTPCLKVIRAVCYMRFLVSKRKFESLPRYDVMDVIBQYSGHLDMLSRKS 583
 Qy 558 LQTRVDQILKGQOTSDSKSREKITAHEETDDLSMLGRVYKVEKQVOSIEKLDCLDI 617
 Db 584 LOSRVDOIVGPAITD-KDRTKGPAEALPEPDSMGRGLGVEKOVLSMEKKLDELVNI 642
 Qy 618 YOQVLRKGSASALALASFOIPPEFC-----EOTSDYOSPVDSKDLGSAONSGCLS 668
 Db 643 YMO--RNG-----IPTEEAIFGAKEPEPAPYPHSPEDSRE---HYDRGCIY 686
 Qy 669 RSTSANISRGLOFTLPNEFSAOTFYALSPTMHSQATOVPIQS-----DGSVAAT 720
 Db 687 KIVSSSSSTG-----QKNFSAP--AAP-----VOCPPSTSMQOSHPRQHGTSIPV 732
 Qy 721 NTIANQINTAPKPAFTLQI-----PP-----PLPAI 748
 Db 733 GDHGSILVRIPPPAHERSLAYGGGNRASMEFLROEDTPGCRPPETGLRDSITSISIPV 792
 Qy 749 KHLRPELHPNPAQLQESISDVTTCLVASKENVOAOS 787
 Db 793 DH----BELERSFSGF--SISO-----SKENLALNS 818

RESULT 13

US-09-813-148-5

; Sequence 5, Application US/09813148
 ; Patent No. US20020076809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHER, Christian
 ; APPLICANT: SCHERER, Constanze
 ; APPLICANT: SEEBOM, Guisard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813,148
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent In version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 872
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-813-148-5

Query Match 34.2%; Score 1620.5; DB 10; Length 872;

Best Local Similarity 42.2%; Pred. No. 1.4e-108;

Matches 396; Conservative 111; Mismatches 258; Indels 173; Gaps 29;

Qy 7 GGEAGGAAGLWVKGAAAAAGGRLGSGMKDVEGSRG-----VLNSAARGDGLL 60
 Db 14 GGGGGGGG-----GGAANPAGGDAAGDEKRGGLAGVDEQYTLAAGADKDGITLL 68
 Qy 61 LGTRAAATLGGGGGLRESRRKOGARMSLCK-PLSTYSOSCRNVKRYVONYLVNVL 119


```

Db      726 RPTVLPITLLDSRVSC-HSQADLGGPYSD-----RISPRQ-----RRSIT 765
Qy      801 MGGELFISVCPMPVPKDLKSLSYONLRSTEEFINLQSGSSGSGSGQDFY- - - - -KWR 856
Db      766 RDSRPPL- - - - -MSVNH- - - - -ELLERSPSGFSISQKDDYVFGINGSSWM 809
Qy      857 ESKLFIIDEEVNGPEETENDTF 877
Db      810 RKRRLAE- - - - -GRTIDPDPF 827

```

RESULT 15
MS-10-131

```

? Sequence 27 Application US/10131665
? Publication No. US20030044912A1
? GENERAL INFORMATION:
? APPLICANT: Blamar, Michael A.
? APPLICANT: Levesque, Paul C.
? APPLICANT: Little, Wayne A.
? APPLICANT: Neubauer, Michael G.
? APPLICANT: Yang, Wen-Pin
? TITLE OF INVENTION: KCMO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
? FILE REFERENCE: DCS6aCON
? CURRENT APPLICATION NUMBER: US/10/131,685
? CURRENT FILING DATE: 2002-07-23
? PRIOR APPLICATION NUMBER: US 09/105,058
? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: US 60/055,599
? PRIOR FILING DATE: 1997-08-12
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 27
? LENGTH: 854
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-131-685-27

```

Query Match	33.9%;	Score 1603.5;	DB 9;	Length 854;
Best Local Similarity	42.7%;	Pred. No. 2.4e-107;		
Matches 393;	Conservative 109;	Mismatches 252;	Indels 167;	Gaps 29

```

QY 472 SSQKPVADADATGALGDVYDEKGGOCQVSDVEDLPEPLTVYIRAIRIMEFNAKRFKET 531
Db 468 SSE-----DAGG----DPAEDRGYGNDDPIEDMPTLKAAIRAVNIIQRLYKFKKEF 519
QY 532 LRPYDVKYIEOYSAGHLDMLCRISLQYRVQDILGKGQITSDDKSR----- 578
Db 520 LRPYDVKYIEOYSAGHLDMLSRIKYLOTRIMIFTPGSPSPKHKSSKGSAFTPPSQ 579
QY 579 ----EKITAHEHTT---DLSMLGRVYKVKOVOSIESKLDLIDYQVLR----- 623
Db 560 SPRNPYPYARPSSTSEIEDQSMGKFEFKVROVODMKKLDPLVDMQHMERLOVOTLEY 639
QY 624 ---KGSASALALASFOIPPECEQTSYSDYSPVDSKDLSSAQNCSLRSSTANSISRLQ 680
Db 640 YPTKTGSS-----PALAEKKKDNKNYS-DLKTICLONYSPTGPEPEPSFH----- 682
QY 661 FILTPNEFSAQTFYALSPTMHOSAOVPIPSOSGSAVAATNTIANOINTAPKRAAPTLLQ 740
Db 683 -QVITDKKSPYGFFAHDP-----VNLPGGSGSGRYOAT-----PPSATTYYE 725
QY 741 IPPPIPAIKHLRPEPHLPNPAIGLOESIDVTTCIVASKENVOVAOSNLTKDRSMKSPD 800
Db 726 RPTVLPILTLBSRSCH-SQADLQGPYSD-----RISPRQ-----RHSIT 765
QY 801 MGGETLLSVYCPMPVKDLKSLSVONLIRSTEELINOLSSGSESSGSGSODFYF---KWR 836
Db 766 RQSDPPLSL-----MSVNH-----EELERSPSGFSISQDRDQYVFENGSGSSMM 809
QY 857 ESKLFIITDEAVGPEETETDTF 877
Db 810 REKRYIAE--GETPDYDTPF 827

```

RESULT

```

US-10-128-870-4
/ Sequence 870, Application US/10128870
/ Patent No. US20020168724A1
/ GENERAL INFORMATION:
/ APPLICANT: Blanan, Michael A.
/ APPLICANT: Dworetzky, Steven
/ APPLICANT: Griboff, Valentin K.
/ APPLICANT: Levesque, Paul C.
/ APPLICANT: Little, Wayne A.
/ APPLICANT: Neubauer, Michael G.
/ APPLICANT: Yang, Wen-Pin
/ TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
/ FILE REFERENCE: DC58ADY
/ CURRENT APPLICATION NUMBER: US/10/128,870
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 09/105,058
/ PRIOR FILING DATE: June 26, 1998
/ PRIOR APPLICATION NUMBER: 60/055,599
/ PRIOR FILING DATE: August 12, 1997
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 300
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: 300 amino acids of human KCNQ2
US-10-128-870-4

```

Query Match	25.5%	score 1207.5;	DB 9;	Length 300;
Best Local Similarity	74.7%	Pred. No. 2.2e-79;		
Matches 227; Conservative	28;	Mismatches 40;	Indels 9;	Gaps 2

```

OY      151 EHTKLASSCLLIEFVMIVPEGGIELIIMWSACCCRRJGMQCHLRFAKPPFCVITYL 210
          | : | : | ||| | ||||| : : ||| : ||||| : ||| : ||||| : ||

```

Db 57 EYKSESGALYIIEIYIVVEGVYRIMAAAGCCCRGRGRGLKFAKRPCEVIDIMVL 116
QY 211 IASIAVSAKTOGNIPTATSLRSLRFLQILRMVMDRGGTWKLLGSVYVAHSEKLITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHSEKLITAM 176
QY 271 YIGFLVLISSFLVYIVVEKDANKFEFTYADALMWGTTITLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLTITIGYDGTPLTWNGRLAAT 236
QY 331 FALIGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296
QY 391 -ATW 393
Db 297 HSTM 300

RESULT 17
US-10-128-870-6
Sequence 6, Application US/10128870
Patent No. US20020168724A1
GENERAL INFORMATION:
APPLICANT: Blanaer, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gridkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC58ADIY
CURRENT APPLICATION NUMBER: US/10/128,870
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 09/105,058
PRIOR FILING DATE: June 26, 1998
PRIOR APPLICATION NUMBER: 60/055,599
PRIOR FILING DATE: August 12, 1997
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 300
TYPE: PRT
ORGANISM: MOUSE
FEATURE:
OTHER INFORMATION: 300 amino acids of murine KCNQ2
US-10-128-870-6

Query Match 25.5%; Score 1207.5; DB 9; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.2e-79;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;
QY 91 GKPLSYTSOSCRNRVYRRQNYLYNLEPRGMATFYHAFFLVFGLISVFSSTIP 150
Db 5 GKPLSYTSOSCRNRVYRRQNYLYNLEPRGMATFYHAFFLVFGLISVFSSTIP 150
QY 151 EHTKLASSCLLIEFWIVVVEGLEFIRIMASAGCCCRGRGRGLKFAKRPCEVIDITVL 210
Db 57 EYKSESGALYIIEIYIVVEGVYRIMAAAGCCCRGRGRGLKFAKRPCEVIDITVL 116
QY 211 IASIAVSAKTOGNIPTATSLRSLRFLQILRMVMDRGGTWKLLGSVYVAHSEKLITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHSEKLITAM 176
QY 271 YIGFLVLISSFLVYIVVEKDANKFEFTYADALMWGTTITLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLTITIGYDGTPLTWNGRLAAT 236
QY 331 FALIGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296

QY 391 -ATW 393
Db 297 HSTM 300

RESULT 18
US-10-131-685-4
Sequence 4, Application US/10131685
Publication No. US20030044912A1
GENERAL INFORMATION:
APPLICANT: Blanaer, Michael A.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC58ACON
CURRENT APPLICATION NUMBER: US/10/131,685
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 09/105,058
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 300
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 300 amino acids of human KCNQ2
US-10-131-685-4

Query Match 25.5%; Score 1207.5; DB 9; Length 300;
Best Local Similarity 74.7%; Pred. No. 2.2e-79;
Matches 227; Conservative 28; Mismatches 40; Indels 9; Gaps 2;
QY 91 GKPLSYTSOSCRNRVYRRQNYLYNLEPRGMATFYHAFFLVFGLISVFSSTIP 150
Db 5 GKPLSYTSOSCRNRVYRRQNYLYNLEPRGMATFYHAFFLVFGLISVFSSTIP 150
QY 151 EHTKLASSCLLIEFWIVVVEGLEFIRIMASAGCCCRGRGRGLKFAKRPCEVIDITVL 210
Db 57 EYKSESGALYIIEIYIVVEGVYRIMAAAGCCCRGRGRGLKFAKRPCEVIDIMVL 116
QY 211 IASIAVSAKTOGNIPTATSLRSLRFLQILRMVMDRGGTWKLLGSVYVAHSEKLITAM 270
Db 117 IASIAVLAAGSGGNVATSLRSLRFLQILRMIMDRGGTWKLLGSVYVAHSEKLITAM 176
QY 271 YIGFLVLISSFLVYIVVEKDANKFEFTYADALMWGTTITLTIGYDGTPLTWLGRLLSAG 330
Db 177 YIGFLCLILASFLVYLAKEKENDHFDYADALMWGLITLTITIGYDGTPLTWNGRLAAT 236
QY 331 FALIGISFPALPAGILGSGFALKVQEOHROKHFEKRRNPANLIQCWRSTAADEKSVSI 390
Db 237 FTLIGVSFPALPAGILGSGFALKVQEOHROKHFEKRRNPAGLIQSAMRFYATNLSRTDL 296
QY 391 -ATW 393
Db 297 HSTM 300

RESULT 19
US-10-131-685-6
Sequence 6, Application US/10131685
Publication No. US20030044912A1
GENERAL INFORMATION:
APPLICANT: Blanaer, Michael A.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

```

: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 676
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-138-316-2

Query Match      23.3%: Score 1102; DB 9; Length 676;
Best Local Similarity 41.9%: Pred. No. 2.9e-71;
Matches 250; Conservative 105; Mismatches 164; Indels 78; Gaps 16

Dy      98  SSOSCRNRVKKR-RVQNZLVNVLEPRGM-AFIYHAFVLLVFGCLILSVSTIBERTKI 155
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      92  SYSTRRPVLARTNVQGRVYVLEFRPTMKCVYHFAVFLVYVCLLISVSTIQYAL 151
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      156  ASSCLLLEFMYIVFGLFIIRMSAGCCCRYRGWGRLFRAPKRFPCVIDTIVLIASIA 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      152  ATGLFWMEIVLVVEFGTEYVVRILMSACGRSKYVGLMGRLRFRARKPDISIIDLIIVASWV 211
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      216  VYSKATQGNIFATSAKRLRFLQILRMVRMDRGSTWMLGSSVYVAHSELITAMVIGL 275
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      212  VLVGSSGQVYFATSAIRGIRFLQILRMVDRQGGTWRLLGSVVEIHRELITTYIGFL 271
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      276  VLISSFLVYVYVEDA-----NKESTYADALMWTITLTITGYGDKPTLVWGLRLSAG 330
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      272  GLIISSTFVYLAEKDAYVESGRVEFGSTADALIMGVAIVYTTITGYGDKVQYTWGKTIA 331
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      331  FALGISFFALPAGILGSGFALKVQEOHROKHFEKRRNPANLIOCWMSYADAEKSVSI 390
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      332  FSVPAISFFALPAGILGSGFALKVQOKOROKHFNQIPAAASLIQTAMRCYAAENPDS- 390
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      391  ATKVPHLAL--HT-CPTNOKLSFKERVNRMASRSGSIKRQASVGRBSPSDITAE 446
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      391  -TWKIYIKKAPRSHLLSPSPK--KKSVAVKKKKFKDKONGVTPGKMLTVPHITD 446
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      447  GSPFKVQKWS--FNDRTRRPSRLKSSOPKPYADIDALGTDDVYDEKGCQCQSVYE 503
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      447  PPERRLDHFESVDGIDSSVKRKSPTL-LEYSMPH-----FMRTNSFAD----LDLEE 494
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      504  DLTPPL-----KTVIRAIRIMKPHVAKRKETLRPYDVAKDIVEQYSAGHIDMLC 553
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      495  TLLRPITRHISLREHNRATIKIVIRMQYFAVAKKFOAKRPKPDVDRVIDEQYSQHILNAY 554
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      554  RIKSLQTRVNDOLKGCQ--TISDKSKREKITAHEHETDLSMLGRVYKVEKQVQSIESL 611
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      555  RIKELQRLDOSIGRPSLEISVSEKSKOR-----GSNTIGARLNRVEDKVTQLDQRL 606
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      612  DCLIDIYQYV-----RKQSA-----SALASFOIPE 641
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy      607  ALITDMHLQLSLHGGSTPGSGGPREGGAHITQPGCGSGSVDPPELLFPLSNILPYTE 663
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-09-840-125-2
: Sequence 2, Application US/09840125
: Patent No. US20020061524A1
: GENERAL INFORMATION:
: APPLICANT: SPLAWSKI, IGOR
: APPLICANT: Keating, Mark T.
: TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQ71 AND
: FILE REFERENCE: 2323-155
: CURRENT FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/634,920
: PRIOR FILING DATE: 2000-08-09
: PRIOR APPLICATION NUMBER: 60/147,488
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 676
: TYPE: PRT

```


US-10-128-870-18

Query Match 22.9%; Score 1085; DB 9; Length 310;

Best Local Similarity 65.3%; Pred. No. 1.6e-70; Mismatches 55; Indels 18; Gaps 3;

Matches 203; Conservative 35; Mismatches 55; Indels 18; Gaps 3;

QY 90 LGRPLSYSSQSCRNVKRYRVONYLVNLEPRGNAPFIYHAFVLLVFGCLLSVFSTI 149

Db 4 LSRPVK-----RNNAKYRRIQTLIYDLEPRGNALVHALVFLVGLLILAVLTTF 56

QY 150 PEHTKLASSCLLIEFVMIYVFGLEFIIRWSAGCCCRRYGMOGRLPFRKPCVIDTIV 209

Db 57 KEYETVSGDWMLLETFALFIFGAEFALRIWAGCCCRKGMGRGLKFAKPLCMDIIFV 116

QY 210 LIASIAVYSAKTQGNIFATSRLRFLQILRMVDRRGCTWKLGSVYVAHSELITA 269

Db 117 LIASIPVAVNGQNVLTLS-LRSLRFLQILRMVDRRGCTWKLGSALICAHSELITA 175

QY 270 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTITLTIGYDKTP 319

Db 176 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTITLTIGYDKTP 235

QY 320 LTVLGRLLSAGFALGIFSFALPAGILSGFALKVQDQKHQKHEKRRNPANLIQCVNR 379

Db 236 KTWEGRLIAATFSLIGVSFFALPAGILSGFALKVQDQKHQKHEKRRNPANLIQCVNR 295

QY 380 SYADEKSVSI 390

Db 296 YYATNPRIIDL 306

RESULT 26

US-10-131-685-18

Sequence 18, Application US/10131685

Publication No. US20030044912A1

GENERAL INFORMATION:

APPLICANT: Blahar, Michael A.

APPLICANT: Levesque, Paul C.

APPLICANT: Little, Wayne A.

APPLICANT: Neubaer, Michael G.

APPLICANT: Yang, Men-Pin

TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: DCS8ACON

CURRENT APPLICATION NUMBER: US/10/131,685

PRIORITY FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 09/105,058

PRIOR FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 18

LENGTH: 310

TYPE: PR

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: 310 amino acids of human KCNQ3

US-10-131-685-18

Query Match 22.9%; Score 1085; DB 9; Length 310;

Best Local Similarity 65.3%; Pred. No. 1.6e-70; Mismatches 55; Indels 18; Gaps 3;

Matches 203; Conservative 35; Mismatches 55; Indels 18; Gaps 3;

QY 90 LGRPLSYSSQSCRNVKRYRVONYLVNLEPRGNAPFIYHAFVLLVFGCLLSVFSTI 149

Db 4 LSRPVK-----RNNAKYRRIQTLIYDLEPRGNALVHALVFLVGLLILAVLTTF 56

QY 150 PEHTKLASSCLLIEFVMIYVFGLEFIIRWSAGCCCRRYGMOGRLPFRKPCVIDTIV 209

Db 57 KEYETVSGDWMLLETFALFIFGAEFALRIWAGCCCRKGMGRGLKFAKPLCMDIIFV 116

QY 210 LIASIAVYSAKTQGNIFATSRLRFLQILRMVDRRGCTWKLGSVYVAHSELITA 269

Db 117 LIASIPVAVNGQNVLTLS-LRSLRFLQILRMVDRRGCTWKLGSALICAHSELITA 175

QY 270 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTITLTIGYDKTP 319

Db 176 WYIGFLVLISSFLVLYVEKDA-----NKEFSTYADALMWGTTITLTIGYDKTP 235

QY 320 LTVLGRLLSAGFALGIFSFALPAGILSGFALKVQDQKHQKHEKRRNPANLIQCVNR 379

Db 236 KTWEGRLIAATFSLIGVSFFALPAGILSGFALKVQDQKHQKHEKRRNPANLIQCVNR 295

QY 380 SYADEKSVSI 390

Db 296 YYATNPRIIDL 306

RESULT 27

US-10-138-316-114

Sequence 114, Application US/10138316

Publication No. US20030054380A1

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, Igor

TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

FILE REFERENCE: 2323-162

CURRENT APPLICATION NUMBER: US/10/138,316

PRIORITY FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/444,295

PRIOR FILING DATE: 1999-11-22

PRIOR APPLICATION NUMBER: 09/135,020

PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: 08/921,068

PRIOR FILING DATE: 1997-08-29

PRIOR APPLICATION NUMBER: 08/739,383

PRIOR FILING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 60/019,014

PRIOR FILING DATE: 1995-12-22

PRIOR APPLICATION NUMBER: 60/094,477

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 114

LENGTH: 570

TYPE: PR

ORGANISM: Homo sapiens

US-10-138-316-114

Query Match 22.9%; Score 1081.5; DB 9; Length 570;

Best Local Similarity 41.6%; Pred. No. 7e-70; Mismatches 105; Indels 77; Gaps 15;

Matches 242; Conservative 105; Mismatches 105; Indels 77; Gaps 15;

QY 112 QNYLVNLEPRGNAPFIYHAFVLLVFGCLLSVFSTIPHTKLASSCLLIEFVMIYV 170

Db 1 QGRVYNLEPRGNAPFIYHAFVLLVFGCLLSVFSTIPHTKLASSCLLIEFVMIYV 60

QY 171 FGLFTIRIMSAGCCCRRYGMOGRLPFRKPCVIDTIVLIASIAVYSAKTQGNIFATSA 230

Db 61 FGLFTIRIMSAGCCCRRYGMOGRLPFRKPCVIDTIVLIASIAVYSAKTQGNIFATSA 120

QY 231 LSLRFLQILRMVDRRGCTWKLGSVYVAHSELITAMWYIGFLVLISSFLVLYVEKDA 290

Db 121 LSLRFLQILRMVDRRGCTWKLGSVYVAHSELITAMWYIGFLVLISSFLVLYVEKDA 180

QY 291 A-----NKEFSTYADALMWGTTITLTIGYDKTPPLTWLGRLLSAGFALPAGI 345

Db 181 AVNESGRVFEFGSYADALMWGTTITLTIGYDKTPPLTWLGRLLSAGFALPAGI 240

QY 346 LGSFALKVQDQKHQKHEKRRNPANLIQCVNRSYADEKSVSIATWPKPLKAL--HT 402

Db 241 LGSFALKVQDQKHQKHEKRRNPANLIQCVNRSYADEKSVSIATWPKPLKAL--HT 298


```

CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325.891
FILING DATE: 23-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/009.492
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/464.340
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36.134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-325-891-13

Query Match
Best Local Similarity 23.38; Score 250; DB 9; Length 539;
Matches 91; Conservative 77; Mismatches 151; Indels 72; Gaps 13:

115 LYNVLEPRGMA---FIYHAFVLVFGCLISVSTIPEHTK-----ASSCLILE 164
173 LMDLEKPPSSVAKLAIISIMFYIUSTALSI-NLPELOSIDFEGOSTDNPOLAVE 231
165 FMYIVFGLEPIIRISAGCCCRYRGWGRLEPRARKPCVYIDTVILASIAVSAKTQGN 224
232 AVCIAMFTMEYLRLFLSSP-----KKW-----KFKGPLNIDLALIPYV-----T 274
225 IFATSLRSL-----RFLQILRMVMDRGRGKWLIGSVYVHAKEL-ITAW 270
275 ILTESNKKVLOPQNVRRVYQIFRIMRLIKLKLARHSTGLQSLGFLRRSYNELGLIL 334
271 YIGFLVLIFSSFLVYLVKDA-NKEFSTYADALMWGTTITLTIGYDGTPLTWLGRLLSA 329
335 FLAMGIMIFSS-LVFEAEKDEDDTKFKSTIPASFWMAITITTYIGYDITKTLIGKIVGG 393
330 GFAILGISFPALPAGILSGFALKVOEQRKHFEKRRNPAANLIQCVMSYADEKSVS 389
394 LCCINGLVIALPIPIIVNFSFYEQRKROEKAIKRR-----DALERAKNGS 442
390 IATWMPHKAHLTSCPTNOKLSFEKERVN-----ASPRGOSIKRSQASVGRRSPSTIDITA 445
443 IVS-----MNNKDAFARSIDEMADIVVEKENGENMKAKDKVQDNHLSPNKWKWT 489
446 EGSPTKVOKSMFNDRTFRPSLRKSSQPK 476
490 KRLTSETSSSKSFETKEOGSPKARSSSPQ 520

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RESULT 38
 US-10-121-746-10
 ; Sequence 10, Application US/10121746

```

Publication NO. US20030036648A1
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OR INVENTION: No. US20030036648A1 Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/10/121.746
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US/09/336.643A
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/038,262
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 646
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(646)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-121-746-10

Query Match
Best Local Similarity 22.58; Score 245; DB 9; Length 646;
Matches 107; Conservative 81; Mismatches 170; Indels 118; Gaps 22:

115 LYNVLEPR---GMAFIYAFVFLVFGCLISVSTIP-----EHTKL 155
172 LWRAFENPHTSTALVFIYVTFGIYV--SVIANVETIICRGARSRSREQPCGERPQ 229
156 ASSCLILEFMAIVHGLEPIIRISAGCCCRYRGWGRLEPRARKPCVYIDTVILIA-SI 214
230 AFEC---MDTACVLIPTGELRLFAA-----PSRCRFLRSVMSLIDVALIPYI 277
215 AVYSAKTQGNIPATSLRSLRFLQILRMVMDRGRGKWLIGSVYVHAKELITAMTYGF 274
278 GLIVK---NDVSGAFVTLRPFVRIRFESHSOGLRILGYTLKSCASEL-----GF 328
275 L-----VLIFSSFLVYLVKDA-NKEFSTYADALMWGTTITLTIGYDGTPLTWLGRLL 326
329 LIFSITMAIIPATVMEY-AEKGNTKNTFTSIIPAAMWYITVITLTIGYDGMVSTIAGKI 387
327 LSAGFALLGISFPALPAGILSGFALKVOEQRKHFEKRRNPAANLIQCVMSYADEKSVS 389
368 FGSISLGSVIVIALPVPVIVNFS---RIYHONQADKRR--AQQKVRILARILAKSGT 442
377 -----VMSYADEKSVS-----ATWKPPLKALH-----TCSPTNOKLSYKER 415
443 TNAFLQYONGNGLEDSGSEBQALCYRNASAEQOHHLHLCLEKTCHEFTDELTFESEA 502
416 VMAFSPROOSIKRSQAS---VG-----DRRSPSTIDITAGSPTKVOKSMFNDRTFR 463
503 LGAVSPGGRTSRSTSVSQPVGPGSLLSSCCPRRAKRAIRILANSYASVSRG-SMGELDM 561
464 FRPSLRKSQPKPYIDTALAGTDVDYDEKQCQD-----VSEDTLPPLKT 511
562 LAGLRSHAPQSRSLNKP-----HDSIDLNDGSRDFAVAILISIP--TPANT 608

```

RESULT 39
 US-10-121-746-4
 ; Sequence 4, Application US/10121746
 ; Publication No. US20030036648A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 60/038,26
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 601
; TYPE: PRT
; ORGANISM: H. sapiens
; US-10-121-746-4

Query Match
Best local Similarity 23.8%; Score 243; DB 9; Length 601;
Matches 82; Conservative 65; Mismatches 109; Indels 88; Gaps 13;

QY 65 AATLGGGGGGLRESRKGAGMSLLGKPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
DB 159 AAGLGDPD-----GKSG-----RWRRLQPRMVALFEDPYS 188
QY 123 -RGMAFYHAHVELLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
DB 189 SRAARFIASFSLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 248
QY 163 LEFMYIVFGLFEFIRMSAGCCCRYRGMRLEFARKPCVDTIVLI-----ASTAVV 217
DB 249 VEGCVVVFTEFELVRYVES-----PNKLEFIKNLINTIDFVALIPFYLEVGLSGL 299
QY 218 SAKTQGNIFATSAIARSLRFLQILRMVMDRGGTAKLGSVVAHSEK-LITAMYIGFLV 276
DB 300 SSKAKAVL--GFLRVRFVRLIRFKLTRHFVGLVGLTLASTNEFLLITLITLALGV 357
QY 277 LIFSEFLVLYVER-----DANKFESTYADALMWGTITLTITGSGDKPTLWLGRL 326
DB 358 LIFAT-MIYAEKRVGAQPDNDPSASEHTQFNIPIGFWMAVVTTLTGDMYPTWISGML 416
QY 327 LSAGFALLGISFFALPAGIL-----GSGFALKVOEQ-----HROKH 362
DB 417 VGALCALAGVLTITAMPVPVIVNFGMYISLAMAKOKLPRKRKH 460

RESULT 40
US-10-024-623-11
; Sequence 11, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; FILE REFERENCE: USE THEREOF
; FILE REFERENCE: MNI-21ACP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-623-11

Query Match
Best local Similarity 23.8%; Score 243; DB 9; Length 638;
Matches 82; Conservative 65; Mismatches 109; Indels 88; Gaps 13;

QY 65 AATLGGGGGGLRESRKGAGMSLLGKPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
DB 195 AAGLGDPD-----GKSG-----RWRRLQPRMVALFEDPYS 224
QY 123 -RGMAFYHAHVELLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
DB 225 SRAARFIASFSLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 284
QY 163 LEFMYIVFGLFEFIRMSAGCCCRYRGMRLEFARKPCVDTIVLI-----ASTAVV 217
DB 285 VEGCVVVFTEFELVRYVES-----PNKLEFIKNLINTIDFVALIPFYLEVGLSGL 335
QY 218 SAKTQGNIFATSAIARSLRFLQILRMVMDRGGTAKLGSVVAHSEK-LITAMYIGFLV 276
DB 336 SSKAKAVL--GFLRVRFVRLIRFKLTRHFVGLVGLTLASTNEFLLITLITLALGV 393
QY 277 LIFSEFLVLYVER-----DANKFESTYADALMWGTITLTITGSGDKPTLWLGRL 326
DB 394 LIFAT-MIYAEKRVGAQPDNDPSASEHTQFNIPIGFWMAVVTTLTGDMYPTWISGML 452
QY 327 LSAGFALLGISFFALPAGIL-----GSGFALKVOEQ-----HROKH 362
DB 453 VGALCALAGVLTITAMPVPVIVNFGMYISLAMAKOKLPRKRKH 496

RESULT 41
US-10-024-623-33
; Sequence 33, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
; TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
; FILE REFERENCE: USE THEREOF
; FILE REFERENCE: MNI-21ACP
; CURRENT APPLICATION NUMBER: US/10/024,623
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-024-623-33

Query Match
Best local Similarity 24.1%; Score 242; DB 9; Length 638;
Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY 70 GGGGGLRESRKGAGMSL-----LGPPLSTSSQSCRNVKRYRVONYLVNLERP-- 122
DB 176 GGGPDDDEDGK--RLGIEDAGLGDPD-----KSGWRKRLQPRMVALFEDPYS 224
QY 123 -RGMAFYHAHVELLVFG-----CL-----ILSVFTIPBHTKLASSCLLI 162
DB 225 SRAARFIASFSLFFILVSTTFCTHEAFNIVKNKTEPVINGTSVYLQYEIETDPALTY 284

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RESULT 44
US-10-062-879-4
; Sequence 4, Application US/10062879
; Patent No. US20020127649A1
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dicks, Daniel W.
; APPLICANT: Chang Ling, Hui-ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; FILE REFERENCE: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-10-062-879-4

```

Query Match 4.8%; Score 229; DB 12; Length 636;

Best Local Similarity 19.7%; Pred. No. 3.3e-08;

Matches 111; Conservative 97; Mismatches 211; Indels 144; Gaps 21;

```

QY 98 SSOSCRNRYKRYRQNYLVNLEPRGMATFYHAFVFLVFG-----CLILSYSTP-- 150
DB 155 NNOSEMPISLSPFQ---MKRAEENPHTSL--ALFYVYTGFFIAVSIVTINVEVPCG 208
QY 151 -----EHTKLASSCLLLEFVMTVVEGLEFIIRIMSAGCCCRGMRGRLRPEAR 199
DB 209 TVPGSKELPCGGRYSVAFC---LDTACVMTFVEYILRLFAA-----PERYRIR 256
QY 200 KPFVIDIVILA-SIAVYSAKTOGNIPTALSRLRFLDILNRVDRRGTKKLIGSV 258
DB 257 SVMSTIDVVALIPYITGLVMTNED--VSGAFVTLRVFVFRIFKFSRHSOGRLIGYT 313
QY 259 VYANSKELITAMYGIFL-----VLIFSSFLVYLVKDKANKKESTYADALMGTITLT 311
DB 314 LKSCASEL-----GFLFSLMTAITTIFATVMTYAKGSSAKFTSIPASWTYIVWT 367
QY 312 IGYDKPTLTMIGRLISAGFALLGISFALPACILISGFALKVOEHRKHFEKRR--- 367
DB 368 LGYGDVMEKTIAGKIFGSIKSLGYLVIALPVEVIVSNFS---RIYHONQBRADRRRAOK 424
QY 368 -----NPAANLIQCWRSYAADEKSVSIATMKPHLALH 401
DB 425 ARLARIRVAKTGSSNAYLHSKRNGLINELELGTPEEEMGKTTSL-IESQHHL--LH 481
QY 402 TCSEPTNOLSEKERYRMAISPRGOSIKRSQASVDRSRSPSTD---ITAESPTVKOKSWS 457
DB 482 CLEKTTNHEFIDEQWF---EQNCMESSMONTPTSRPSLSSHPLGLTTCCSRKSKTTH 537
QY 458 FNDSTRPRLSKSQKRPVADATLCTDQVYDEKCCOCDDVSDVLPPLKTVIRAIR 517
DB 538 LPNSN--LPATRLRMQELSTHIO---GSEQ-----PSLTSRSLSLN 575
QY 518 IMKPHVAKRKFEKTLRPYDVKVIQYSGHDMLCRIKSIOIRVDOILKGGTSSKKS 577
DB 576 L-----KADDGLRPN-----CKTSQITTAIISIPPPALTPGES 610
QY 578 REKITAHEHTTDDLMLGRVVKV 600
DB 611 RPPASPGPMNTNIPSTISNVK 633

```

RESULT 45
US-10-121-746-18
; Sequence 18, Application US/10121746
; Publication No. US20030036648A1

```

; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 477
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-18

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Query Match 4.7%; Score 224; DB 9; Length 477;

Best Local Similarity 23.7%; Pred. No. 5.1e-08;

Matches 84; Conservative 65; Mismatches 139; Indels 66; Gaps 12;

```

QY 91 GKPLSTSSOSCRNRYKRYRQNYLVNLEPRGMATFYHAFVFLVFGCLILSYSTP 150
DB 163 GQPLG-----NFRQL-WLALDNGYSYLSR-----VFSLISLVYMGSIITMCLNSLP 210
QY 151 EHTKLASS-----CLILEFWIIVVPGLEFIIRIMSAGCCCRGMRGRLRPEAR 203
DB 211 DQIPDSQNGEDPREIIEHGIAMFTFELVARFAVA-----PDFLKFKNALN 261
QY 204 VDT-----VLIASIAVSAKTOGNIPTALSRLRFLDILNRVDRRGTKKLIG 256
DB 262 LIDMLSVPTITLVNLYVVESTTLNGLVAVQ--LRMKIRFIILAKRSTGLRSIG 319
QY 257 SVYANSKELITAMYGIFLVIFL-----SLVYLVKDKANKKESTYADALMGTITLT 310
DB 320 ATEKYSYK-----GCLLLYLVSGISIFSVAYTTEKEBNEGATIPACWMAVTSMT 373
QY 311 TIGYDKPTLTMIGRLISAGFALLGISFALPACILISGFALKVOEHRKHFEKRRPA 370
DB 374 TWGYGVVPGTTAGKLTASACILAGILVVPITLIFNKFS-----HYRRKQL 423
QY 371 ANLIQ-CVWRSYAADEKSVSIATMKPHLALHTCPTN-----OKLSFKRVR 417
DB 424 ESAMRSCDGDGDKKEVPSVNLRYIAHKVSLMASLNMSSSELSLNDSLR 477

```

RESULT 46
US-10-121-746-8
; Sequence 8, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

Query Match	4.7%	Score 223	DB 9	Length 500
Best Local Similarity	28.2%	Pred. No. 6.4e-08		
Matches	80	Conservative 47	Mismatches 107	Indels 50
				Gaps 10
QY	111	VONTLYVNERP-----RGMAFLYHAFVPLLVGCLLSVFSTIPERTKLASSCLLIE	164	
	: : : :	: : : :	: :	: :
Db	192	VROKLMLEKPGSSTARIFGVISIIIVVSIINMALMSA-----EKSMIDLQLELEIE	246	
QY	165	FNAIIVGFLFEIIRIWSAGCCCRFYRQMGRLRFARPCPCVIDIYLINSIAVYSAKTQGN	224	
	: : : :	: : : :	: :	: :
Db	247	YVCIISWFTGGEVLR-----LCVR-----DKREFKPNIIIDLAIEFFYITLLVVESTSG	297	

Query Match	4.4%	Score 206.5;	DB 9;	Length 494;
Best Local Similarity	23.28%	Pred. No. 9.8e-07;		
Matches 64; Conservative	57;	Mismatches 122;	Indels 33;	Gaps 6

```

QY      107 KYRQVNNLYLVVLRPRGM--AFIHA107VELFLPFCGLIIVSTP117-----EHRK127LAS 157
      160 RMRRQCQCMVKFLKRPSSPCAPVA160VELSP170LLIVSSVYMCMDIT180DELQYLDNAEGNRV190EH 219
QY      158 SC168LIIEFVNVVGLF178IIIRISAGCC188RRKGMGRLEFAK198PCVID208ITYI218-----A 212
      220 P230LENVETACI240GMT250LELLR260FS-----PNK270LHFA280LSEMN290IVLV300LIP310YVSL 270
Db

```

QY 213 STAVSAKTOGINFATSLRFLQILRMVRMDRGSTWKLGSVYVAHSEKEL-ITAWY 271
Db 271 TLTHLGARMELTNVOQAVQALRIRKIRIKFLARHSSGLQTLTYALKRSFKELGLIMY 330
QY 272 IGEVLVLFSSFLVYLVKEDANKREFTYADALMWGTTTLTIGYDKTPPLTWIGRLLSAGF 331
Db 331 LAVGIFVFESALGYTMQSHPELTFKNIPQSEFWMAITMTVGYGDYIPKTLTKLMAAIS 390
QY 332 ALLGTSFFLPAGILGSGFALKVQEOHQHKEKRR 367
Db 391 FLGCVIAIALPPIHPINNFEV-----RYNKKOR 417

RESULT 49

US-10-143-002-4
; Sequence 4, Application US/10143002
; Patent No. US20020132775A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
; CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/143,002
; FILING DATE: 13-May-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,493
; FILING DATE: <unknown>
; APPLICATION NUMBER: US/08/468,533
; FILING DATE: 6 JUNE 1995
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: <unknown>
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-143-002-4
Query Match 4.4%; Score 206.5; DB 12; Length 494;
Best Local Similarity 23.2%; Pred. No. 9.8e-07;
Matches 64; Conservative 57; Mismatches 122; Indels 33; Gaps 6;
QY 107 KYRVRQNTLYNVLEPRGW--AFIYHAFVFLVFGCLISVFSTIP-----EHTKLAS 157
Db 160 RWRRCQKCVWFKLEPRSSCPRVVAELSLFLIVSVVCMPTIPLQYLDAGNRYEH 219
QY 158 SCLILEFVMIVFGLFPIIRIWSGCCCRYRGMOGRAPRRPFCVITIVLI-----A 212

Db 220 PLENEVEACIGMETLELYLRFS-----PNKLRALSFMNIWDLVLAIPFVSL 270
QY 213 STAVSAKTOGINFATSLRFLQILRMVRMDRGSTWKLGSVYVAHSEKEL-ITAWY 271
Db 271 TLTHLGARMELTNVOQAVQALRIRKIRIKFLARHSSGLQTLTYALKRSFKELGLIMY 330
QY 272 IGEVLVLFSSFLVYLVKEDANKREFTYADALMWGTTTLTIGYDKTPPLTWIGRLLSAGF 331
Db 331 LAVGIFVFESALGYTMQSHPELTFKNIPQSEFWMAITMTVGYGDYIPKTLTKLMAAIS 390
QY 332 ALLGTSFFLPAGILGSGFALKVQEOHQHKEKRR 367
Db 391 FLGCVIAIALPPIHPINNFEV-----RYNKKOR 417

RESULT 50

US-09-875-321-13
; Sequence 13, Application US/09875321
; Publication No. US20030049724A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM
; CHANNEL FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-061001
; CURRENT APPLICATION NUMBER: US/09/875,321
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 532
; TYPE: PRP
; ORGANISM: Mus musculus
US-09-875-321-13

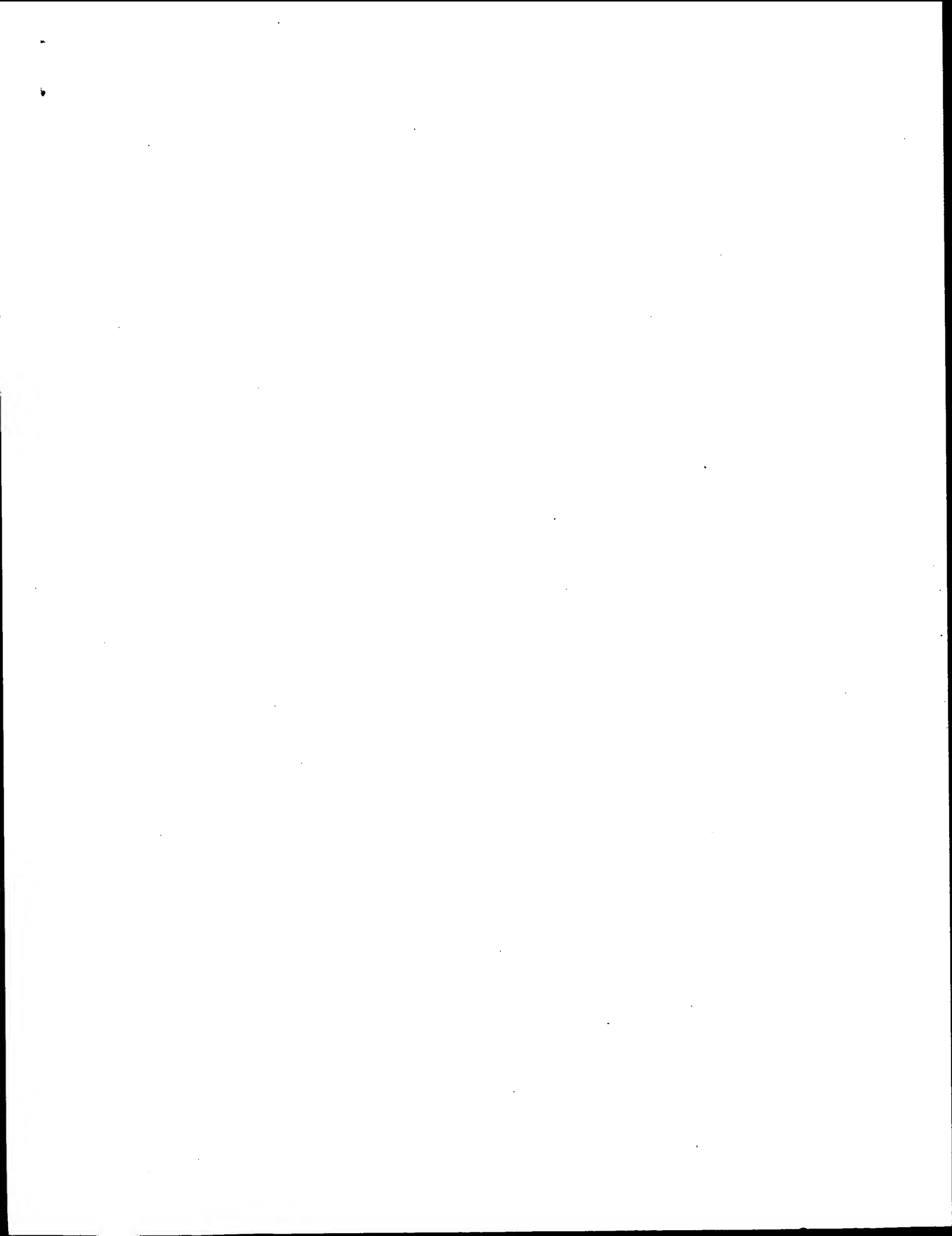
Query Match 4.4%; Score 206.5; DB 9; Length 532;
Best Local Similarity 21.3%; Pred. No. 1.1e-06;
Matches 101; Conservative 74; Mismatches 148; Indels 151; Gaps 19;

QY 3 RHHAGEEGAGLWYK---SGAAAAAGGRLGSKMKDVSGRGVLLNSAARGDGL 59
Db 52 RHRRTPDWGG-CGVGATRPPTGRGCRHGAIVPAALRCE---RLVLNVAGLFE--- 103
QY 60 LGTRATLTGGGGGGLRESRRKOGARM--SLGKPLSYTSQSCRNVKRYRQNYLYN 117
Db 104 ---TRATLG-----RFPDTLGDV-----RRSRFDGARAEYFF 136
QY 118 VLERPRGMAFIYH-----AFVFLVYF-----GCLT----- 142
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'Fri Jun 20 09:08:48 2003

Search completed: June 14, 2003, 17:54:01
Job time : 63 secs

us-09-825-147-2.rapb



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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 10:10:41 ; Search time 376 Seconds
(without alignments)
10818.373 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772

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Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues 2085038

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2772	100.0	3111	10	US-09-825-147-3
3	2723.8	98.3	3074	10	US-09-813-148-1
4	2662.8	96.0	2667	10	US-09-810-796-3
5	2635.4	95.1	3071	10	US-09-810-796-1
6	2635.2	94.7	2694	10	US-09-810-796-2
7	478.8	17.3	2169	9	US-10-128-870-22
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9	465.4	16.8	896	9	US-10-128-870-1
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13	428.4	15.5	3287	9	US-10-131-685-19
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25	267.6	9.6	2821	10	US-09-880-107-3358	Sequence 3358, Ap
26	130.4	4.7	416	10	US-09-960-352-13343	Sequence 13343, A
27	104.2	3.8	429	10	US-09-783-590-4509	Sequence 4509, Ap
28	90.2	3.3	477	9	US-09-918-995-27819	Sequence 27819, A
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31	58.4	2.1	1844	9	US-10-016-647-3	Sequence 3, Appl
32	58.4	2.1	2561	9	US-09-976-740-48	Sequence 48, Appl
33	58.4	2.1	2561	12	US-10-023-529-48	Sequence 48, Appl
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66	48.6	1.8	249487	9	US-10-026-188-3	Sequence 3, Appl
67	48	1.7	2288	9	US-09-989-920-103	Sequence 103, App
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78	46.6	1.7	3454	9	US-10-171-581-312	Sequence 312, App
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Sequence 87, App
Sequence 251, App
Sequence 1043, A
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Sequence 1, Appl
Sequence 3800, Ap
Sequence 3802, Ap
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Sequence 6, Appl
Sequence 574, App
Sequence 574, App

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? APPLICANT: Zambrowicz, Brian
? APPLICANT: Sands, Arthur T.
? TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
? TITLE OF INVENTION: Polynucleotides Encoding the Same
? FILE REFERENCE: LEX-0160-USA
? CURRENT APPLICATION NUMBER: US/09/835.147
? CURRENT FILING DATE: 2001-04-03
? PRIOR APPLICATION NUMBER: US 60/194,255
? PRIOR FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 2772
? TYPE: DNA
? ORGANISM: homo sapiens
US-09-825-147-1

Query Match          100.0%; Score 2772; DB 10; Length 2772;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1
US-09-825-147-1
Sequence 1, Application US/09825147
Patent No. US20020042505A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Kleke, James Alvin
APPLICANT: Turner, C. Alexander J.
APPLICANT: Neffs, Michael C.
APPLICANT: Friedrich, Glenn

```

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RESULT 2
 US-09-825-147-3
 ; Sequence 3, Application us/09825147
 ; Patent No. US20020042505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, YI
 ; APPLICANT: Kieke, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.

QY	1861	GTCCCTTGAGAAAGGCTTGCTCGAGCCCTGCTTGGCTTATTCAGATCCAGCTTTT	1920
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QY	2641	CCGAGAGCTGCACAGAGAACTGCTTTTGATCAACACTCTCTAAGAGACTGGAAAGTCAAG	2700
Db	2700	CCGAGAGCTGCACAGAGAACTGCTTTTGATCAACACTCTCTAAGAGACTGGAAAGTCAAG	2759
QY	2701	TCATCTCAGAGCAATTTGTAAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTC	2760
Db	2760	TCATCTCAGAGCAATTTGTAAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTC	2819
QY	2761	AAACTGAAATTA 2772	
Db	2820	AAACTGAAATTA 2831	
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US-09-813-148-1			
: Sequence 1, Application US/09813148			
: Patent No. US20020076809A1			
: GENERAL INFORMATION:			
: APPLICANT: STEINMEYER, Klaus			
: APPLICANT: LERCHHE, Christian			
: APPLICANT: SCHERER, Christian			

```

1  APPLICANT: SEEBOHM, Guiscard
2  APPLICANT: BUSCH, Andreas E.
3  TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF
4  TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
5  FILE REFERENCE: 38005-119
6  CURRENT APPLICATION NUMBER: US/09/813,148
7  CURRENT FILING DATE: 2001-03-21
8  PRIOR APPLICATION NUMBER: DE 100 13 732.6
9  PRIOR FILING DATE: 2000-03-21
10 PRIOR APPLICATION NUMBER: US 60/194,041
11 PRIOR FILING DATE: 2000-04-03
12 NUMBER OF SEQ ID NOS: 6
13 SOFTWARE: PatentIn version 3.0
14 SEQ ID NO 1
15     LENGTH: 3074
16     TYPE: DNA
17 ORGANISM: Homo sapiens
18 US-09-813-148-1

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	Query Match	98.3%;	Score 2723.8;	DB 10;	Length 3074;	
	Best Local Similarity	98.8%;	Pred. No. 0;			
	Matches 2765;	Conservative	0;	Mismatches	7;	Indels 27; Gaps 1.
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OY	61	GGCGCAGCGCGCGCGCGCGCGCGCGCGCTTGGGCACGCGCATAGAAGATTGGAG	120			
Db	170	GGCCACAGCGCGCGCGCGCGCGCGCGCTTGGGCACGCGCATAGAAGATTGGAG	229			
OY	121	TGCGGCGCGGGCAGGGGTCTGTAACTCGGCACGCGCACGGGGGAGCGGCTGTACTG	180			
Db	230	TGCGGCGCGGGCAGGGGTCTGTAACTCGGCACGCGCACGGGGGAGCGGCTGTACTG	289			
OY	181	CTGGGCAACCCCGCGGCGCCACGCTCGGTGGCGCGCGCGGTGGCTTAGAGSAGACCCGCG	240			
Db	290	CTGGGCAACCCCGCGGCGCCACGCTTGTTGGCGCGCGCGGTGGCTTAGAGSAGACCCGCG	349			
OY	241	GGCAAAGACGGGGGCCCGGATAGCCTGCTGGSGAAGCCGCTCTTAACAAGATTAGCCAG	300			
Db	350	GGCAAAGCAGGGGGGCCCGGATAGCCTGCTGGSGAAGCCCGCTCTTAACAAGATTAGCCAG	409			
OY	301	AGCGCGCGGCGCAACGTCATACTAACCGGGGGTGACAACTACGTCACGTCGTGGAG	360			
Db	410	AGCGCGCGGCGCAACGTCATACTAACCGGGGGTGACAACTACGTCATACTGTGGAG	469			
OY	361	AGACCCCGCGGCTGAGCGCTTCATCATCACACCTTTCGTTTTCTCTGTCTTGGTTGC	420			
Db	470	AGACCCCGCGGCTGAGCGCTTCATCATCACACCTTTCGTTTTCTCTGTCTTGGTTGC	529			
OY	421	TTGATTTTGTGAGTTTCTTACCAATCCGTAGACACACAAAATTGGCTCAAGTTGCCTC	480			
Db	530	TTGATTTTGTGAGTTTCTTACCAATCCGTAGACACACAAAATTGGCTCAAGTTGCCTC	589			
OY	481	TTGATCTCGAGGTTCTGATCATTTGCTCTTGGTTTGGAGTTATCATTCGAATCTGG	540			
Db	590	TTGATCTCGAGGTTCTGATCATTTGCTCTTGGTTTGGAGTTATCATTCGAATCTGG	649			
OY	541	TCTCGGGGTCTGTGTGCAATATAGAGATAGGCAAGAAAGCTAGGTTGCTGGAAG	600			
Db	650	TCTCGGGGTCTGTGTGCAATATAGAGATAGGCAAGAAAGCTAGGTTGCTGGAAG	709			
OY	601	CCCCTCTCTGTTATAGATACCATATGTTCTTATCCGCTTCAATAGACAGTTGTTCTGCAAAA	660			
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Db	770	ACTCAGGGTAATATTTTGGCCACGCTCAGACCTCAGAAAGTCTCCGTTCTTCCAAGATCTCTC	829			
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Db	830	CGATGTGGCCATGAGCAGCAAGGGGAGGCACCTTGGAANAATTA	CTGGTTACGTGGTTAT	889
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Db	890	GCCTCACAGCAAGGAATTAATCACAGCTTGCTACATAGAAATTTT	GGTTATTTTTCG	949
QY	841	TCCTTCCCTGTGCTATGCTGGTGAAGAAAGTGGCAATAAAGAGT	TTTCTACATATGCAGAT	900
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QY	1201	CACACCTGGACGCCCTTACCAC-----TCAGAACTAAGT		1233
Db	1310	CACACCTGGACGCCCTTACCACAAAGAAAGAGGAAAGCAT	CAAGCAAGTTCAGAAACCTAAGT	1366
QY	1234	TTTAAAGAGAGAGTGGCCATGGCTAGCCGCCAGAGCAAGT	TTTAAAGAGCCGCAAGCC	1293
Db	1370	TTTAAAGAGAGAGTGGCCATGGCTAGCCGCCAGAGCAAGT	TTTAAAGAGCCGCAAGCC	1429
QY	1294	TCAGTAGGTGACAGAGGTCCCAAGACCCGACATCACAG	CCGAGGGCAGTCCCAACCA	1353
Db	1430	TCAGTAGGTGACAGAGGTCCCAAGACCCGACATCACAG	CCGAGGGCAGTCCCAACCA	1489
QY	1354	GTCACAGAAAGCTGGAGCTTTAAAGCAGCAACCCGCTT	CCGGCCCTTGCCTGCGCTCA	1413
Db	1490	GTCACAGAAAGCTGGAGCTTTAAAGCAGCAACCCGCTT	CCGGCCCTTGCCTGCGCTCA	1549
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Db	1550	AGTTCTCAGCAAAAACCAAGTATGATGCTGACACAGCC	CTTGGCACTGATGATGTAT	1609
QY	1474	GATGAAGAAAGATGCCAGTGTGATGTATCAGTGGAAG	AGACCTCACCCACCACTTAAACT	1533
Db	1610	GATGAAGAAAGATGCCAGTGTGATGTATCAGTGGAAG	AGACCTCACCCACCACTTAAACT	1669
QY	1534	GTCATTCGAGCTATCAGAAATTTATGAAATTTTCA	TGTGGCAAAACGGAAGTTTAAAGAAACA	1593
Db	1670	GTCATTCGAGCTATCAGAAATTTATGAAATTTTCA	TGTGGCAAAACGGAAGTTTAAAGAAACA	1729
QY	1594	TTACGTCACATATATGTAAGAAAGATGTCATTTGA	CAATATTTGCTGGTCACTGCGAATG	1653
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Db	2210	ACTTTCTACGCGCTTTAGCCCTACTATGCAAGTCAAGCAACAGAGTGGCAATTAGTCA	2269
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RESULT 4
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US2020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.

[illegible]

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 2701 TAA 2703

RESULT 6
 US-09-810-796-2
 ; Sequence 2, Application US/09810796
 ; Patent No. US20020102677A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jega, Timothy James
 ; APPLICANT: IChagen, Inc.
 ; TITLE OF INVENTION: KCM05, a No. US20020102677A1 Potassium Channel
 ; FILE REFERENCE: 018512-00501005
 ; CURRENT APPLICATION NUMBER: US/09/810,796
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: US 60/190,954
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 2694

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human outwardly-rectifying, voltage-gated
 OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
 NAME/KEY: CDS
 LOCATION: (1)..(2694)
 OTHER INFORMATION: KCM05-1
 US-09-810-796-2

Query Match 94.7%; Score 2625.2; DB 10; Length 2694;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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 Db 961 GAAACAACCCGCAAGAAACCTTTGAGAAAAAGAGAAACCAAGCTGCCAATTCAG 1020
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 Db 1021 TGTGTTGGGCTGTTAGAGAGTGAAGAAATCTGTTTCATTCGAACTGGAAGCA 1080
 QY 1186 CACTTGAAGGCTTTCGACACCTGCGAGCTTACCA 1220
 Db 1081 CACTTGAAGGCTTTCGACACCTGCGAGCTTACCAAGAAAGAAAGGGAAGCATCAAGC 1140
 QY 1221 --TCAAGAGTAAATTTAAAGAGCGAGTGGCTAGCCCGAGGCGCAGATTT 1278
 Db 1141 AGTCAAGAGTAAATTTAAAGAGCGAGTGGCTAGCCCGAGGCGCAGATTT 1200
 QY 1279 AAGAGCGAGAACCTGAGTAGGTGACAGAGGTCCCAAGACCGAGATCAGACCGAG 1338
 Db 1201 AAGAGCGAGAACCTGAGTAGGTGACAGAGGTCCCAAGACCGAGATCAGACCGAG 1260
 QY 1339 GGCAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCCGCGCC 1398
 Db 1261 GGCAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCCGCGCC 1320
 QY 1399 TCGCTCGGCTCAAAAGTCTCAGCGAAACCAAGTATGATGCTGACACAGCCTTGGC 1458
 Db 1321 TCGCTCGGCTCAAAAGTCTCAGCGAAACCAAGTATGATGCTGACACAGCCTTGGC 1380
 QY 1459 ACTGATGATATATGATGAGAAAGAGATGCCAGTGTATGATGCTGGAAGACCTCAC 1518
 Db 1381 ACTGATGATATATGATGAGAAAGAGATGCCAGTGTATGATGCTGGAAGACCTCAC 1440
 QY 1519 CCACCACTTAAACGTGATTCGAGTATGAGAAATTTATGAAATTTGATGCAAAACGG 1578
 Db 1441 CCACCACTTAAACGTGATTCGAGTATGAGAAATTTATGAAATTTGATGCAAAACGG 1500
 QY 1579 AAGTTAAGAAACATTTAGCTCCATATGATGATTAAGATGTCATTTGAACAATTTCTGT 1638
 Db 1501 AAGTTAAGAAACATTTAGCTCCATATGATGATTAAGATGTCATTTGAACAATTTCTGT 1560
 QY 1639 GGTATCTGAGCAATGTTGTGTAGATTAAGAAACCTTCAACACGCTGATCAAAATCTT 1698
 Db 1561 GGTATCTGAGCAATGTTGTGTAGATTAAGAAACCTTCAACACGCTGATCAAAATCTT 1620
 QY 1699 GGAAGAGGCAATCAGATCAGATTAAGAAAGCGAGAGAAATTAACAGCAGACATGAG 1758
 Db 1621 GGAAGAGGCAATCAGATCAGATTAAGAAAGCGAGAGAAATTAACAGCAGACATGAG 1680
 QY 1759 ACCACAGAGATTCAGATATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1818
 Db 1681 ACCACAGAGATTCAGATATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
 QY 1819 ATGAATCCCAAGCTGAGCTGCTCTAGACATTCATCAACAGGCTCTCGAAAGGCTCT 1878
 Db 1741 ATGAATCCCAAGCTGAGCTGCTCTAGACATTCATCAACAGGCTCTCGAAAGGCTCT 1800
 QY 1879 GCGTCAGCCCTCGCTTGGCTTATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1938
 Db 1801 GCGTCAGCCCTCGCTTGGCTTATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
 QY 1939 GACTATCAAGCCCTGCTGATAGCAAGATCTTTCGGGCTTCGCGCAAAACAGTGGCTGC 1998
 Db 1861 GACTATCAAGCCCTGCTGATAGCAAGATCTTTCGGGCTTCGCGCAAAACAGTGGCTGC 1920
 QY 1999 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTCGAGTTCTATCTGAGCGCAAT 2058
 Db 1921 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTCGAGTTCTATCTGAGCGCAAT 1980


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Db 1027 GCCTGAGATTTATGCTACTTAACCTCTCAGCAGCCAGCTGCACTCCACGCGAGTAC 1086
OY 1189 T----- 1189
Db 1087 TAGAGCGGAGCACTCACTGTCCCATGTACAGACTCATCCACTCTGACACGCTGGAG 1146
OY 1190 -----TGAGGCGCTTGACACACTGC 1209
Db 1147 CTGCTGAGAAATCTCAAGACCAATCTGACTCAGCTTCAGGAGAGCCAGCCAGCAGAG 1206
OY 1210 ACCCCATCAATCAGAAAGCTAAGTTTAAGAGGAG---TCCGATGGCTAGCCCCAG 1266
Db 1207 CCATCACCAGTACAGAGGTGAGTGAAGATGTGCTTCTCTCAGCCCGAGGAGCAG 1266
OY 1267 GCGCAGAGATTTAAGAGCCGACCAAGCTCAGTAGGTGACAGAGTCCCAAGCAGCAG 1326
Db 1267 GCTGCCAAGGAAAGGGGTCTCCCGAGCCAGAGCGGTCCGGGTCCCGCAGTGGAT 1326
OY 1327 ATCAGAGCCGAGGAGGCTCCACCAAAAGTGCAGAGAGCTGAGCTTCAGCAGCAG 1386
Db 1327 CAGAGTCTTGATGTACAGCCCGACAGAGGTGCCCAAGAGCTTGAGCTTGGTGACG 1386
OY 1387 GCTTCCGCGCCCTCGCTGGCCCTCAAAAGTCTCAGCCCAAAACAGATGATGATCTGAC 1446
Db 1387 CGCAGACGCGCAGGCTTCCGATCAGAGGAGTGTGCTGATCCGCGAGATTCAGAAAGCAG 1446
OY 1447 ACAGCCCTTGAGCAGTGTATGTATGTATGATGATAAAAGAGATCCAGTGTATCAGTG 1506
Db 1447 C---TCCCTGGGAGAGACATGTAGAGGACACAGAGAGCTTAAGTGGAGTTTGTACT 1503
OY 1507 GAAGACCTTACCCCACTTAAAGTGTGATGAGCTTACAGATTAAGAAATTTGAT 1566
Db 1504 GAGAGTCTTACCCCTGCGCTCAAAAGTGTAGATCAGAGCTGTGTGTATGCTGGTCTTG 1563
OY 1567 GTTGAAAGAGAGTAAAGATTAAGAAATTAAGTATGATGATGATGATGATGATGATGAT 1626
Db 1564 GATATTAACCGAAAGTTCAGAAAGAGAGTGTGCGCCATATGATGATGATGATGATGATGAT 1623
OY 1627 CAATATCTGCTGTGCTGATGTGACATGTTGTGAAATTAAGAGCTTCAAAAGAGTGT 1686
Db 1624 CAGTACTCGCTGTGACATGTGATGTGTGTCCCGATCAAGAGCTGCAATGCCAGATG 1683
OY 1687 GATCAAAATCTTGGAAGAGGCAATCAGATCAGATTAAGAGAGCCGAGAGAAATTAACA 1746
Db 1684 GACCGATTGTGGGGGGGGCCCAACAAATTAACGATTAAGA---TCCGACCAAAAGGCCCA 1740
OY 1747 GCAGAAATGAGAGCCAGACAGATCTCAGTATGCTGTGGGTGGTCAAGGTGAAATAA 1806
Db 1741 GCGGAAAGAGAGCTGCCCAAGAGCCAGCATATGAGGAGGCTTGGGAGAGTGAGAAA 1800
OY 1807 CAGGTACAGTCAATGAAATCCAGCTGAGCTGCTACTAGACATCTATCAACAG 1860
Db 1801 CAGGCTGTGTCATGGAAGAAAGCTGCACTTCTTGTGTGAGCATCTATACACAG 1854

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RESULT 8

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US-10-131-685-22
; Sequence 22, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blamner, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DCS8aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599

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; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: MOUSE
US-10-131-685-22

Query Match      17.3%  Score 478.8  DB 9:  Length 2169;
Best Local Similarity 57.1%  Pred. No. 1.8e-138;
Matches 1024; Conservative 0; Mismatches 662; Indels 108; Gaps 4;

OY 169 GGCCTGTACTGTGGGACCCGCGGCGATGAGCTGTGGGAGGCGGAGTGGCTGAGG 228
Db 67 GCGTTCGTGGGCGTGGAGACCCGCGCGCCGCGGATGAGCTGAGAGCGGCGGCTGATC 126
OY 229 GAGAGCCGCGGGGCGAGCAGGAGGCGCGGATGAGCTGTGGGAAAGCCGCTCTTAC 288
Db 127 GCGGCTCCGAGGCGCCCGCAAGCGCGCAGCGTTTGAGCAAGCCGCGAGCGGCGG 186
OY 289 ACAGATGCGCAGACTGCGGCGGCGAGCTCAAGTACAGTCCGCGGCTGAGAACTCTGAT 348
Db 187 GGAAGCGGGAAGCCCGGAGCGCAGAGCTTCTACCGAGCTGCAAGATTTCTCTAC 246
OY 349 AACGTGCTGAGAGACCCGCGGCGTGGCGTTCATCTACAGCTTTCCTTCTCTCT 408
Db 247 AAGGTGTAGAGGCGGCGCGCGGCGGCGGCTTCATCTACAGCTTTCCTTCTCT 306
OY 409 GTCTTTGGTGTCTGATTTTGTCAAGTCTTCTACAGCTTCTGAGCAGCAAAATTTGCC 468
Db 307 GTCTTCTCCGCTTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
OY 469 TCAAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
Db 367 GAGGCGGCGCTTCAATCTTGAATCTGATGATGATGATGATGATGATGATGATGATGAT 426
OY 529 ATTGGAATGCTGTGCGGCGTGTGCTGTGATGATGATGATGATGATGATGATGATGATGAT 588
Db 427 GTGAGGATCTGGGCTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 486
OY 589 TTTGCTGAAAGCCCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
Db 487 TTTGCGAGGAGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
OY 649 GTTTCGCAAAATCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Db 547 CTGGCTGTGCTTCCAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
OY 709 CTACAGATCTCTCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
Db 607 TTGCAAAATCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
OY 769 TCAAGTGTATGCTCAGAGCAAGAAATTAATCAGAGCTGTGTATGATGATGATGATGAT 828
Db 667 TCGTGTGTACAGCTCAGAGCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 726
OY 829 CTATTTTCTTGTCTTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 888
Db 727 CTATCTGCGCTTCTATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
OY 889 ACATATGAGATGCTCTGCTGTGGGCAACAATTAATTAATTAATTAATTAATTAATTAATTAAT 948
Db 787 ACCTAGCAGATGACACTGTGTGGGTGTGATACCTGAGAGACATTTGCTACGCGGAGC 846
OY 949 AAAATCCCTTAATCTGCTGGGAGAGATGCTTCTGAGAGCTTGTGACCTCTTGTGAT 1008
Db 847 AAGTACCTCAGAGCTGGAAGGAGGAGCTGTGAGAGGAGCTTATTAACCTATGATGATGAT 906
OY 1009 TCTTCTTGTGACCTTCTGCGGATCTTGTGCTGAGGTTTGTGATTAAGTACAGAA 1068
Db 907 TCGTCTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966

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QY 178 CTGCTGGGACCCCGGCGCACGCTCGGTGGCGGCGGTGGCTGAGGAGAGCGG 237
 Db 103 GTACACTGTGGGCTGGGGCCCGGAGCCGACAAAGAGGAGACCTGCTGGAGGGCGG 162
 QY 238 CGGGGCGAGGAGGCGGCGGATGAGCTGCTGGGAGCGCTCTTTACAGAGTAGC 297
 Db 163 GGGCGCGAGGAGCGGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 222
 QY 298 CAGAGCTGCGC-----GGCGCAAGCTGAGTACCGGCGGCGGTGGAGAGTACCTGAC 348
 Db 223 CTGAGCGCGCGGACGTCAGAGAGAAACAGCGCAAGTACCGGCGATCCAACTTTGATCTAC 282
 QY 349 AACGTGCTGAGAGACCCCGGCGGCTGGGCGGTTCATCTACACAGCTTTCTTTCTCT 408
 Db 283 GACGCGCTGGAGAGACCGGCGGCGGTGGCGGCTGCTTACACAGCGGTGCTGCTGAT 342
 QY 409 GTCTTTGGTTCGCTGATTTTGTCACTGTTTCTACCATCTCGAGACACAAATGTCG 468
 Db 343 GTCTGGGGGTCTGATTTGCTGCTGCTGACACATTCAGAGAGTATGAGACTGCTG 402
 QY 469 TCAAGTTCCTCTGATCTGAGTTCGATGATGTTGCTGCTGCTGCTGCTGCTGCTG 528
 Db 403 GGAAGACTGGCTTCTGTTACTGAGACATTTGCTATTTCTATCTTTGAGCGAGTTGCT 462
 QY 529 ATTGCAATCTGCTGCGGGGTTGCTGTTGCTGATATAGAGATGGCAAGAGACTGAG 588
 Db 463 TTGAGATCTGGGCTGCTGATGTTGCTGCGGATCAAAAGGCTGGCGGGCGGAGTGA 522
 QY 589 TTTTGTGGAAGGCTCTGCTGATATAGATACATTTGCTTATGCTTCAATAGACAT 648
 Db 523 TTTTGTGGAAGGCTCTGCTGATATAGATACATTTGCTTATGCTTCAATAGACAT 582
 QY 649 GTTTCGCAAAACTCAGGGTATATTTTGCACGCTGACGCTGACGAGAGTCTGCTG 708
 Db 583 GTTGTCTGGGAAACCAAGGATGTTCTGGCACCT---CCCTCGAAGCTTGGCTG 639
 QY 709 CTACAGATCTCCGATGTTGCGCATGAGACCGAAGGAGGAGGACTTGAATTAAGT 768
 Db 640 CTGCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
 QY 769 TCAGTGTATGCTCAGAGAGAAATATATCAAGCTGCTGCTGCTGCTGCTGCTGCT 828
 Db 700 TCAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
 QY 829 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873
 Db 760 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
 QY 874 -----AATAAGATTCTTCAATATGAGATGCTCTGCTGCTGCTGCTGCTGCT 918
 Db 820 CAAGAGAGAGATGAAAGAGAGATTTGAGACCTATGAGATGCTGCTGCTGCTGCTG 879
 QY 919 ATTACATGACACTATGCTATGAGAGACAAACTCCCACTGCTGCTGCTGCTGCTGCT 978
 Db 880 ATACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
 QY 979 CTCTTGCAGGCTTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
 Db 940 ATTGCGCGCCACTTTTCTTAAATGCGCTCTCTTTTCTGCTGCTGCTGCTGCTGCT 999
 QY 1039 GGTCTAGGTTTTCATTTAAAGTACAAAGACACCGCCGCAAAACTTTGAGAAAAGA 1098
 Db 1000 GGGTCTGGGGTGGCGCTCAAGGTGACAGAGACACCGCTGCAAGACTTTGAGAAAAG 1059
 QY 1099 AGGAACCCAGCTGCAACTCATTTGCTGTTGGGTGTTGGGAGTGCAGCTGATGAGAAA 1158
 Db 1060 AGGAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
 QY 1159 TCTGTTTCAATG-----CAACTGGAAGCCACACTTGAAGGCTTGCACACTGCT 1209
 Db 1120 AGGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179

QY 1210 AGCCCTACCAATCAGAGCTAGTTTAAAGAGCGGAGCGCATGGCTAGCCCCAGGGC 1269
 Db 1180 AGGAAGACAGCTGAGAGGAGCATCCAGCCAAAGAGCTGGCTTTGGATCGGGTTGCG 1239
 QY 1270 CAGAGTATTAAGAGCCGCAAGAGCTCAGTAGGTGACAGAGAGGTCCCAAGCAGCATC 1329
 Db 1240 CTCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299
 QY 1330 ACAGCCGAGGAGCTCCACCAAGTGCAGAGAGCTGAGCTTCAAGCAGCAACCGC 1389
 Db 1300 GCCATTAAGAAAGTCTCTTAAAGAAACCAAGCCCTGTTGGCTTAAACAATTAAGAG 1359
 QY 1390 TTCGGCCCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1449
 Db 1360 TTCGGCAGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
 QY 1450 GCCCTGGCAGCTGATGATATGATGATGATGATGATGATGATGATGATGATGATG 1509
 Db 1420 ACAGGTAGCCCATAGG-----GGAAGACAGGGGCTATGGGAATGACTTCCCATGCA 1473
 QY 1510 GACCTACCCCGACCTTAAAGCTGCTATGAGCTATGAGATATGAAATTTATGTT 1569
 Db 1474 GACATGATCCCGACCTGAGAGCGGCGCATCGAGCCGCTGACAAATTTCAATTTCTG 1533
 QY 1570 GCAAAAGGAGTATTAAGAAACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1629
 Db 1534 TATTAATAAATAATTAAGAGAGCTTTGAGGCTTATGAGTATGAGAGATGATGATG 1593
 QY 1630 TATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1689
 Db 1594 TATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1653
 QY 1690 CAATTTCT 1697
 Db 1654 ATGATTTT 1661

RESULT 12
 US-10-131-685-26
 ; Sequence 26, Application US/10131685
 ; PUBLICATION NO. US20030044912A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blau, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ACON
 ; CURRENT APPLICATION NUMBER: US/10/131,685
 ; PRIOR FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 26
 ; LENGTH: 2565
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-131-685-26

Query Match 15.5%; Score 428.8; DB 9; Length 2565;
 Best Local Similarity 56.8%; Pred. No. 9.2e-123;
 Matches 924; Conservative 0; Mismatches 647; Indels 57; Gaps 5;
 QY 118 GAGTCGGCGGGGCGAGGAGTCTGATCTGATCTGCAAGCCGCAAGGCGGAGCTGCTA 177
 Db 43 GCGGCGGCGGCGGCGGAGGAGCGGAAAGTGGGCTGGCGCGCGGCGGAGCTGAGACAA 102
 QY 178 CTGCTGGGACCCCGGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237


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QY 289 ACGAGTACCGAGAGTGGCGGCAACGTCAAGTACCGGGGCTGAGAACTACTGTAC 348
Db 247 GGGCCCGGGAGAGCCCGCCCAAGCGCAACGGCTTCTACCGCAAGCTGAGAAATTTCCCTAC 306
QY 349 AAGTGGGAGAGAGAGCCCGGGGCTGGGCTGATCTACACAGCTTTCTTCTCT 408
Db 307 AAGCTGGAGAGAGAGCCCGGGGCTGGGCTGATCTACACAGCTTTCTTCTCT 366
QY 409 GTCTTGGTGTGATTTGTCTGATGTTTCTACATCCCTGAGCACAATAATGGCC 468
Db 367 GTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 426
QY 469 TCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 528
Db 427 GAGGGGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486
QY 529 ATTGGAATCTGCTGCGGGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db 487 GTGGGATCTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
QY 589 TTTCTGGAAGCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
Db 547 TTTCTGGAAGCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606
QY 649 GTTCTGCAAAACTCAGGTAATATTTTGGCAGCTCTGCACTGAGAGTCTCCGTTT 708
Db 607 CTGGCCCGGCGCTCCAGGCGCAACGCTTTGGCAGCTCTGCGCTCGGAGCTCGGCTT 666
QY 709 CTACAGATCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db 667 CTGAGATCTGCGGATGATCCGATGAGCGGCGGAGGAGCCTGAGAGCTGCTGCTG 726
QY 769 TCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
Db 727 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
QY 829 CTATATTTTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 888
Db 787 CTATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
QY 889 ACATATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 948
Db 847 ACCTACCGGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 949 AAAACTCCCTTAATCTGCTGGAAGATTTCTGAGCTTTGCACTCTCTGCTCAT 1008
Db 907 AAGTACCCCGAGAGCTGGAAGGCAAGCTCTCTGCGGCACTTCACTCTCTCTCT 966
QY 1009 TCTTTCTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1068
Db 967 TCTTTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1026
QY 1069 CAACACCGGAGAGAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
Db 1027 CAGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
QY 1129 GTTGGCGGTAGTTACGC 1145
Db 1087 GCCTGAGATTTTACGC 1103

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; FILE REFERENCE: DC58aCON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-685-19

Query Match      15.5%: Score 428.4; DB 9; Length 3287;
Best Local Similarity 64.8%: Pred. No. 1.5e-122;
Matches 633; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

QY 169 GACCTGTACTGCTGGGACCCCGGCGGCAAGCTCGGTGGGCGGCGGTGCTGAG 228
Db 127 GGCTTCTGGGCTGTGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGATC 186
QY 229 GAGAGCCGCGGCGGCAAGCAGGGGCGCGGATGAGCTGTGGGAGCCGCTCTTAC 288
Db 187 GCGGCTCTCGAGGCGCCCAAGCGGCGGAGATCTCAGCAAACTCGGCGGCGGCGGCG 246
QY 289 ACGAGTACGAGAGCTCGGCGGCAAGCTCAGTACGCGGCGGTGCAAACTACTGTC 348
Db 247 GCGCGCGGGAAGCCCGCCCAAGCGGCGGCAAGCTCTTCAAGCGGCGGCGGCGGCG 306
QY 349 AAGTGTGTGAGAGAGCCCGGCGGCGGCGGCTTCACTACAGCTTTGCTTCTGCT 408
Db 307 AAGTGTGTGAGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 366
QY 409 GTCTTGTGCTGTGATTTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
Db 367 GTTCTCTGCGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426
QY 469 TCAAGTGTCTCTGATCTCTGATCTGTGATGTGTGTGTGTGTGTGTGTGTGTGT 528
Db 427 GAGGGGCGCTCTCAATCTGGAATCGTACTATCGTGTGTGTGTGTGTGTGTGTGTGT 486
QY 529 ATTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Db 487 GTGCGATCTGTGGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
QY 589 TTTGCTGGAAGCCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
Db 547 TTTGCGCGGAAACGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606
QY 649 GTTCTGCAAAACTCAGGTAATATTTTGGCAGCTCTGCACTGAGAGTCTCCGTTT 708
Db 607 CTGGCGCGGCTCTCCAGGGCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
QY 709 CTGAGATCTCTCGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768
Db 667 CTGAGATCTCTCGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
QY 769 TCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
Db 727 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 786
QY 829 CTATATTTTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 888
Db 787 CTATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
QY 889 ACATATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 948
Db 847 ACCTACCGGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 949 AAAACTCCCTTAATCTGCTGGAAGATTTCTGAGCTTTGCACTCTCTGCTCAT 1008

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Db 907 AAGTACCCCAAGACCTGGAAGGAGGAGGCTCTTGGGCAACCTTACCCCTCATCGGTGTC 966
QY 1009 TCTTTCTTTCGACCTTCCTGCGGCGATCTTGGCTCAGGTTTGGATTAAAGTCAAGAA 1068
Db 967 TCTTCTTTCGCGCTTCCTGAGGACATCTTGGGCTTGGGTTGCCCGGAGGTTGAGAG 1026
QY 1069 CACACCCCGGCAAGAACCTTTGAGAAAGAGAACCCAGCTGCGCAACCTCATTCAGTGT 1128
Db 1027 CAGCAGAGGAGAGACACTTTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1086
QY 1129 GTTGGCGGTAGTACGC 1145
Db 1087 GCTGAGAGATTTTACGC 1103

RESULT 15

US-10-128-870-3
; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiv
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

Query Match 15.2%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 8.4e-121;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 299 AGAGTCGCGGCGCAAGTCAAGTACCGGCGGTGCGAAGTACTGTAACAGTGTG 358
Db 17 AGCCCCCAAGGCAAGCGCTTCTACCGCAAGCTGCAAGATTCTCTACACAGCGCTG 76
QY 359 AGAGACCCCGGCGGTGCGGTATCATCTACACGCTTCTCTCTCTCTCTCTCTCT 418
Db 77 AGCGGCGCGCGCGGTGCGGTATCATCTACACGCGCTTCTCTCTCTCTCTCTCTCT 136
QY 419 GCTTATTTTGCAGTCTTCTTACCATCTCTGAGCAGACAAATTTGGCCCAAGTTCC 478
Db 137 GCTGCTGCTGCTGCTTCTTCCACATCAAGAGATGAGAAAGCTGGAAGGGGCGCC 196
QY 479 TCTTATCTCTGAGTTCGTATGATGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 538
Db 197 TCTACATCTCTGAAATCGTACATGCTGTGTTTGGCGTGGATCTACTGCTGGGATCT 256
QY 539 GGTCTGCGGCTGCTGCTGCTGCTATATAGAGATGCGAAGAGACTGAGTTGCTGCA 598
Db 257 GGGCGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 316
QY 599 AGCCCTCTGCTGCTTATAGATACCATGCTTCTTCTGCTTCTTCTTCTTCTTCTTCT 658
Db 317 AACGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 376

QY 659 AACCTCAGGATATATTTTGGCCAGCTGCTGCTCAGAGATCTCCGTTCTCTACAGATTC 718
Db 377 GCTCCAGGAGCAAGCTTCTTCCCATCTTGGGCTTCCGAGGCTTGGCTTCTCTGAGATTC 436
QY 719 TCCGATGTGCGCATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 778
Db 437 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
QY 779 ATGCTCAGCAGAGATATATGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
Db 497 ATGCCACAGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
QY 839 CGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
Db 557 CCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
QY 899 ATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
Db 617 ATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
QY 959 TACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
Db 677 AGACTGGAACGAGGCTCTTGGCGGCAACCTTCACTCATCTGCTGCTGCTGCTGCT 736
QY 1019 CACTTCTGCGGCGCATCTTGGCTCAGGTTTGGATTAAAGTACAGAACACACCGCC 1078
Db 737 CGCTGCTGAGGAGCTTCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 796
QY 1079 AGAAGCACTTTGAG 1138
Db 797 AGAAGCACTTTGAG 856
QY 1139 GTTACGC 1145
Db 857 TTTACGC 863

RESULT 16

US-10-131-685-3
; Sequence 3, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blanaer, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58acon
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-131-685-3

Query Match 15.2%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 8.4e-121;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 299 AGAGTCGCGGCGCAAGTCAAGTACCGGCGGTGCGAAGTACTGTAACAGTGTG 358
Db 17 AGCCCCCAAGGCAAGCGCTTCTACCGCAAGCTGCAAGATTCTCTACACAGCGCTG 76

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QY 359 AGAGACCCCGGCGCTGGGCTTCATCTACACGCTTTCGTTTCTCTCTGTTGTT 418
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 AGCGCGCGCGGCGCTGGGCTTCATCTACACGCTTTCGTTTCTCTCTGTTGTT 136
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 419 GCTGATTTTCTGCTGTTTCTTACCATCTGAGCAGCAACAAATTGGCCTCAAGTTGCC 478
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 GCGTCTGCTGCTGTTTCTTCCACCATCAGAGATGAGAGAGCTCGGAGGGGCC 196
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 479 TCTTGATCTGAGTTCGATGATGCTGTTGCTTGTGAGTTCATCATCTGATCT 538
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 TCTACATCTTGAAATCGTACTATGCTGTTGCTGCTGCTGCTGCTGCTGCTGCT 256
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 539 GGTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 GGGCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
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QY 599 AGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 AACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 659 AAACCTGAGGATATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 GCTCCAGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 719 TCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 778
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 TGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 779 ATGCTACAGCAGAGATATATACAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 ATGCCACAGCAGAGATATATACAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 839 GCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 CCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 899 ATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 617 ATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
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QY 959 TAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1018
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Db 677 AGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1019 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 737 CACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1079 AGAACACTTGTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138
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Db 797 AGAAGCACTTGTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
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QY 1139 GTTACGC 1145
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 857 TTTACGC 863
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: PRIOR APPLICATION NUMBER: 09/105,058
: PRIOR FILING DATE: June 26, 1998
: PRIOR APPLICATION NUMBER: 60/055,599
: PRIOR FILING DATE: August 12, 1997
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 5
: LENGTH: 900
: TYPE: DNA
: ORGANISM: MOUSE
: FEATURE:
: OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-128-870-5

Query Match      15.2%  Score 420.6: DB 9: Length 900:
Best Local Similarity 68.7%: Pred. No. 1.5e-120:
Matches 579: Conservative 0: Mismatches 264: Indels 0: Gaps 0:

QY 309 GCGCAAGCTCAAGTACCGGCGGCTGAGAGACTGATCAACGTGCTGAGAGACCGG 368
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 GCGCAAGCTCTTACCGGAGCTGAGAGATTTCTCTCAACGTGCTGAGAGACCGG 86
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CGGCTGGCGTTCATCTACACGCTTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 428
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Db 87 CGGCTGGCGTTCATCTACACGCTTGTGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 146
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 GTCAGTGTCTTACCATCCCTGAGCAGACAAATTTGGCTCAAGTTGGCTGCTGATCT 488
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Db 147 TTTGCTGTTTCCACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 489 GAGTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 GGAATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 549 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
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QY 609 TGTATATATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 TGTATATATATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 669 TAATATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
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Db 387 CAATCTCTTGGCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
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QY 729 GCGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 788
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Db 447 CCGTATGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 789 CAAGGATTAATCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 CAAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 849 TGTATATGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 GGTGATCTTGGCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626
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QY 909 GTGGGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 968
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 627 GTGGGCTGTAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
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QY 969 GGGAGATTTGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAG 1028
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Db 687 GGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1029 CGGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 747 TGGCATTTTGGGATCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
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QY 1089 TGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 807 TGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 866
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



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Db      192 AGACTGCTCTGTTACTGAGACATTTGCTATTTTCATCTTTGAGCCGAGTTTCTT 251
Qy      531 TCGATCTGCTGCTGGGCTGCTGTTGCTGATATAGAGATGCAAGAACTGAGTT 550
Db      252 GAGATCTGGGCTGCTGATGTTGCTGCTGATACAAAGGCTGGGCGGCTGAGATT 311
Qy      591 TGTCTGAAAGCCCTTCTGTTATAGATACCATTTGCTTATCGCTCAATAGCACTTGT 650
Db      312 TGCAGGAAGCCCTTCTGATGTTGACATCTTTGCTGATTTGCTTCTGCTGCTGCT 371
Qy      651 TTCTGCAAAAACCTAGGTAATATTTTTCACAGTCTGCACTGAGATCTCCGTTCT 710
Db      372 TGTCTGGAAGAACCAAGCAATGTTCTGCGCACCT---CCCTGCAAGCCTGGCTTCT 428
Qy      711 ACAATCTCGGCAATGTTGGCCATGAGACCAAGGAGGAGGACCTTGAATTTACTGGTTC 770
Db      429 GCAATCTCTGCGCATGCTGGGATGAGCCGAGAGGAGGACCTGAGACCTTCTGGGCTC 488
Qy      771 AGTGGTTATGCTACAGCAAGAAATTAATACAGCTTGTACATAGATTTTGTGCTCT 830
Db      489 AGCATCTGTGCTCCACCAAGAACTCATCAGGCTGTACATGCTTCTGACACT 548
Qy      831 TATTTTTCCTTCTCTTCTGCTATCTGCTGAGAAAGATGCC-----873
Db      549 CATCTTCTTCTTCTTCTTCTTCTTCTGAGAAAGCTCCAGAGTGTGATGCACA 608
Qy      874 -----AATAAAGATTTTCTACATATGCAATGCTCTCTGCTGGGCACT 920
Db      609 AGGAGAGGATGAAGAGAGATTTGAGACCTATGCAAGTGGCTGTGGGCTGTAT 668
Qy      921 TACATTGACAATATTTGGCTATGAGACAAACTCCCTAATGCTGTGGAAGATTGCT 980
Db      669 CACATCTGGCCACATTTGGCTATGAGACAAAGCAAAAGCTGGGAAGGCGCTGTAT 728
Qy      981 TTCTGCAAGCTTTCACCTTGGCATTTCTTCTTCTTCTGACCTTCTGCGGCACTTCTG 1040
Db      729 TGCGGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 788
Qy      1041 CTCAGTTTTCATTAAGTACAAAGACACACCGGCAAGAACTTTGAGAAAGAA 1100
Db      789 GTCCGGGCTGGCCCTCAAGGTGACAGAGACACACCTTGAAGAAAGAG 848
Qy      1101 GAACCCAGCTGCAACTCATTCAGTGTGTTGGCGGTATATGCG 1145
Db      849 GAAGCCAGCTGCTGAGCTCATTCAGGCTGCCCTGGAGGATATTATGC 893

RESULT 20
US-10-131-685-17
; Sequence 17, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaumer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KONO PORASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: D05880N
; CURRENT APPLICATION NUMBER: US/10/131,685
; PRIORITY FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 17
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; OTHER INFORMATION: 930 nucleotides of human KCNQ3
US-10-131-685-17
Query Match
Best Local Similarity 13.1%, Score 363.8; DB 9; Length 930;
Matches 580; Conservative 0; Mismatches 272; Indels 33; Gaps 2;

Qy      291 GAGTAGCAGAGCTGCGCGCCCAACGTAAGTACCGGGGGGAGAGAACTACTGTACAA 350
Db      12 GAGCGGCCCACTCAAGAAACCAACGCAAGTACCGGCGCATCAAACTTGATGTACGA 71
Qy      351 CGTCTGAGAGAGACCCGCGGCTGATCTATACACAGCTTCTGTTTCTCTCTGT 410
Db      72 CGCCCTGGAAGAGACCGCGGGCTGCGGCTGCTTACACAGCGGTGTGTTCTGATGT 131
Qy      411 CTTTGTTGCTTGAATTTTGTACAGTTTCTTACCATCCCTGAGACACAAATAGCCCTC 470
Db      132 CTTGGGGTCTTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
Qy      471 AAGTTGCTCTGATCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 530
Db      192 AGACTGCTTGTGTTACTGAGACATTTGCTATTTTCTTCTTCTTCTTCTTCTTCTT 251
Qy      531 TCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
Db      252 GAGATCTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
Qy      591 TGTCTGAAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
Db      312 TGCAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
Qy      651 TTCTGCAAAAACCTAGGTAATATTTTTCACAGTCTGCACTGAGATCTCCGTTCT 710
Db      372 TGTCTGGAAGAACCAAGCAATGTTCTGCGCACCT---CCCTGCAAGCCTGGCTTCT 428
Qy      711 ACAATCTCGGCAATGTTGGCCATGAGACCAAGGAGGAGGACCTTGAATTTACTGGTTC 770
Db      429 GCAATCTCTGCGCATGCTGGGATGAGCCGAGAGGAGGACCTGAGACCTTCTGGGCTC 488
Qy      771 AGTGGTTATGCTACAGCAAGAAATTAATACAGCTTGTACATAGATTTTGTGCTCT 830
Db      489 AGCATCTGTGCTCCACCAAGAACTCATCAGGCTGTACATGCTTCTGACACT 548
Qy      831 TATTTTTCCTTCTCTTCTGCTATCTGCTGAGAAAGATGCC-----873
Db      549 CATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 788
Qy      874 -----AATAAAGATTTTCTACATATGCAATGCTCTCTGCTGGGCACT 920
Db      609 AGGAGAGGATGAAGAGAGATTTGAGACCTATGCAAGTGGCTGTGGGCTGTAT 668
Qy      921 TACATTGACAATATTTGGCTATGAGACAAACTCCCTAATGCTGTGGAAGATTGCT 980
Db      669 CACATCTGGCCACATTTGGCTATGAGACAAAGCAAAAGCTGGGAAGGCGCTGTAT 728
Qy      981 TTCTGCAAGCTTTCACCTTGGCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1040
Db      729 TGCAGCAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 788
Qy      1041 CTCAGTTTTCATTAAGTACAAAGACACCGGCAAGAACTTTGAGAAAGAA 1100
Db      789 GTCCGGGCTGGCCCTCAAGGTGACAGAGACACACCTTGAAGAAAGAG 848
Qy      1101 GAACCCAGCTGCAACTCATTCAGTGTGTTGGCGGTATATGCG 1145
Db      849 GAAGCCAGCTGCTGAGCTCATTCAGGCTGCCCTGGAGGATATTATGC 893

RESULT 21
US-10-128-870-7
; Sequence 7, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:

```

; APPLICANT: Blanaar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribokoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubaer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ADIY
 ; CURRENT APPLICATION NUMBER: US/10/128,870
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 7
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: RAT
 ; US-10-128-870-7

Query Match 12.1%; Score 334.2; DB 9; Length 735;
 Best Local Similarity 68.4%; Pred. No. 1.5e-93;
 Matches 462; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 477 CCTCTGATCCGAGTTCGATGATGCTGCTGTTGGAGTTCATTCGAT 536
 DB 30 CCTCTGATCCGAGTTCGATGATGCTGCTGTTGGAGTTCATTCGAT 89
 QY 537 CTGCTGCGGGTTCGTTGATATAGAGATGCAAGAGAGAGTTCGTCG 596
 DB 90 CTGCGGCGAGGCTGCTGCGGATATGAGGCTGAGGCGCGGCTCAAGTTGCGAG 149
 QY 597 AAGCCCTTCTGTTATAGATACATGTTCTTATGCTTAATGACATGTTCTGC 656
 DB 150 GAAGCCATTCGTGTGATGATGATGCTGCTGATGCTGCTGCTGCTGCTGCTG 209
 QY 657 AAAAATCGAGGATATATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
 DB 210 TGGCTCCAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
 QY 717 CCTCCGATGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
 DB 270 CTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 329
 QY 777 TTATGCTACAGCAAGATTAATACAGCTTGTATGATGATGATGATGATGATGAT 836
 DB 330 CTACGCTACAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
 QY 837 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 DB 390 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
 QY 897 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
 DB 450 GGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
 QY 957 CCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
 DB 510 TCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
 QY 1017 TGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
 DB 570 CGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
 QY 1077 CCAGAACACTTTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
 DB 630 GCAAAAG 689
 QY 1137 TAGTTAG 1151

DB 690 ATTCTATGCTACTATA 704

RESULT 22

; Sequence 7, Application US/10131685
 ; Publication No. US20030044912A1
 ; GENERAL INFORMATION:

; APPLICANT: Blanaar, Michael A.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubaer, Michael G.
 ; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58ACON

; CURRENT APPLICATION NUMBER: US/10/131,685
 ; PRIOR FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: US 09/105,058
 ; PRIOR FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 60/055,599
 ; PRIOR FILING DATE: 1997-08-12

; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 7

LENGTH: 735

TYPE: DNA

ORGANISM: RAT

US-10-131-685-7

Query Match 12.1%; Score 334.2; DB 9; Length 735;
 Best Local Similarity 68.4%; Pred. No. 1.5e-93;
 Matches 462; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 477 CCTCTGATCCGAGTTCGATGATGCTGCTGTTGGAGTTCATTCGAT 536
 DB 30 CCTCTGATCCGAGTTCGATGATGCTGCTGTTGGAGTTCATTCGAT 89
 QY 537 CTGCTGCGGGTTCGTTGATATAGAGATGCAAGAGAGAGTTCGTCG 596
 DB 90 CTGCGGCGAGGCTGCTGCGGATATGAGGCTGAGGCGCGGCTCAAGTTGCGAG 149
 QY 597 AAGCCCTTCTGTTATAGATACATGTTCTTATGCTTAATGACATGTTCTGC 656
 DB 150 GAAGCCATTCGTGTGATGATGATGCTGCTGATGCTGCTGCTGCTGCTGCTG 209
 QY 657 AAAAATCGAGGATATATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
 DB 210 TGGCTCCAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
 QY 717 CCTCCGATGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
 DB 270 CTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 329
 QY 777 TTATGCTACAGCAAGATTAATACAGCTTGTATGATGATGATGATGATGATGAT 836
 DB 330 CTACGCTACAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
 QY 837 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
 DB 390 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
 QY 897 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
 DB 450 GGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
 QY 957 CCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
 DB 510 TCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
 QY 1017 TGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
 DB 570 CGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629


```

QY 448 CTTGAGCAGACAAAATTGGCCTCAAGTTGCTTGTGATGCTGGATGATGTC 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GAGACAGATATGCCCCCTGGCCACGGGAGCTCTCTTGATGAGATCGTGCTG 657
QY 508 GTCCTTGGTTTGAAGTTCATCATTCGATCTGCTGCGGTTGCTGTTGATATAGA 567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 TTTCTGGGAGAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 568 GGATGGCAGGAAGATGATGTTGCTGGAAGCCCTGCTGCTGCTGCTGCTGCTG 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 GGCCTTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
QY 628 CTTATCCCTTCAATATAGCAGTTGTTCTGCAAAAACCTGAGGGTAAATATTTTGGCCAGCTCT 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 778 GTCCTGGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
QY 688 GCACTGAGAGTCTCCGTTTCTTACAGATCTCCGCTGCTGCTGCTGCTGCTGCTG 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 GGCATCAGGGGAGATCCGCTTCTGCAAGATCTGAGGATCTACACGTCGACCCGACAGGA 897
QY 748 GGCACCTTGGAAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 GGCACCTGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
QY 808 TGATACATAGGATTTTGTCTTATTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTG 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 958 CTGATACATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
QY 868 GATCCCAATATA-----GAGTTTCTACATATGACAGATGCTCTGCTGCTG 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1018 GACCCGCTGAGAGTACAGGCGCGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 1077
QY 913 GGCACATTTACATATGACATTTGCTTGTGAGACAAAACCTCCCTTACCTTGGCTGGA 972
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1078 GGGGTGGTCAAGTATACCAACCTGCGCTATGGGAGACAAAGTGGCCCAAGAGTGGTGGG 1137
QY 973 AGATTGCTTCTGACAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1138 AAGACATATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
QY 1033 ATTCTGGCTCAGGTTTGGCATTAAGATCAACAAACACGCGCAAGAAACCTTTGAG 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1198 ATTCTGGCTCAGGTTTGGCATTAAGATCAACAAACACGCGCAAGAAACCTTTGAG 1257
QY 1093 AAAAGAGGAAGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCTAGTTACGACGTGA 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1258 CGGAGATCCCGGGGCGAGGCTCAGCTCATTCAGAACGCAATGAGTGTATGTCGCGA 1316

```

RESULT 25

```

US-09-880-107-3358
; Sequence 3358, Application us/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3358
; LENGTH: 2821
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U049090
US-09-880-107-3358

```

```

Query Match          9.6%; Score 266.6; DB 10; Length 2821;
Best Local Similarity 59.3%; Fied. No. 6.5e-72;
Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

```

```

QY 329 GGGTGCAGAACTACCTGATCAACAGTGTGAGAGACCCCGGCGCTGG---GCTTCACT 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 GGGGCGAGGCGCGCTGCTCAACTTCTGCAAGCTGCCACCGGCTGGAAATGCTTGGT 175
QY 386 ACCAGCTTTCGTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 ACCACTTCCCGCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
QY 446 TCCCTGAGACACAAAATTGGCTCAAGTGGCCCTTGTATCTGAGTGGTGGATGATG 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 TCGAGCAGTATGCGCCCTGGCCACGGGAGCTCTTCTGATGATGAGATGCTGCTG 295
QY 506 TCGCTTGTGTTGAGATTCATTCATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 TGTCTTGGGAGAGAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
QY 566 GAGATGCAAGGAGAGAGTGTGCTGCAAAAGCCCTTCTGCTTATATATACATG 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 TGGGCTCTGGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
QY 626 TTTCTATCCCTCAATAGCAGTGTGTTCTGCAAAAACCTGAGGTAATTTTGGCCAGCT 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 TGTCTGCTGCTCCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
QY 686 CTGACATCAAGAGTCTCCGTTTCTTACAGATCTCCGCTGCTGCTGCTGCTGCTGCTG 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 GGGGCTATGAGGAGCTCCGCTTCTGCAAGTCTGAGAGTCTACAGTCAAGCCGACAG 535
QY 746 GAGGCACTTGAATTAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 536 GAGGCACTTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 595
QY 806 CTGATCAATAGGATTTTGTGCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 CCTGTACATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
QY 866 AGAGTCCCAATATA-----GAGTTTCTACATATGACAGATGCTCTGCTG 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 AGAGTCCCAATATA-----GAGTTTCTACATATGACAGATGCTCTGCTG 915
QY 911 GGGGCAATTAATGATGACAACTATGCTATGAGCAAAACCTCCCTAATCTGGCTG 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 GGGGCTGTGTCACAGTACCAACATGCGCTATGAGGAGCAAGGTGCGCAGAGTGGCTG 775
QY 971 GAAGATGCTTCTGACAGGCTTGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 GGAAGACATGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
QY 1031 GCATTTCTGCTCAGGTTTGGCATTAAGTACAGAAACACCGCCAGAAACCTTTG 1090
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 GGAATTTCTGCTGAGGTTTGGCTTGAAGGTGAGCAAGAACAGAGGAGCAAGCACTTCA 895
QY 1091 AGAAAGAGGAAGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCTAGTTACGACGTG 1150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 ACCGCGAGATCCCGGGGCGAGGCTCAGCTCATTCAGAACGCAATGAGTGTATGCTGCGG 955

```

RESULT 26

```

US-09-960-352-13343
; Sequence 13343, Application us/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

```

```

: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT APPLICATION NUMBER: US/09/960.352
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 13343
: LENGTH: 416
: TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 57-LIB3058-010-Q1-K1-G2
US-09-960-352-13343

```

```

Query Match          4.7%; Score 130.4; DB 10; Length 416;
Best Local Similarity 62.4%; Pred. No. 6.7e-30;
Matches 256; Conservative 0; Mismatches 121; Indels 33; Gaps 2;

```

```

QY 616 GATACATTTCTTATGCTTACATAGCATGTTTTCGAAAAACATCAGGTAATTT 675
   || || || || || || || || || || || || || || || || || || || ||
Db 2 GACATCTTTGTGCTGATGCGCTCGCTGCTGTTGCCGGAACCAAGGCGACGCTC 61
   || || || || || || || || || || || || || || || || || || || ||
QY 676 TTTCGCAAGTCTGACAGAGTCTCCGTTTCTACAGATCCCGCATGTCGCGCATG 735
   || || || || || || || || || || || || || || || || || || || ||
Db 62 CGGGCCACGCT---CCCTCGGAGTCTGCGCTTCCTGAGATCTTGATGCTGCGAATG 118
   || || || || || || || || || || || || || || || || || || || ||
QY 736 GACCGAAGGAGGACGACTTGGAAATTAAGTGGTTCAGTGGTTTATGCTCAGCAAGAA 795
   || || || || || || || || || || || || || || || || || || || ||
Db 119 GACCGAGGGGCGGACCTGGAAGTCTCGGCTCGGCGCATCTGGCCACAGCAAGAAAG 178
   || || || || || || || || || || || || || || || || || || || ||
QY 796 TTAATCACAGCTTGGTATAGATTTTGGTTCTTATTTTTCGCTTCTTCTGCTAT 855
   || || || || || || || || || || || || || || || || || || || ||
Db 179 CTCATCACCGCTGCTGATGCGCTCGCTGCTGTTGCCGGAACCAAGGAGATGAAAGATTT 238
   || || || || || || || || || || || || || || || || || || || ||
QY 856 CTGCTGGAAGAGATG-----CCATTAAGAGATT 885
   || || || || || || || || || || || || || || || || || || || ||
Db 239 CTGCTGGAAGAGATGCTCGGAGTGGATGCCCAAGGAGAGATGAAAGAGATTT 298
   || || || || || || || || || || || || || || || || || || || ||
QY 886 TCTACATATGCAATGCTCTCTGCTGGGCGACAAATTAATGCAACATATGCTATGGA 945
   || || || || || || || || || || || || || || || || || || || ||
Db 299 GAGACCTACGACATGCTGCTGCTGGGCGCTGATCACATGCGCACCATGCTACGGA 358
   || || || || || || || || || || || || || || || || || || || ||
QY 946 GACAAAACCTCCCTAATCTGCTGGGAGATGCTTTTCGACGCGCTTTC 995
   || || || || || || || || || || || || || || || || || || || ||
Db 359 GACAAAGCGCCCAAAAGCTGGGAGGCGCTGATGAGCCACCTTTTC 408
   || || || || || || || || || || || || || || || || || || || ||

```

```

RESULT 27
US-09-783-590-4509
: Sequence 4509, Application US/09783590
: Patent No. US20020110850A1
: GENERAL INFORMATION:
: APPLICANT: Dillon, Patrick J.
: APPLICANT: Haselaine, William A.
: APPLICANT: Li, Haodong
: APPLICANT: Rosen, Craig A.
: APPLICANT: Rudeen, Steven M.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
: FILE REFERENCE: PO-16.2C1
: CURRENT APPLICATION NUMBER: US/09/783.590
: PRIOR FILING DATE: 2000-07-15
: PRIOR APPLICATION NUMBER: 08/420,856
: PRIOR FILING DATE: 1995-04-12
: PRIOR APPLICATION NUMBER: 08/346,731
: PRIOR FILING DATE: 1994-11-21
: NUMBER OF SEQ ID NOS: 12485
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4509
: LENGTH: 429
: TYPE: DNA

```

```

: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (25)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (31)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (54)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (130)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (181)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (214)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (253)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (287)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (313)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (314)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (346)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (355)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (358)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (366)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (392)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (400)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (407)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (422)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-4509

```

```

Query Match          3.8%; Score 104.2; DB 10; Length 429;
Best Local Similarity 58.6%; Pred. No. 1.1e-21;
Matches 197; Conservative 0; Mismatches 124; Indels 15; Gaps 1;

```

```

QY 665 AGGTAATATTTTGGCCACGCTCAGTCAGAAAGTCTCCGTTTCTACAGATCTCCGCA 724
   || || || || || || || || || || || || || || || || || || || ||
Db 15 AGGGGAGGTTTTCNACGTCACAGGCGCATCCNCTCTGACATCCCAAGGA 74
   || || || || || || || || || || || || || || || || || || || ||
QY 725 TGGTGCCATGAGCCAGGAGGAGGACCTTGGAATTAATGAGTTTCACTGTTATGCTC 784
   || || || || || || || || || || || || || || || || || || || ||
Db 75 TGCTACACGCTGACACCGCCAGAGGACACCTGAGGCTCTCTGCTCCGTCTTATTC 134
   || || || || || || || || || || || || || || || || || || || ||
QY 785 ACAGCAAGGAATTAATCAGAGCTTGTACATAGATTTTGGTTCTTATTTTCGCTCT 844
   || || || || || || || || || || || || || || || || || || || ||
Db 135 ACCGCCAGAGCTGATTAACACACCTGTACATCGGCTTCTGCGCTTATCTTCCTCGT 194
   || || || || || || || || || || || || || || || || || || || ||

```


[illegible]

```

: APPLICANT: Haselbeck, Robert
: APPLICANT: Wall, Daniel
: APPLICANT: Gross, Molly
: TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
: FILE REFERENCE: ELITRA.010A
: CURRENT APPLICATION NUMBER: US/10/032,393
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/7259,434
: PRIOR FILING DATE: 2000-12-27
: PRIOR APPLICATION NUMBER: 09/948,993
: PRIOR FILING DATE: 2001-09-06
: PRIOR APPLICATION NUMBER: 60/7230,335
: PRIOR FILING DATE: 2000-09-06
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 47
: LENGTH: 12733
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Vector pEPR14
US-10-032-393-47

Query Match      2.1%; Score 57.6; DB 9; Length 12733;
Best Local Similarity 48.5%; Pred.No.6,3e-06;
Matches 159; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY      16 GCGGAGAGAGAGAGGCGCGCCCGCCTGTGTGAGAGACGCGCGCACGCGCGGCG 75
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5088 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5147
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      76 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 135
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5148 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5207
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      136 GTGCTGCTGAACCTGGCGACGCCGCCAGGGGGGCGACGAGCCTCTACTACTGTGGGCAACCCGCGCG 195
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5208 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      196 GCCACGCTGCTGTGCGGCGGGGGGGGTGTGAGGGAGAGCCCGGGGGCGAACAGAGGGGCGC 255
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5268 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5327
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      256 CGATGAGCCTGTGCTGGGGGAGCCCGCTCTTTACACGAGTAGCCAGAGCTGCGGCGCAAC 315
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5328 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5387
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      316 GTCAAGTACCGGGGGGGGTCCAGACATACC 343
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      5388 CTTCGGGTGGGCGCGGGGCGCATGACTATC 5415
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 36
US-10-032-393-8
Sequence 8, Application US/10032393
Publication No. US20030027286A1
GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Wall, Daniel
: APPLICANT: Gross, Molly
: TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
: FILE REFERENCE: ELITRA.010A
: CURRENT APPLICATION NUMBER: US/10/032,393
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/259,434
: PRIOR FILING DATE: 2000-12-27
: PRIOR APPLICATION NUMBER: 09/948,993
: PRIOR FILING DATE: 2001-09-06
: PRIOR APPLICATION NUMBER: 60/230,335
: PRIOR FILING DATE: 2000-09-06
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8

```

LENGTH: 12739
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Vector pEPR1
US-10-032-393-8

Query Match 2.1%; Score 57.6; DB 9; Length 12739;
Best Local Similarity 48.5%; Pred. No. 6.3e-06;
Matches 159; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 16 GCGGAGAGAGAGAGCGCGCGCGCGCGCTGCTGTAAGAGCGCGCAAGCGCGCG 75
DB 5094 GGG 5153
QY 76 GCGGCGGG 5213
DB 5154 GGG 5213
QY 136 GTGCTGCTGAACCTGCGCAGCGCGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCG 195
DB 5214 GGG 5273
QY 196 GCCACCTCGGTGCGCGCGCGCGCGCTGCTGTAAGAGAGCGCGCGCGCAAGCGGGCC 255
DB 5274 GGG 5333
QY 256 CGGATGAGCTGCTGCGGGAAGCGCGCTGCTTACAGAGTACAGAGCTGCCCGCGCAAC 315
DB 5334 GGG 5393
QY 316 GTCAAGTACCGCGCGGTGCGCAACTACC 343
DB 5394 CTCCGGTGGCGCGGGGCGATGACTATC 5421

RESULT 37
US-09-963-285-9/c
Sequence 9, Application US/09963285
Patent No. US20020090707A1
GENERAL INFORMATION:
APPLICANT: Enerbck, Sven
APPLICANT: Krook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Wasserman, Wyleth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1503)
US-09-963-285-9

Query Match 2.0%; Score 56.4; DB 10; Length 1506;
Best Local Similarity 53.4%; Pred. No. 2.8e-06;
Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 23 GAGAGAGAGGCGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCGCGCGCGCGCG 82
DB 1114 GAGCGCTCAGGGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCGCGCGCGCG 1055

QY 83 GCGGGGGCGCGCTTGGGACAGCGGCATGAAGATGTGAGTCCGGCGCGCGCGCGCG 142
DB 1054 GCGGAGACACATGTGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 995
QY 143 TGAACCTGCGCAGCGCGCGCGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCGCG 202
DB 994 TGCACCT-GGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 936
QY 203 TCGGTGGCG 262
DB 935 GCGGCGGGCG 876
QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
DB 875 CCGGCCCGCGCGCGCTCAGCTCTC 854

RESULT 38
US-09-963-285-8/c
Sequence 8, Application US/09963285
Patent No. US20020090707A1
GENERAL INFORMATION:
APPLICANT: Enerbck, Sven
APPLICANT: Krook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Wasserman, Wyleth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 3289
TYPE: DNA
ORGANISM: Homo sapiens
US-09-963-285-8

Query Match 2.0%; Score 56.4; DB 10; Length 3289;
Best Local Similarity 53.4%; Pred. No. 5.2e-06;
Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 23 GAGAGAGAGGCGCGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCGCGCGCGCGCG 82
DB 2310 GAGCGCTCAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2251
QY 83 GCGGGGGCGCGCTTGGGACAGCGGCATGAAGATGTGAGTCCGGCGCGCGCGCGCG 142
DB 2250 GCGGAGACACATGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2191
QY 143 TGAACCTGCGCAGCGCGCGCGCGCGCGCGCTGCTGTAAGAGCGCGCGCGCGCG 202
DB 2190 TGCACCT-GGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2132
QY 203 TCGGTGGCG 262
DB 2131 GCGGCGGGCG 876
QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
DB 2071 CCGGCCCGCGCGCGCTCAGCTCTC 2050

RESULT 39
US-09-963-285-3/c
Sequence 3, Application US/09963285

Patent No. US20020090707A1
 GENERAL INFORMATION:
 APPLICANT: Eneidck, Sven
 APPLICANT: Kirook, Katarina
 APPLICANT: Rondahl, Lena
 APPLICANT: Masserman, Wyeth
 TITLE OF INVENTION: PROMOTER SEQUENCES
 FILE REFERENCE: 13425-042001
 CURRENT APPLICATION NUMBER: US/09/963,285
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: SE 0004102-0
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: US 60/238,897
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: SE 0003435-5
 PRIOR FILING DATE: 2000-09-26
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 4158
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (187)...(1437)
 US-09-963-285-3

Query Match 2.0%; Score 56.4; DB 10; Length 4158;
 Best Local Similarity 53.4%; Pred. No. 6.2e-06;
 Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 23 GAGAGGAGGCGGCGCGGCGCTCTGGGTGAAGAGCGCGGCGCGCGCGCGCG 82
 DB 1048 GAGCGCTCAGGGGCGGCGGCGCGCTCTGGGTGTCGAGAGGCGCTCTCGAGGCGG 989
 QY 83 GCGGGGCGGCTTGGGCGAGCGCGCATGAGATGTGAGTGGGCGGCGGCGCGGCGG 142
 DB 988 GCGGAGCGACATGTGCGCGCGCGCGCTCGCGCGCGGTGACAGGCTCATCGCTCGCATGC 929
 QY 143 TGAATCGGAGCGCGCGGCGGCGAGCGCGTCTGCTACTGCTGGGCGACCGCGCGCGCGCG 202
 DB 928 TGCACCT-GGTACCTCCCGCGCGCGCGCGCTCCAGGCGCTGAGCGCGCTGGCGCTAG 870
 QY 203 TCGGTGCGGCGCGGCGGCTGTGAGAGAGCGCGCGGCGGCGGCGCGCGCGATGA 262
 DB 869 GCGGCGGCGCGCGCGCGCGCGGTGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCT 810
 QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
 DB 809 CCGGCGCGCGCGCGCTCAGCTCTC 788

RESULT 40
 US-09-963-285-1/c
 Sequence 1, Application US/09963285
 Patent No. US20020090707A1
 GENERAL INFORMATION:
 APPLICANT: Eneidck, Sven
 APPLICANT: Kirook, Katarina
 APPLICANT: Rondahl, Lena
 APPLICANT: Masserman, Wyeth
 TITLE OF INVENTION: PROMOTER SEQUENCES
 FILE REFERENCE: 13425-042001
 CURRENT APPLICATION NUMBER: US/09/963,285
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: SE 0004102-0
 PRIOR FILING DATE: 2000-11-09
 PRIOR APPLICATION NUMBER: US 60/238,897
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: SE 0003435-5
 PRIOR FILING DATE: 2000-09-26
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1
 LENGTH: 6458
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (2235)...(3737)
 US-09-963-285-1

Query Match 2.0%; Score 56.4; DB 10; Length 6458;
 Best Local Similarity 53.4%; Pred. No. 8.8e-06;
 Matches 140; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 23 GAGAGGAGGCGGCGCGCGGCGCTCTGGGTGAAGAGCGCGGCGCGCGCGCGCG 82
 DB 3348 GAGCGCTCAGGGGCGGCGGCGCGCTCTGGGTGTCGAGAGGCGCTCTCGAGGCGG 3289
 QY 83 GCGGGGCGGCTTGGGCGAGCGCGCATGAGATGTGAGTGGGCGCGCGCGCGCGGCTGTC 142
 DB 3288 GCGGAGCGACATGTGCGCGCGCGCTCTGGGTGTCGAGAGGCGCTCTCGCATGC 3229
 QY 143 TGAATCGGAGCGCGCGGCGGCGCATGAGATGTGAGTGGGCGCGCGCGCGCGCG 202
 DB 3228 TGCACCT-GGTACCTCCCGCGCGCGCGCGCTCCAGGCGCTGAGCGCGCTGGCGCTAG 3170
 QY 203 TCGGTGCGGCGCGGCGGCTGTGAGAGAGCGCGCGGCGGCGGCGCGCGCGATGA 262
 DB 3169 GCGGCGGCGCGCGCGCGCGCGGTGATGAGCGCGCGCGCGCGCGCGCGCGCGCT 3110
 QY 263 GCCTGCTGGGGAAGCGCGCTCTC 284
 DB 3109 CCGGCGCGCGCGCGCTCAGCTCTC 3088

RESULT 41
 US-10-184-644-202
 Sequence 202, Application US/10184644
 Publication No. US20030044930A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C227
 CURRENT APPLICATION NUMBER: US/10/184,644
 CURRENT FILING DATE: 2002-06-28
 Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 202
 LENGTH: 440
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-184-644-202

Query Match 2.0%; Score 56.2; DB 9; Length 440;
 Best Local Similarity 21.7%; Pred. No. 1.2e-06;
 Matches 60; Conservative 75; Mismatches 142; Indels 0; Gaps 0;

QY 10 CACACGCGGAGAGAGAGAGCGCGCGCGCGCTCTGGGTGAAGAGCGCGCGCGCG 69
 DB 128 VRSWQGVNPGHSGAMETSGHGIRFGSGGLGCGGNGSLGTPVWHGYPGNSAGSFGNN 187
 QY 70 GCGGCGGCGCGCGCGCGCGCGCTTGGGCGAGCGCGCATGAGATGTGAGTGGCGCGCG 129

Db 188 PGAPWGGGNGNPNFTNTGAVNAQPGYGVASVNASONEGCTNPPSSGSGSSNSGGG 247
QY 130 GGGAGGGGCTGCTGTAACCTGCGACGCGCGGAGGGGCGGCTGCTACTGCTGGGACG 189
Db 248 SGGSGSSGSSGSGNDNNSS 307
QY 190 GCGCGGCGCACGCTGCTGCGCGGCGGCTGCGCTGAGGAGAGCCGCGCGGCGCAAGCAG 249
Db 308 SSMGSSSTGSSGHNHGGSGGNGHKPCCEKPCGNARSGSGGCTGCGFPGCGVSSNMRETSKE 367
QY 250 GGGGCGCGGATGAGCCTGCTGCGGGAAGCCGCTCTT 286
Db 368 GNRLLGSGDNYRGOGSSSWGSGGDAVGAVNTVNSSET 404

RESULT 42

US-10-184-634-202
; Sequence 202, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184, 634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-202

Query Match 2.0%; Score 56.2; DB 9; Length 440;
Best Local Similarity 21.7%; Pred. No. 1.2e-06;
Matches 60; Conservative 75; Mismatches 142; Indels 0; Gaps 0;

QY 10 CACACGCGGAGAGAGAGAGGCGCGCGCGGCTGCTGGAAGCGCGGACG 69
Db 128 VHSQMGVPHSGAMETSGHGFSGSGGIGGOGGPGGLGTPWVHGPGNSAGSFGMN 187
QY 70 GGGGCGCGCGCGCGCGCGCGCTGCGGAGCGGATGAGATGAGAGTGGGCGG 129
Db 188 PGAPWGGGNGNPNFTNTGAVNAQPGYGVASVNASONEGCTNPPSSGSGSSNSGGG 247
QY 130 GCGAGGGTCTGCTGTAACCTGCGACGCGCGGAGGGGCGGCTGCTACTGCTGGGACG 189
Db 248 SGGSGSSGSSGSGNDNNSS 307
QY 190 GCGCGGCGCACGCTGCTGCGCGGCGGCTGCGCTGAGGAGAGCCGCGCGGCGCAAGCAG 249
Db 308 SSMGSSSTGSSGHNHGGSGGNGHKPCCEKPCGNARSGSGGCTGCGFPGCGVSSNMRETSKE 367
QY 250 GGGGCGCGGATGAGCCTGCTGCGGGAAGCCGCTCTT 286
Db 368 GNRLLGSGDNYRGOGSSSWGSGGDAVGAVNTVNSSET 404

RESULT 43
US-09-804-682-29/C
; Sequence 29, Application US/09804682
; Patent No. US20020106765A1

; GENERAL INFORMATION:
; APPLICANT: Kinders, Robert
; APPLICANT: Corey, Michael J.
; TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR
; FILE OF INVENTION: MODULATING THE SAME
; FILE REFERENCE: 130001.406
; CURRENT APPLICATION NUMBER: US/09/804, 682
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 5, 6, 10, 21, 24, 25, 33, 39, 72, 110, 209, 214, 231, 232,
; LOCATION: 235, 237, 238, 244, 245, 246, 256, 282, 292, 297, 306, 319,
; LOCATION: 321, 323, 330, 334, 340, 349, 354, 355, 363, 372, 376, 378,
; LOCATION: 397, 405, 432, 437, 454, 455, 457, 458, 459, 468, 470
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562,
; LOCATION: 583, 600, 611, 613, 623, 624, 632, 654, 674, 681, 687, 691,
; LOCATION: 694, 701, 713, 716, 720, 721, 725, 731, 734, 735, 739, 743,
; LOCATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,
; LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,
; LOCATION: 1043, 1047, 1049, 1051, 1054, 1056
; OTHER INFORMATION: n = A,T,C or G
US-09-804-682-29

Query Match 2.0%; Score 54.6; DB 10; Length 1064;
Best Local Similarity 46.5%; Pred. No. 7.8e-06;
Matches 120; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 16 GCGGAGAGAGAGAGAGGCGCGCGCGGCTGCTGCTGTAAGAGCGCGGCGGCGG 75
Db 645 GGGGCGGCGGAGAGAGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGAGG 586
QY 76 GCGGCGGCGGCGGCGGCTTGGGCGAGCGGCGGAGAGATGAGATCGGCGGCGGCGG 135
Db 585 GANAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526
QY 136 GTGCTGCTGTAACCTGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 195
Db 525 GNGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
QY 196 GCCAGCGCTGCTGCGCGCGCGGCGGCTGAGGAGAGAGCGCGGCGGCGGCGGCGG 255
Db 465 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 406
QY 256 CGGATGAGCCTGCTGCGG 273
Db 405 NCGAGGCGGCGGAGGCGG 388

RESULT 44
US-09-954-456-292
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954, 456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233, 617
; PRIOR FILING DATE: 2000-09-18

QY 28 GAGGCGCGCCCGCCGCTCTGGGTGAAGACGCGCGCGCGCGCGCGCG 87
 Db 25554 GCGGGGCGCGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25613
 QY 88 GGGCGCTGGGCGCGCGCATGATGATGATGATGATGATGATGATGAT 147
 Db 25614 GGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25673
 QY 148 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 207
 Db 25674 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25733
 QY 208 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 267
 Db 25734 TGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25793
 QY 268 CTGGGCGAGCCGCTC 282
 Db 25794 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25808

RESULT 47

US-10-098-841-34/c
 ; Sequence 34, Application US/10098841
 ; Publication No. US20020197679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Xu, Chongjun
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhao, Qing-A.
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Drmanac, Radolje T.
 ; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
 ; FILE REFERENCE: Polypeptides
 ; CURRENT APPLICATION NUMBER: US/10/098,841
 ; PRIOR APPLICATION NUMBER: 2002-03-13
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 331
 ; SOFTWARE: PL_genes Version 1.0
 ; SEQ ID NO 34
 ; LENGTH: 4176
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1508)..(3430)
 ; US-10-098-841-34

Query Match 1.9%; Score 52.6; DB 9; Length 4176;
 Best Local Similarity 52.0%; Pred. No. 9.7e-05;
 Matches 141; Conservative 0; Mismatches 129; Indels 1; Gaps 1;

QY 27 GGAAGGCGCGCGCGCGCGCTCTGGGTGAAGACGCGCGCGCGCGCGCG 86
 Db 1798 GAAGTTCGCGCGCGCGCGCGCTCTGGGTGAAGACGCGCGCGCGCGCG 1739
 QY 87 GGGGCGCTGGGCGAGCGCGCATGAAGATGTGAGTTCGCGCGCGCGCGCGCG 146

Db 1738 GGCCTCGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1679
 QY 147 CTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 206
 Db 1678 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1619
 QY 207 TGGCGCGCGCGCGT-GGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 265
 Db 1618 GCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1559
 QY 266 TGCTGGGGAAGCGCGCTCTTACACAGATG 296
 Db 1558 GTCCGGGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1528

RESULT 48

US-10-095-407-16/c
 ; Sequence 16, Application US/10095407
 ; Patent No. US20020164330A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 09404/052001
 ; CURRENT APPLICATION NUMBER: US/10/095,407
 ; PRIOR APPLICATION NUMBER: 2002-03-11
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: US 60/091,650
 ; PRIOR FILING DATE: 1997-08-04
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16
 ; LENGTH: 152331
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1)..(152331)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-10-095-407-16

Query Match 1.9%; Score 52.4; DB 9; Length 152331;
 Best Local Similarity 49.6%; Pred. No. 0.0019;
 Matches 119; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 16 GCGGAG 75
 Db 22102 GGGGCGGGGCGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG 22043
 QY 76 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 135
 Db 22042 GGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGG 21983
 QY 136 GTGCTGCTGAACCTGGGAGCGCGCGCGCGCGCGCGCGCGCGCG 195
 Db 21982 GGGGCGGGGCGGTGGGGGCGGGGCGGGGCGGGGCGGGGCGGG 21923
 QY 196 GCCACGCTGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 255
 Db 21922 GCMGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGG 21863

RESULT 49

US-10-198-846-8585
 ; Sequence 8585, Application US/10198846
 ; Publication No. US20030099974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steimann, Kathleen

	APPLICANT:	Kank, David R.	
	APPLICANT:	Hanzel, David K.	
	TITLE OF INVENTION:	HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR	
	TITLE OR INVENTION:	GENE EXPRESSION ANALYSIS BY MICROARRAY	
	FILE REFERENCE:	Aeomica-X-1	
	CURRENT APPLICATION NUMBER:	US/09/864,761	
	PRIOR FILING DATE:	2001-05-23	
	PRIOR APPLICATION NUMBER:	US 60/180,312	
	PRIOR FILING DATE:	2000-02-04	
	PRIOR APPLICATION NUMBER:	US 60/207,456	
	PRIOR FILING DATE:	2000-05-26	
	PRIOR APPLICATION NUMBER:	US 09/632,366	
	PRIOR FILING DATE:	2000-08-03	
	PRIOR APPLICATION NUMBER:	GB 24263,6	
	PRIOR FILING DATE:	2000-10-04	
	PRIOR APPLICATION NUMBER:	US 60/236,359	
	PRIOR FILING DATE:	2000-09-27	
	PRIOR APPLICATION NUMBER:	PCT/US01/00666	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00667	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00664	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00669	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00665	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00668	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00663	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00662	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00661	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	PCT/US01/00670	
	PRIOR FILING DATE:	2001-01-30	
	PRIOR APPLICATION NUMBER:	US 60/234,687	
	PRIOR FILING DATE:	2000-09-21	
	PRIOR APPLICATION NUMBER:	US 09/608,408	
	PRIOR FILING DATE:	2000-06-30	
	PRIOR APPLICATION NUMBER:	US 09/774,203	
	PRIOR FILING DATE:	2001-01-29	
	NUMBER OF SEQ ID NOS:	49117	
	SOFTWARE:	Annomax Sequence Listing Engine vers. 1.1	
	SEQ ID NO:	1804	
	LENGTH:	998	
	TYPE:	DNA	
	ORGANISM:	Homo sapiens	
	FEATURE:		
	OTHER INFORMATION:	MAP TO AL035685.13	
	OTHER INFORMATION:	EXPRESSED IN BRAIN, SIGNAL = 4.3	
	OTHER INFORMATION:	EXPRESSED IN BT474, SIGNAL = 3.4	
	OTHER INFORMATION:	EXPRESSED IN FETAL LIVER, SIGNAL = 5	
	OTHER INFORMATION:	EXPRESSED IN HBL100, SIGNAL = 3.3	
	OTHER INFORMATION:	EXPRESSED IN HELA, SIGNAL = 3.2	
	OTHER INFORMATION:	EXPRESSED IN HEART, SIGNAL = 2.8	
	OTHER INFORMATION:	EXPRESSED IN LUNG, SIGNAL = 3.3	
	OTHER INFORMATION:	EXPRESSED IN BONE MARROW, SIGNAL = 4.8	
	OTHER INFORMATION:	EXPRESSED IN ADULT LIVER, SIGNAL = 3.6	
	OTHER INFORMATION:	EXPRESSED IN PLACENTA, SIGNAL = 3.6	
	US-09-864-761-1804		
Query Match	1.9%;	Score 51.8;	DB 10; Length 998;
Best Local Similarity	52.6%;	Pred. No. 5,6e-05;	Mismatches 113; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
DB	449	TTAGGATCTTCCAGCCTTGCTTCCTGTCTGGAAGAAGATGCCAAATAAGAGATT	886
OY	827	TTCCTATTTTTCGGCTTCCCTGCTACTGCGGAAAAGATGCCAAATAAGAGATT	886
DB	449	TTAGGATCTTCCAGCCTTGCTTCCTGTCTGGAAGAAGATGCCAAATAAGAGATT	390
OY	887	CTACATATGCAGATGCTCTGCTGGGCAACAATTACATTCGACCACTATGGCTATGGAG	946

Db	389	AAAGCATCCAGCCTTTCTGTGGGCCACCATGACTACTGTGGGTATGAG	330
OY	947	ACAAACTCCCTTACTTGGCTGGGAGATGCTTTGCAAGCTTTGCACCTCTTGGA	1006
Db	329	ACATCTACCCAGAGACTCTCCTGGGAAATGTTGGGGACTCTGTCATTCAGAG	270
OY	1007	TTCTTTCTTTGCACTTCCTGCGGCAATTTGGC	1041
Db	269	TCCTGGTATGCTCTTCCCATCCCATCATGTC	235

Search completed: June 19, 2003, 13:32:23
 Job time : 391 secs

101	43.4	1.6	68750	4	US-09-567-969-1	Sequence 1, Appl1
102	43.4	1.6	68750	4	US-09-568-480-1	Sequence 1, Appl1
103	43.4	1.6	68750	4	US-09-568-486-1	Sequence 1, Appl1
104	43.4	1.6	68750	4	US-09-568-472-1	Sequence 1, Appl1
105	43.4	1.6	68750	4	US-09-567-899-1	Sequence 1, Appl1
106	43	1.6	1805	1	US-07-955-916-6	Sequence 1, Appl1
107	43	1.6	2439	4	US-09-233-989-1	Sequence 6, Appl1
108	43	1.6	2443	1	US-08-452-362-1	Sequence 1, Appl1
109	43	1.6	2443	1	US-08-774-550-1	Sequence 1, Appl1
110	43	1.6	2443	5	PCT-US96-07528-1	Sequence 1, Appl1
111	43	1.6	8438	1	US-07-945-283-1	Sequence 1, Appl1
112	42.8	1.5	226	4	US-09-105-058C-9	Sequence 9, Appl1
113	42.8	1.5	696	4	US-09-220-528-2	Sequence 1, Appl1
114	42.8	1.5	696	4	US-08-483-533-36	Sequence 2, Appl1
115	42.8	1.5	1337	4	US-08-283-471A-36	Sequence 36, Appl1
116	42.8	1.5	1337	4	US-08-681-129-1	Sequence 36, Appl1
117	42.8	1.5	1578	1	US-09-220-528-68	Sequence 1, Appl1
118	42.8	1.5	1652	4	US-09-220-528-69	Sequence 68, Appl1
119	42.8	1.5	1652	4	US-09-220-528-69	Sequence 69, Appl1
120	42.6	1.5	2352	4	US-08-997-251-3	Sequence 3, Appl1
121	42.6	1.5	329	4	US-09-056-556-168	Sequence 168, App
122	42.6	1.5	329	4	US-09-072-596-163	Sequence 163, App
123	42.6	1.5	1056	4	US-09-524-162-1	Sequence 1, Appl1
124	42.6	1.5	1335	2	US-08-585-090-3	Sequence 1, Appl1
125	42.6	1.5	1335	3	US-09-165-543-1	Sequence 3, Appl1
126	42.6	1.5	2689	2	US-08-985-090-3	Sequence 1, Appl1
127	42.6	1.5	2689	4	US-09-165-543-1	Sequence 1, Appl1
128	42.6	1.5	5328	4	US-09-428-517-1	Sequence 15, Appl1
129	42.6	1.5	43380	2	US-08-804-227C-1	Sequence 1, Appl1
130	42.6	1.5	50937	4	US-09-428-517-1	Sequence 1, Appl1
131	42.4	1.5	4488	4	US-08-406-030-3	Sequence 1, Appl1
132	42.4	1.5	11219	1	US-07-642-734C-1	Sequence 1, Appl1
133	42.4	1.5	11219	3	US-08-439-009A-1	Sequence 1, Appl1
134	42.2	1.5	5011	1	US-08-141-893-1	Sequence 1, Appl1
135	42.2	1.5	5011	1	US-08-463-0928-1	Sequence 1, Appl1
136	42.2	1.5	5011	1	US-08-463-0928-3	Sequence 3, Appl1
137	42.2	1.5	5011	2	US-08-462-109A-1	Sequence 1, Appl1
138	42.2	1.5	5011	2	US-08-462-109A-3	Sequence 3, Appl1
139	42.2	1.5	5011	2	US-08-460-9078-3	Sequence 1, Appl1
140	42.2	1.5	5011	3	US-08-463-179A-1	Sequence 1, Appl1
141	42.2	1.5	5011	3	US-08-461-384A-1	Sequence 1, Appl1
142	42.2	1.5	5011	3	US-08-461-384B-3	Sequence 1, Appl1
143	42.2	1.5	5011	3	US-08-407-207A-1	Sequence 1, Appl1
144	42.2	1.5	5011	3	US-08-318-193-69	Sequence 69, Appl1
145	42.2	1.5	508	4	US-09-398-193-98	Sequence 98, Appl1
146	42	1.5	5515	4	US-08-785-420-1	Sequence 98, Appl1
147	42	1.5	15378	3	US-09-836-643A-9	Sequence 9, Appl1
148	41.8	1.5	3424	4	US-08-845-998-7	Sequence 7, Appl1
149	41.8	1.5	4524	2		
150	41.8	1.5				

```

RESULT 1
US-09-177-650-88
: Sequence 88, Application US/09177650
: Patent No. 6413719
:
: GENERAL INFORMATION:
: APPLICANT: Leppert, Mark F.
: APPLICANT: Singh, Nanda
: APPLICANT: Charlier, Carole
: TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
: TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
: TITLE OF INVENTION: AND OTHER EPILEPSIES
: FILE REFERENCE: 2323-134
: CURRENT APPLICATION NUMBER: US/09/177, 650
: CURRENT FILING DATE: 1998-10-23
: EARLIER APPLICATION NUMBER: 60/063,147
: EARLIER FILING DATE: 1997-10-24
: NUMBER OF SEQ ID NOS: 129
: SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
US-09-177-650-88

Query Match: 17.8%; Score 492.4; DB 4; Length 2273;
Best Local Similarity: 57.2%;
Pred. No. 5,3e-120;
Matches 1022; Conservative 2; Mismatches 665; Indels 99; Gaps 4

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Query Match	Best Local	Similarity	17.8%	Score	492.4	DB	4	Length	2273
Matches	1022	Conservative	2	Mismatches	665	Indels	99	Gaps	4
QY	169	GGCTTCCTACTGCTG6GACCCGCGCGGCACCTCGTGCGGCGCGGCTGAGG	228						
Db	67	GGCTTCGTGGGGGTGGACCCCGCGCGCCGAGNATCACAACGCGAGCGMCNCTACTCATC	126						
QY	229	GAGAGCCCGCGGGGACAGCAGGGGGCCGGATGAGCTCTGGGGAAGCCGCTCTTAC	288						
Db	127	GGGGGCTCCGAGGGCCGCCAAGGGCGGCACNNTTTAGCAAGCCGCGGACGGCGGCGG	186						
QY	289	ACGAGTAGCCAGAGCTGCGGGCGCAACGTCAGTACGCGGGGTGAGAACTACCTGTAC	348						
Db	187	GGANCCGGGAAGCCCCCNANANGCAACGCCCTTCTACCAAGCTGAGATTCCTCTAC	246						
QY	349	AACGTGCTGAGAGACCCCGCGGCTGGGCTTCATCTACACGCTTCGTTTTCTCCCT	408						
Db	247	AACGTGCTAGACGGCGCCCGCGGCTTGGGCTTCATCTACAGCGCTACGTCGTCG	306						
QY	409	GTCCTTGCTGCTGATTTTGTCAAGTCTTTTACCATCCCTGAGCACAANAATGGCC	468						
Db	307	GTTTTCTCGCTGCTTGTCTCTGTGTTTCACCATCAAGAGTACAGAAAGACCTT	366						
QY	469	TCAAATTGCTCTTAACTCTGAGTTCGATGATTTGCTGCTTGGTTTGGATTTATC	528						
Db	367	GAGGGGGCCCTTACATCTGGAATACTCGATCTACGTCGTCGTCGTCGTCGTCGTCG	426						
QY	529	ATTGCAATCTGCTGCGGGTTCGTGTGTCGATATAGAGATGAGCAAGAACTGAGG	588						
Db	427	GTAGAGATCTGGGCTGACAGGCTGCTGTGGCCGTCATGAGGCTGGAGGGGACGCTCAAG	486						
QY	589	TTTGTCTGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATGCTTCAATAGCACTT	648						
Db	487	TTTGCAGAGAACCCCTTCTGTGTGATTAATATCATGTCGTCGATTCCTCATTTCTGTG	546						
QY	649	GTTTTCGAAAAACACGAGGTAATTTTTTGGCAGCTCGACCTGACAGAGTCCGCTTC	708						
Db	547	CTGGTCTGCTGTTCCCAAGGCAATCTCTTGGCAATCTGCGCTTGGAGCTTGGGCTTC	606						
QY	709	CTACAGATCTCCCGCATGGTGGCATGAGACCGAAGGGGAGGCACTTGGAAATTAATCTGGGT	768						
Db	607	TTGCAAAATCTTGGCGATGATCCGTATGAGCCGAGGGGTGGCACTGAGAGCTCTGGGA	666						
QY	769	TCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTTGGTT	828						
Db	667	TGCGTAGTCTACGCTCACAGCAAGAGCTGGTAGCTGCTGGTACATTTGGCTTCTCTGCG	726						
QY	829	CTTATTTTTTGGCTCTTTCCTGTCATCTGATGAGGAAAAAGAAAGAAATTAAGAGTTTCT	888						
Db	727	CTCATCTCTGCGCTCATTTCTTGGTGTACTTGGCAGAAAAAGGTGAGAAATGACCACTTTAC	786						
QY	889	ACATATGCAATGCTCTCTGCTGGGAGCAATTAATCAATGAGCAATATGCTATGAGAGC	948						
Db	787	ACCTAGAGATGCACTCTGCTGGGGTGTATCAACCTGAGACCATTTGGCTACGGGAGC	846						
QY	949	AAAACTCCCTAACTTGGCTGGGAGATTCGTTCTGCGAGCTTTGCACTCTTGGCAAT	1008						
Db	847	AAGTACCTCTGAGACTGTGAGAGGAGGCTGTGACAGGACCTTACCTCATTTGGTGTCTC	906						
QY	1009	TCTTTCTTTGCACTTCTCGCGGCAATCTTGGCTCAGGTTTGGATTTAAAGTACAAGAA	1068						
Db	907	TGCTTTTGTCTCTTTCGCGCTGGATTTTGGGATTCGGCTTTGCCGTAAGTCCAAAGG	966						

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QY 1069 CAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCACCTCATTCAGTGT 1128
    || || || || || || || || || || || || || || || || || || || || || ||
Db 967 CACATCTGGGAAAACCTTTGAGAAAAGCGGAAACCTCGGGCAGGTCTGATTCAGTCT 1026
QY 1129 GTTTGGCGTAGTACGAGCTGAT----- 1152
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1027 GCCTGGAGATTCATGCTACTAACCTCTCACGCAACCCAGCTGCACTCCACGTCGAGTAC 1086
QY 1153 ----GAGAAATCTGTTTCCATTGCACTGGAAAGCCACACTTGAAGCCCTTGCACACTTC 1209
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1087 TAGAGAGGAAACACTGCTGCTCCATGTACAGTCCAAACTCAAAACCTATGCGGCTTC 1146
QY 1210 AGCCCTAC-----AATGAGAGCTAAGTTTAA 1237
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1147 AGACTCATCCCACTCTGTAACCACTGAGCTGCTGAGGAATCTCAAGACAAATCTGGA 1206
QY 1238 AGGAGCAGATGCGCATGCTGATGCCCCAGGGCCAGAGTATTAAAGACCGCAAGCCTGAC 1297
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1207 CTCACCTTCAGAGAGAGAGCCACAGCCAGAGCCATCACAAGCCCGGAGCATGCTGCC 1266
QY 1298 TAGGTGACAGAGAGTCCCCCAAGCACCCGATCAGAC----- 1334
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1267 AAGGGAAGAGGGGTCTCCCAAGCCAGAGCGGTCCGGCGTCCCAAGTGGGATAGAGT 1326
QY 1335 --CGAGGAGAGTCCCAAGAGTGCAGAGAGCTGAGCTTCAAGCAGCCAGCCGCTTC 1392
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1327 CTGATACAGAGCCGAGAGAGTGCACCAAGCTGAGAGTGTGGAGCCGAGCCGAGCA 1386
QY 1393 CGGCGCTGCTGCGCTTCAAAAGTTCAGCCAAAACAGATGATGATCTGACACAGCC 1452
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1387 CGCGAGAGCTTCCGATCAGAGGCTGCTATCCCGGAGAAATTCAGAAACCAAGCCATC 1446
QY 1453 CTGCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1447 CTTGGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
QY 1513 CTCACCCCAACCACTTAAACATGCTATTCAGCTATCAGATTAAGAAATTTGATGGA 1572
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1507 CTTACCCCTGCGCTCAAAAGTATAGATCAGAGCCGTGTGTATGATGATGATGATGATGATGAT 1566
QY 1573 AAACGGAATTTAAAGAAACATTTACGCTCATATGATTAAGAAAGTCTATTGACATAT 1632
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1567 AAGGGAAGTTCAAAGAGAGTCTGCGCCATATGATGATGATGATGATGATGATGATGATGAT 1626
QY 1633 TCTGCTGCTCATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1627 TCGGCTGAGACCTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
QY 1693 ATTCTTGAAGAGGCAATATCATCATTAAGAAAGCCAGAGAAATAATTAACAGCAGAA 1752
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1687 ATTGCGGGCGGGGCGCCCAACATATACGATTAAGAA--TCGCAACCAAGGCGCAGGGA 1743
QY 1753 CATGAGACCAAGAGATCTCATGATGCTCGGTGCGGTGCTCAAGTTGAAAAACAGGTA 1812
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1744 ACGGAGCTGCCCGAAGAGCCAGCATGATGAGGACGCTTGGGAGATGAGAAACAGGTC 1803
QY 1813 CAGTCCATAGAAATCCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1860
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Db 1804 TTGCTGAGGAAAGAGAGCTGAGCTTCTTGTGAGCATCTATACAG 1851

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; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
; US-09-105-058C-22

Query Match      17.3%  Score 478.8:  DB 4;  Length 2169;
Best Local Similarity 57.1%:  Pred. No. 2e-116;
Matches 1024:  Conservative 0;  Mismatches 662;  Indels 108;  Gaps 4;

QY 169 GGCCTGCTACTGCTGCGGACCCGCGGCGCCACGCTCGGTGGCGGGGCTGAGG 228
    || || || || || || || || || || || || || || || || || || || || || ||
Db 67 GGCCTGCTGGGGGCTGAGACCCCGGCGCCGACATCCACAGCGGAGCGGCTACTCATC 126
QY 229 GAGAGCCCGCGGCGCAAGCAGGGGGCCGATGAGCTGCTGGGGAACCCGCTCTTAC 288
    || || || || || || || || || || || || || || || || || || || || || ||
Db 127 GCGGGCTCCGAGAGCCCGCCAGCGGCGAGCGTCTTGAAGCAAGCCGAGCGGCGCG 186
QY 289 ACGAGTACAGAGACTCGCGCGCGAGCTCAAGTACCGCGGAGTACAGACTGATAC 348
    || || || || || || || || || || || || || || || || || || || || || ||
Db 187 GAGAGCCGGAAGCCCGCGAGAGCGAGCGCTTCTACAGAGCTGATCTCTAC 246
QY 349 AAGCTGCTGAGAGAGACCCCGGCGGCTGCTCATACCAAGCTTGTCTTCTCT 408
    || || || || || || || || || || || || || || || || || || || || || ||
Db 247 AAGCTGCTAGAGCGCGCGCGCGGCTGAGCTTCACTACAGCTGATGCTCTTAA 306
QY 409 GTCTTGTGCTGCTGATTTTGTCAAGTCTTCTACCACTCCCTGAGACACAAATTTGGCC 468
    || || || || || || || || || || || || || || || || || || || || || ||
Db 307 GTCTTGTGCTGCTGCTGCTTGTGCTTGTTCACATCAAGAGATGAGAGAGCTCT 366
QY 469 TCAAGTTCCTGCTGATCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 528
    || || || || || || || || || || || || || || || || || || || || || ||
Db 367 GAGGGGGCGCTCTACATCTTGGAAATCGTACATGATGATGATGATGATGATGATGATGATGAT 426
QY 529 ATTGGAATGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
    || || || || || || || || || || || || || || || || || || || || || ||
Db 427 GTGAGGATGCTGCGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
QY 589 TTTCTGGAAGACCCCTTGTGCTGATATGATATGATATGATATGATATGATATGATATGATATGAT 648
    || || || || || || || || || || || || || || || || || || || || || ||
Db 487 TTTCCAGGAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
QY 649 GTTCTGCAAAACATCAAGGTAATATTTTGGCACGCTGCACTGAGAGTCTCGCTTC 708
    || || || || || || || || || || || || || || || || || || || || || ||
Db 547 CTGCTGCTGCTTCCAGGGCAATGCTTGTGCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 709 CTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
    || || || || || || || || || || || || || || || || || || || || || ||
Db 607 TTGCAAAATCTGCGATGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
QY 769 TCACTGCTTATGCTCAAGAGAGAAATTAATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
    || || || || || || || || || || || || || || || || || || || || || ||
Db 667 TCGGTAGCTTACGCTCAGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
QY 829 CTTATTTTCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888
    || || || || || || || || || || || || || || || || || || || || || ||
Db 727 CTGATCTCGGCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 889 ACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
    || || || || || || || || || || || || || || || || || || || || || ||
Db 787 ACTAGCAGATGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 949 AAAATCCCTTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
    || || || || || || || || || || || || || || || || || || || || || ||
Db 847 AAGTACCTCAGACCTGGAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906

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RESULT 2

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US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blamir, Michael A.
; APPLICANT: Dmowski, Steven
; APPLICANT: Glibkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-pin

```

OY	1009	TCCTTCTTGGACCTCCGCGGGGCAATCTGTGGCTCAGCTTTTGGCATTAAGTACAGAA	108
Db	907	TCGTTCTTTGCTCTTCTGCTGGCATTTTGGGATCCGGCTGGCTCCCTGCAAACTCCAAAG	966
OY	1069	CAACACCGCCAGAAAACACTTTTGAGAAAAGAAAGAACCCAGCTGCCAACTCCATTCAGTGT	1122
Db	967	CAGCATCGGCAAAAACACTTTTGAGAAAGCGGGAACCCCTGCGGCAAGTGTGATCCAGTCT	1022
OY	1129	GTTTGGCGTAGTTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCCACAC	1188
Db	1027	GCCGTGGAATTTCTATGCTACTTAACCTTCACGACCCGACCTGCTCACTCCACGTGGAGTAC	1088
OY	1189	T-----	1188
Db	1087	TACGAGCGGACAGTCACGTCTCCCATGTACAGACTATCCACTTCGAAACCGAGCTGAG	1144
OY	1190	-----TGAGGCCCTTGGACACCTGC	1209
Db	1147	CTGCTGAGGAATCTCAGAGCAAACTCTGGACTCACTTCAGGAAGAGGACACAGCCAGAG	1208
OY	1210	AGCCCTACCAATCAGAGCTAAGTTTAAAGACGAG--TGCGCATGGTACGCCACAG	1266
Db	1207	CCATCACCMAATCGAAGAGGTGATGTTGAAAGATCGTCTCTTCTCCAGCCCCGAGGCAATG	1266
OY	1267	GGCCAGATATTAAAGAGCCGCAAGACCTCAGTAGGTGACAGAGGTCCCCAGCACCGAC	1322
Db	1267	GCTGCCAAGGSAAGGGGTCTCCCAAGGCCAGAGAGGTCCGGGGTCCCCCAGTGGCAT	1322
OY	1327	ATCAGACGCGAGGGGCAATCCCAACCAATGCGAGAGACTGAGAGTTCAAGACCGCAAC	1388
Db	1327	CAGAGTCTTGAATGACAGCCCAAGAGAGGTGCCCAAGAGCTGAGCTTTGGTGAACCGCAGC	1388
OY	1387	CGCTTCGGGCCCCCTGCTGCGGCTCAAAAGTTCTAGCCCAACAGTAGTAGTACTGAC	1448
Db	1387	CGCACAGCGCCAGGCTTCCGATCAAGGGTCTGTGATCCCGGAGCAATTCAGAGACGAC	1448
OY	1447	ACAGCCCTTGGCACTGATGATGTATATGATAAAAAGATGCCAGTGTGATGATCACTG	1506
Db	1447	C---TCCCTGGGAGGACATGTAAGAGCAACAAGACCTTAATCTGCAATTTGTGTACT	1503
OY	1507	GAAAGACCTCACCCACCACTTAAACTGTCAATTCGAGCTATCAGAAATTAAGAAATTCAT	1566
Db	1504	GAAATCTTACCCCTGGGCTCAAAAGTTAGCATCAGAGCTGTGTGTGTTATGCGGTTCTTG	1563
OY	1567	GTTGCAAAAAGGGAAGTTAAGAAAACATTAAGTCAATATGATGTAAAAAGATGATTTGAA	1628
Db	1564	GTATCTAAGGCAAGATTCAAAGAGAGAGTCCGCAATATGATGTAGTAGAGTCAATGAA	1623
OY	1627	CAATATTCCTGTGTCATCTGAGACATGTGTGTGAAATTAAGACCTTCAAAACAGTGT	1686
Db	1624	CAGTACTCTGGGTGACACTTGGGATATGTGTCCCGCATCAAGACCTGCACTCCAGAGTG	1683
OY	1687	GATCAAAATTTCTGGAAGAAAGGCAAAATCAATCAATTAAGAAAGACCCGAGCAAAATAACA	1746
Db	1684	GACCAAGATTGGGGGGGGGGCCCAACAATTAAGSATTAAAG--TCCGACCAAAAGGCCCA	1740
OY	1747	GCAGAACATGAGACCAAGAGATCTCAGTAGTCTGCTGGGTGATCAAGGTTGAAAAA	1806
Db	1741	GCAGAAACGAGAGCTGCCGAAAGACCCAGCATATGATGAGAGCGCTTGGGAAGGTGAGAAA	1800
OY	1807	CAGGTACAGTCCATAGAAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAG	1860
Db	1801	CAGGTCTTGTCCATGAAAGAAAGACCTGACTTCTTGGTGAACATCTATACACAT	1854

```

1  APPLICANT: Grilckoff, Valentin K.
2  APPLICANT: Levesque, Paul C.
3  APPLICANT: Little, Wayne A.
4  APPLICANT: Neubauer, Michael G.
5  APPLICANT: Yang, Wen-Pin
6  TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
7  FILE REFERENCE: 3053-4052
8  CURRENT APPLICATION NUMBER: US/09/105,058C
9  CURRENT FILING DATE: 1998-06-26
10 PRIOR APPLICATION NUMBER: US 60/055,599
11 PRIOR FILING DATE: 1997-08-12
12 NUMBER OF SEQ ID NOS: 28
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 1
15
16 LENGTH: 896
17
18 TYPE: DNA
19
20 ORGANISM: Artificial Sequence
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22 FEATURE:
23
24 OTHER INFORMATION: Description of Artificial Sequence:Consensus
25 OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
26 OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
27 OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
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Query Match	16.8%;	Score 465.4;	DB 4;	Length 896;
Best Local Similarity	53.7%;	Pred. No. 4.3e-113;		
Matches 460;	Conservative 231;	Mismatches 162;	Indels 4;	Gaps 2;

QY	295	ACCCAGAGCGTGGCGGGGACATCAAGTACGCGGGGGGTCCAGAACTACCTGTACAAACG	354
Db	13	RSMSMCCMSYTAAGKMAACCCMMWSTACCSMSMTSCARMMTTSMTCTACRAGYS	72
QY	355	CTGAGAGAGACCCCGGGGCTGGGCGTTCATCTACCAACGCTTGTGTTTCTCCGTCTT	414
Db	73	CTRGAAGMRCSCSGSGCTGGCGGYTSMYTCACCAAGCTSGWSGTGTCTBHTDYYYS	132
QY	415	GGTTCCTGATTTTTCMGAGTGTTCCTACCATCCCTGAGACACAAATTTGGCCCTCACT	474
Db	133	KSTGCTBYRKYCTKCTCTGTS-YKMCACAMTTCAGGAATAAGAGAMKKRYTCBRRGHS	191
QY	475	TGCCCTTGATCCTCGAGTTCGTGATGATATGTCGATTCGTTTGGAGTTCATCAATCGA	534
Db	192	KSSCTYYMSWMTYTGARAYMKTKRCAYATYKTSRVTYTGHGIBGAGWYRYTYTGMR	251
QY	535	ATCTGCTCGCGGGTCTGTTGTGATATAGAGATGGCAAGAACTGAGTTTGGCT	594
Db	252	ATCTGGGCGCGMTGYTSYTCGGRACMMGCTGGGGGGGSMGRTCSAAGTTCGCC	311
QY	595	CGAAGACCCCTTGTGTATAGATACCAATGTTCCTTATCGCTCAATAGCAATGTTCCT	654
Db	312	MGAARCCVCTGYRTGMTBAYATCMTKKGICTSATYGGCTCYRTSCBDSGTGKCY	371
QY	655	GCAAAACTCAGGGTAATATATTTTCCACAGTCTGCATCAGAAAGTCCGTTTCCTAACG	714
Db	372	GYBGHMMWCCARGGCAAGYATYTKCYACVTCY--CTBCGNAAGCYTSCGSTTCYTRCAR	428
QY	715	ATCCGCCCATAGTTCGCGATGAGCCAGGAAGGGGAGCCACTGTGAAATTCATGGGTCCAGMG	774
Db	429	ATYTRGCSATGMSCSGATGTGACCGGMRGSHGCACCTGSAAGCTBYTGGMTCDDIV	488
QY	775	GTTTATGCTCACAGCAAGCAATTAATCACAGCTTGGAATATGAAATTTTGGTCTTATTT	834
Db	489	RTCTRYGCGYCAAGCAARGARTSRTSACKCSGTGTCATATYAGGYTCTCTBMSHCTCANC	548
QY	835	TTTTGCTTCCCTTGCTATCTGTTGGTGAAGAAAGATATGCCAATMAAGATTTTTCATAT	894
Db	549	CTKCYTDRITTYCTKGTSTACTTGGYWARARSSDGAHMBGAISSMTTYYGASACCTAY	608
QY	895	GCAGATGCTCTGTGGGGGACAAATTCATTTGACAATATTTGGTATAGAGACAAACT	954
Db	609	GCAGATGCMCHSTGSGGGGCGYCTGATCAVCYTGKRVACATTTGGTATAGGAGACAAGMM	668
QY	955	CCCCTAATTGGCTGGGAAGATTGCTTCTTCAGAGCTTTCGCATCTCCTTGCAATTTCTTTC	1014

Db	669	CCYARACSTGGRAMGSGMKCSTHTDGCVCACASTTYMCCYMAHYGGTGTCTCVTTY	728
Qy	1015	TTTGCACCTTCCCTGCCGGCATTCCTTGCGTCAGGTTTTCATTAAAGTACAAACACAC	1074
Db	729	TTTGCBCCTCKMGCDGGCATYTTTGCGRCYGGSTTKGGCCCSAARGTBCAAGACARAY	788
Qy	1075	CGCCAGAAACCTTTGAGAAAAAGAAACCCAGCTGCCACCTATTCAGTGTGTTGG	1134
Db	789	MGRKARAARCACTTTGAGAAAMGGMGABCCDGCDCGWRBCTSATYCAKCKKCCITGG	848
Qy	1135	CGTAGTTACGACGCTGA	1151
Db	849	AGRTWYTAIGCYACATA	865

```

RESULT 4
US-09-177-650-6
: Sequence 6, Application US/09177650
: Patent No. 6413719
: GENERAL INFORMATION:
: APPLICANT: Leppert, Mark F.
: APPLICANT: Singh, Nanda
: APPLICANT: Charlier, Carole
: TITLE OF INVENTION: KCON2 AND KCON3 - POTASSIUM CHANNEL GENES WHICH ARE
: TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
: TITLE OF INVENTION: AND OTHER EPILEPSIES
: FILE REFERENCE: 2323-134
: CURRENT APPLICATION NUMBER: US/09/177.650
: CURRENT FILING DATE: 1998-10-23
: EARLIER APPLICATION NUMBER: 60/063,147
: EARLIER FILING DATE: 1997-10-24
: NUMBER OF SEQ ID NOS: 129
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 2914
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (19)..(2634)
: FEATURE:
: NAME/KEY: allele
: LOCATION: (840)
: OTHER INFORMATION: The polymorphism of a T to a C at this position
: OTHER INFORMATION: has appeared in one individual.
: FEATURE:
: NAME/KEY: mutation
: LOCATION: (947)
: OTHER INFORMATION: The missense mutation from a G to a T occurs at
: OTHER INFORMATION: this position in a BFNC family.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (678)
: OTHER INFORMATION: This position is polymorphic for C or T.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (750)
: OTHER INFORMATION: This position is polymorphic for T or C.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (1089)
: OTHER INFORMATION: This position is polymorphic for G or C.
: FEATURE:
: NAME/KEY: allele
: LOCATION: (2598)
: OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Query Match      15.8%; Score 438.2; DB 4: Length 2914;
Best local Similarity 56.6%; Pred. No. 12e-105;
Matches 967; Conservative 0; Mismatches 683; Indels 59; Gaps 6

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QY	35	CGCCGGGCTCTGGGGTGAAGAGCGGCGAGCGGGGGCGGGCGGGGGGGCGCTTTGGG	98
Db	34	CGAGGGGGGGGGGGGGCGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	93
QY	99	CAGGCGCATGAAGAGATGTGGAGTGGGGCGCGG--GGCAGGGTGGCTGGTAATCGCAGCC	156
Db	94	GCTAACCCAGCCGGAGGGAGACGCGCGCGCGCGCGACAGAGAGGGGAAGTGGGGCTTG	153
QY	157	GCCAGGGGGCAGGGCGCTGCTACTGCTGGGACACCCGGCGGGCACGCTGGTGGCGGGC	216
Db	154	GGCGCCGGCGACGTGGAGAGCAAGTCACTTGGCGGCTCGGGGCGCGAGCGCAAAAGACGG	213
QY	217	GGTGGCTGAGGGAGAGACCCCGGGGGACAGACGGGGGCCGGAGTGAAGCTGGCGGGGAAG	276
Db	214	ACCCTGTGCTGGAGGGGGGGCGGGCGGACAGGGGGAGCGAGGGAGACCCGCGAGGGATC	273
QY	277	CCGCTCTCTTACAGAGTGAAGCAAGCGTCCG-----GGGCAACGCTCAAGTACCG	327
Db	274	GGGCTCTGGGCGCAAGACCCCGCTAGCGCGCCCACTCAAGAGAAACACAGCCAGTACCG	333
QY	328	CGGGTGCAAGACTACCTGTATACACAGTGTGTGAGAGACCCCGGGGCTGGCTTCATCTAC	387
Db	334	CGCATCCAACTTTGATCTACAGACGCCCTGGAGAGACCGGGGGCTGGGCGCTGTCTTAC	393
QY	388	CACGCTTTCGTTTTCTCTCTGTCTTTGGTGGTGTGATTTGTTCAGTGTTTCTACATC	447
Db	394	CACGGTGTGGTTCCTGATTTGTCTGGTGGGCTGTGATTCGGCTGTCTGACCAATTC	453
QY	448	CCTGAGCACAAATAATGGGCTCAAGTGGCTTGATTCGGAGTTCGATGATGTG	507
Db	454	AAGGAGTATGAGACTGTCTCGGAGACTGGCTTCTGTACTGGAGACATTTGCTATTTC	513
QY	508	GTCCTTGGTTTGAAGTATCATTCAGATTCGATGTGTGTGGGGTTGCTGTGCATATAGA	567
Db	514	ATCTTTGAGCGAGTTGTTGTTGAGATCTCGGGCTGTGGATGTGTGCTGGCATACAA	573
QY	568	GGAGGCAAGAGAACTGAGTGTGTGCTGGAAGCCCTTCTGTATATAGATCAATTTGT	627
Db	574	GGCTTGGCGGGGGCGGCTAGTGTGTGCCAGGAAGCCCTGTGCATGTTGGAACTTTGTG	633
QY	628	CTTATCGGTTCAATGAGAGTGTGTGTGCCAAAACCTCAGGGTATATTTTGGCACGCT	687
Db	634	CTGATTTGCTCTGTGCCAGTGGTGTCTTGGGAAACCAAGGCAATTTCTGGCCACT--	691
QY	688	GCACCTCAAGAGTCTCCGTTTCTCAAGATCCCTCGCATGTGCGCATGGACCGAAGGGGA	747
Db	692	-CCCTGGCAGAGCTCGCTTCTCTGAGATCTCGGCAATCGTGGGATGGAGCGGAGAGGT	750
QY	748	GGCAGCTGGAATTAAGTGGGTCAAGTGTATGTCTACAGACAGGAATTAATCAAGCT	807
Db	751	GGCAGCTGGAAGCTCTGGGGCTACAGCCATCTGTGGCCCAACAAAGAACTATCAACGGC	810
QY	808	TGGTACATAGAAATTTTGGTCTTATTTTTCGCTTCCCTGGTCTATCTGGTGGAAAG	867
Db	811	TGGTACATCGGTTTCTTGACACTCACTCTTCTTATTTCTGTCTACCTGGTGGAGAA	870
QY	868	GATGCC-----ATAAAGATTTTCTACATATGCA	897
Db	871	GAGCTCCCAAGAGTGGATGACACAGAGAGAGATGAAGAGAGATTGAGAACTATGCA	930
QY	898	GATGCTCTGTGGTGGGGACAATTAATTAACAACTATGTGCTATGAGACAAACTGCC	957
Db	931	GATGCCCTGTGGTGGGGCTGTGATCACTAGTGGCCACCAATTTGGCTATGGAGCAACACC	990
QY	958	CTAAGCTGGCTGGGAAGATGCTTCTGACAGGCTTGGACGTCCTTGGCATTTCTTCTT	1017
Db	991	AAAGCTGGAGAGCGCTGTATTTCCGCCACCTTTTCTTAATTTGGCTCTCTTTT	1050
QY	1018	GCATTTCCGCGCGCATCTTGGGCTCAGGTTTGTGATTAAGTACAAGAACACACGC	1077
Db	1051	GCCCTTCCAGCGGGCATCTGGGGTCCGGGGTCCGACCAAGTGGACAGAACACACCGT	1110
QY	1078	CAGAAACACTTTGAGAAAAAGAGAACCCAGCTGCCAACTTCATCTAGTGTGTTGGCGT	1137

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Db 1111 CAGAGCACTTGTAGAAAAGAGAGCCAGCTGCTGATTCATTCAGGCTGCGTGGAG 1170
QY 1138 AGTTACGACGCTGATGAGAAATCTGTTCCATTCG-----CAACCTGGAAGCCACAC 1188
Db 1171 TATTATGCTACCAACCCCAAGAGATTCAGCTGTGGCGACATGAGATTTTATGAATCA 1230
QY 1189 TTGAAGCCCTTGCACACCTGACGCCCTTACCATCAGAAAGCTTAAGTTTAAGGACGAGT 1248
Db 1231 GTCGCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1290
QY 1249 CGCATGCTAGCCCAAGGGCCAGAGTATTAGAGCCGACAGCCCTCAGTAGTGACAG 1308
Db 1291 GGTCTCTTGGATCGGGGCTTCCCTTCTTAATCCCTGTGTAGCAATACTAAAGGAAGCTA 1350
QY 1309 AGTTCGCCAGACGACATCAACAGCCGAGGGAGGAGTCCCAAAAGTGCAGAAAGCTGG 1368
Db 1351 TTTACCCCTTGAATGTAGATGCTCATAGAAAGATCTTCTTAAGAAACCAAGCCCTGTT 1410
QY 1369 AGCTTCAACGACCGAACCCTTCGCGCCCTGCTGCGCTCAAAAAGTTCTCAGCCAAA 1428
Db 1411 GGCCTTAACAAATTAAGAGGCTTTCGCGACGCGCTTCCGATGAAGCTTACGCTTCTGG 1470
QY 1429 CCACTGATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGATGC 1488
Db 1471 CAGAGTCTGAAGATGCGGAGAGTGAACCCCATGGCGAA-----GACAGGGCTAT 1524
QY 1489 CAGTGTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1548
Db 1525 GGGATGATGCTTCCCATGAGACATGATCCCATCCCTGAGAGCCGCGCATCCGAGCCCTG 1584
QY 1549 AGAATTTATGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1608
Db 1585 AGAATTTATGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1644
QY 1609 GTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1668
Db 1645 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1704
QY 1669 AGCCTTCAACACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1697
Db 1705 TACCTTCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1733

RESULT 5
US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BRNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)..(2811)
US-09-177-650-90

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Query Match 15.6%; Score 432; DB 4; Length 2814;
 Best Local Similarity 56.7%; Pred. No. 5e-104;

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Matches 962; Conservative 3; Mismatches 673; Indels 58; Gaps 7;
QY 50 GGGTGAAGAGCGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 109
Db 225 GCGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 284
QY 110 AGGATGTGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 169
Db 285 AGG-GGAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 343
QY 170 GCGTGTACTGTGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229
Db 344 TGGAGGAAGTACACTTGGCGCTAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 403
QY 230 AGAGCCGCGGGGCGAAGCAGAGGGGGCGGATGAGCTGTGTTGGGAGGCGCTCTTCTTACA 289
Db 404 AGGGCGGTGGCGCGCGAAGAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
QY 290 CGAGTAGCGAGACTCGC-----GGCGCAACGTCAAGTACCGGGGGGGTGCAGACT 340
Db 464 AGACCCCTTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 523
QY 341 AACTGTACAACTGCTGAGAGAGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 400
Db 524 TGATCTATGACGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
QY 401 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 460
Db 584 TCTTGATTTCTTGGAGATGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 643
QY 461 AATTTGCTCAAGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 520
Db 644 CTGTCTGTGAGAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 703
QY 521 AGTTATCAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
Db 704 AGTTGCTTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
QY 581 GACTGAGTTTGTGCAAGAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 640
Db 764 GCTTAAGTTTGTGCAAGAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 823
QY 641 TAGAGTTTCTTGTCAAAACTCAGGGTAAATATTTTGTGCAAGCTGCACTCAAGATC 700
Db 824 TCCAGATGTTGCGCGTGGGAAACAGAGCAATGCTTGGCCACT---CCCTGGGAAGCC 880
QY 701 TCCGTTTCTAAGATTCCTCCGATGCTGCGCATGACCGAAGGGAGGACCTTGGAAAT 760
Db 881 TTGCGCTTCTGAGATTCCTGCGCATGCTTGAATGATGAGAGGGGTGGCACCTGGAAGC 940
QY 761 TACTGGTTCACTGTTTATGCTCACAGCAAGGAATTAATCAACGCTTGTATCATATGAT 820
Db 941 TCTTGCGCTGCTATCTTCTGCGCACAGCAAAACATCAATCACTGCTGGTATGATGATG 1000
QY 821 TTTTGGTTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 871
Db 1001 TCTTGCACTATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1060
QY 872 -----CCAATAAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 910
Db 1061 TGGATGCCCAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120
QY 911 GGGGCAATATTCATTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970
Db 1121 GGGGCTGATATCACTGCGCACACATTTGATATGAGACRAGACCTTAATAACCTGGGAAG 1180
QY 971 GAAGATGCTTCTTCAAGGCTTTCGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1030
Db 1181 GAGCTGATGCTGCGCACCTTTCTTATATGCGGCTCTCTTTTGGCTTCCGCGAG 1240
QY 1031 GCATTTCTGGCTCAGGTTTTCATTAAGATACAGACACACCGCGAGAAACCTTTG 1090
Db 1241 GCATCTTTGGCTCAGGACTGGACATGAAGTTTCAGAGACAGCACCGCTCAAGAACACTTTG 1300

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QY 1091 AGAAGAAGGAGCCAGTCCCAACCTCATTCAGTGTGGCGTATGACGAGCTG 1150
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Db 1301 AGAAGAAGGAGGAGCCAGTCCCAACCTCATTCAGTGTGGCGTATGACGAGCTG 1360
QY 1151 A--TGAGAATCTGTTTCCATTCAGTGTGGCGTATGACGAGCTG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1361 ACCCAACAGAGTGTGATCTGTGGCGTATGAGATCTTATGAAATCAGTGTGCTTCC 1420
QY 1202 ACACCTGCAGCCCTACCATCAGAGTAACTTTAAGAGCGAGTGGCGTATGAC 1261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1421 CATTTCTTCAGGAAAGAACTGTGACAGCAGCAGCAGCAAAAGCTGTGCTTGAATC 1480
QY 1262 CCAGGGGCGGAGGATTAAGAGCGGACAGCAGCAGCAGCAGGAGTGGCGTATGAC 1321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1481 GGGTGTGCTTTTCTTATCTCTGTGTGAGTAAAGTAAAGTAAATTTACCTTGA 1540
QY 1322 CCAGCATCAGAGCGGAGGAGTCCCAAAAGTGCAGAGAGTGTGAGCTTCAACGAGC 1381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1541 ATGTAGATGCGATAGAGAAAGGCTTCCAAAGAGCCAGCAGTGTGCTTAAACATA 1600
QY 1382 GAACCGGCTTCCGCGCTGCTGCTGCTCAAAAGTCTCAGCCAAACAGTATGATG 1441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1601 AAGAGGCTTCCGAGCGCTTCCGATGAAGGCTTCTGCGCAGAGTCTGAG 1660
QY 1442 CTGACACAGCGCTTGGCAGTATGATGATGATGATGATGATGATGATGATGAT 1501
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Db 1661 ATCTGGGAGACAGCGAGCCAGTCA-----GAAGACAGGCGCTATGAGTCACTGCTC 1714
QY 1502 CAGTGAAGACCTCAGCCCAACCTTAACCTGATTCAGTATGAGTATGAGTATGAGT 1561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1715 TCATTTGAGACATGATGCTTCCCTTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1774
QY 1562 TTGATGTGCAAAAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1775 TCGCTCTATATATAAAAGTCAAGAGAGGAGGCTGATGATGATGATGATGATGATGAT 1834
QY 1622 TTGACATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1835 TTGAGCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1894
QY 1682 GTGTTGATCAATCT 1697
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1895 GAATGATATGATTTT 1910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCON2 AND KCON3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation

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; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred K1504.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1591)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1846)
; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1469)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K1525.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1094)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K4443.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1125)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K4516.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (2736)..(2737)
; OTHER INFORMATION: There is an insertion of GGGCC between these two
; OTHER INFORMATION: nucleotides in K3963.
US-09-177-650-1

Query Match 15.5%; Score 429.4; DB 4; Length 3232;
Best Local Similarity 61.5%; Pred. No. 2,6e-103;
Matches 707; Conservative 0; Mismatches 436; Indels 6; Gaps 1;

QY 3 GCCCGCCACACCGGAGAGAGAGGCGCGCGCGCGCTCTGCTGGAAGAGCGG 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 GCATGCGGCTCCGCGCGGCGCGCTGCGTGGGCGCGCGCGCGCGCGCGCTCGC 81
QY 63 CGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 141
QY 123 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 GCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 201
QY 177 ACTGCTGGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 202 GGGCGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 261
QY 237 CCGGCGCAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321

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Db	802	CTATGGCCACAGCAAGGAGCTGGTCACTGCCTGGTAACTGGCTTCCCTTTGTCATCCT	861
QY	837	TTGCTCTTTCTCTTCTATCTGGTGGAAAGAGATGCCAATTAAGAGTTTCTACATATGC	896
Db	862	GGCCTCGCTCTCTGGTGTACTTGGGAGAGAAAGGGGAGAAACACCACCTTTGACACCTACGC	921
QY	897	AGATGCTCTCGTGGGGGACAAATTAATTAATACAACTATTTGGCTATGGAGACAAACATCC	956
Db	922	GGATGGCACTCTGGTGGGGCCCTGATCAGCAGCTTACCAACCATTTGGCTACGGGGACAAAGTACC	981
QY	957	CCTAACCTGGCTGGGAAGATTGCTTTTTCAGAGCTTTGCACTCTTGGCAATTTCTTCTT	1016
Db	982	CCAAACCTGGGAACGGCAGGCTCCTTTGGGGCCAACTCCTCATCGGTGCTCTCTTCTT	1041
QY	1017	TGCACTCTCTGCGCGCATTTCTTGGCTCAGTTTGGCATTTAAAGTACAAGAACCAACACCG	1076
Db	1042	CGCGCTCTGCTCAGAGCATCTTGGGGGTCTGGGTTTGCCCTGAAGGTTTCAGAGGACAGACACAG	1101
QY	1077	CCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAATCTCAATCAGTGTGTTGGCG	1136
Db	1102	GCAGAAACACTTTTGAAGAGAGGCGGAACCCGGCAGAGGCGCTGATCCAGTGGCGCTGGAG	1161
QY	1137	TAGTTACGC	1145
Db	1162	ATTCTACGC	1170

RESULT 8
US-09-105-058C-26

```

Sequence 26 Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blamar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-pin
TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 2565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-105-058C-26

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Query Match	15.5%	Score 428.8;	DB 4;	Length 2565;
Best Local Similarity	56.8%	Pred. No. 3.3e-103;		
Matches 924; Conservative	0;	Mismatches 647;	Indels 57;	Gaps 5

[illegible]

QY	349	AACGCTGAGAGACCCCGGGGGGCTTCATCTCCACGAGCTTCCTTCCTT	408
Db	283	GAGCGCCCTGGAGAGACCCGGGGCTGGGCGCTCTTACACGCTTGGTCTGATT	342
QY	409	GTCCTTGGTGGCTGATTTTGTCACTGTTTTCTACCATCCCTGAGCACAAATTTGGCC	468
Db	343	GTCTGGGGGTGCTGATTCTGTGCTCTCCGACCACTCAAGAGATGAGACTCTCG	402
QY	469	TCAAGTGGCTCTTATCTCGAGTCTCGATGATTGTCGCTTGGTTTGGAGTTTCACT	528
Db	403	GGAGACTGGCTTCCTTACTGGAGACATTTGCTATTTTCACTTTTGGAGCCGAGTTTGGCT	462
QY	529	ATTCAAACTGGTCTGCGGGTTCCTGTTTGCATATAGAGATGGCAGAGAACTGAG	588
Db	463	TTGAGGATCTGGGCGTGTGATGTTGTGCGGATATCAAAAGGTGGCGGGCGAGTAAG	522
QY	589	TTTGCTCGAAAGCCCTTCTGTGTTTAAATATACATTTGTTCTTATCGCTTCAATAGCACTT	648
Db	533	TTTGGCAGGAAGCCCTGTGCATGTTGGACATCTTTGGCTGATTTGCCCTGTGGCAATG	582
QY	649	GTTCCTGCAAAAACTCAGAGGTAAATTTTGGACAGCTGTCAGACTAGAACTCCGTTTC	708
Db	583	GTTGCTGTGGGAACCAAGCAATGTTCTGGCCACT---CCCTCGAAAGCTGGGCTTC	639
QY	709	CTACAGATCTCTCCGATGGTGGCATGAGACCGAAGGGAGGCACTTGGAAATTAATCTGGGT	768
Db	640	CTGCAGATCTTCGCACTGCTGGAGTGAACCGGAAGGTGGCACTGGAAAGCTTGGGGC	699
QY	769	TCAGTGGTTTATGCTCACAGCAAGGAATTAATACAGCTGGTACATAGAAATTTTGGTT	828
Db	700	TCAGCAATCTGGCCACAGCAAAACATCACTACAGGCTGGTACATGGATTCTCTGACA	759
QY	829	CTTATTTTTCGTCCTTTCCTCTGCTCATCTGATGGTGAAGAGATGCC-----	873
Db	760	CTCATCTTCTCTCATTTCTGTCTTACCGTGTGAAGAGAGCTCCAGAGGTGATGCA	819
QY	874	-----AATBAAGATTTTCTATCATATGCAAGATGCTCTCTGGTGGGACACA	918
Db	820	CAAGGAGAGAGATGAAGAGAGATTTGAGACTATGAGAGACCTGTGGTGGGGCCTG	879
QY	919	ATTACATTGACAACTATTGGCTATGAGAGCAAAACTCCCTCACTTGGCTGGAGATTTG	978
Db	880	ATCACAATCTGGCCACTATGGCTATGTAGAGACAAAGACACCMAAACGTGGGAAGCGGTCTG	939
QY	979	CTTTCTGACAGGCTTTGCACTCCCTTGGCACTTCTTTCTTGGCACTTCTGCGGCAATCTT	1033
Db	940	ATTGCGCGCACTTTTCCCTTAATTTGGCGCTCTCTTTTGGCCCTTCCAGCGGGCACTCTG	999
QY	1039	GGCTCAGGTTTGGCAATTAAGTATACAAGAAACAACCGGCANAAACACTTTGAGAAAGA	1099
Db	1000	GGGTCCGGGGCTGGCCCTCAAGGTGACGAGGACACACCGCTCABACACACTTTGTAGAAAGG	1055
QY	1099	AGGAACCCAGCTGCCCAACTCATTCATAGTGTGTTTTGGCGTATGTTACGCAAGCTGATAGAAA	1155
Db	1060	AGGAAGCCAGCTGTGTAGCTCATTCAGGCTGCCGTGGAAGGTATTTGTATCCAAACCCCAAC	1111
QY	1159	TCTGTTTCCATTG-----CAACCTGGAAGCCACACTTAAAGGCTTGGACACTCG	1205
Db	1120	AGGATTTGACCTGTGGGCGACATGGAGATTTTGTGATCAGTGTCTTTTTCCTTTCTTC	1177
QY	1210	AGCCCTACCAATCAGAGCTAGTTTTTAAAGAGCGAATGGCGATGGCTAGCCCAAGGGCC	1266
Db	1180	AGGAAGAAGCACTGGAGGCAAGCATTCAGCCCAAAAGCTGTGCTCTTGTGATCGGGTTGCG	1233
QY	1270	CAGAGTATTAAAGCGCGACAGACCTCATAGTGTGAAGAGGTTCCCAAGACCGCAATC	1322
Db	1240	CTTTCTAATTCCTGCTGTGTAGCAATTAATTAAGAAAGACTATTTACCCCTCTGATATAGAT	1299
QY	1330	ACAGCCGAGGCGATGCCACCAAAAGTGCAGAAAGACTGGAAGTCTAAAGACCGAAGCCCGC	1389
Db	1300	GCCATTAGAAAGAAAGTCTTTCTTAAGAACCAACCAAGGCTGTTGGCTTTAAACAATTAAGAGGCT	1355


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-09-105-058C-3

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Query Match      15.2%; Score 421.4; DB 4; Length 900;
Best Local Similarity 68.7%; Pred. No. 1.7e-101;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

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QY 299 AGAGTCCGCGGCAAGTACAGTACGCGGCGGCGAGCACTACTGACACGCTGCG 358
DB 17 AGCCCCCAAGCCAGCCAGCTTACCGCAAGCTGCAAAATTCCTTACACGCTGCG 76
QY 359 AGAGACCCGCGGCGCTGGCGCTTACATACACGCTTCTGTTCTCTGCTTGGTT 418
DB 77 AGCGGCGCGGCGCTGGCGCTTATACACGCGCTACGCTTCTGCTGCTTCTCTCT 136
QY 419 GCTTGAATTTGTAGTGTCTTACATCCCTGACACACAAATTTGGCTCAAGTTGCC 478
DB 137 GCTCGTGTGCTGTGTGTTCACCAAGAGTATGAGAGAGCTCGGAGGGGCCCC 196
QY 479 TCTTGAATCCGAGTGTGATGATGTGTGCTTGTGGTTGGAGTATCATTTGGAATCT 538
DB 197 TCTACATTCCTGGAATGCTGACTATGCTGTGTGTGGCTGAGAGTACTTCTGCGGATCT 256
QY 539 GGTCTGCGGGGTGCTGTGTGATATAGAGATGCGAAGAGACTAGGTTGCTCGAA 598
DB 257 GGGCCGCGAGGCTGCTGCTGCGGTACCGTGGCTGGAGGGGGCGCTCAAGTTTCCCGGA 316
QY 599 AGCCCTTCTGTGTATAGATACATTTGTTATCGCTTCANATGCAAGTTGTTCTGCA 658
DB 317 AACCGCTGTGTGATGATGATGATGATGCTCATCGCTCATTCGCGTGTGCGCGCG 376
QY 659 AAACCTGAGGATATATTTTGGCCAGCTGCTACAGCAAGCTCCGTTTCTTACAGATCC 718
DB 377 GCTCCAGGCGCAAGCTTCTTGGCCAGCTGCTGCTGCGAGCTGCGCTTCTTACAGATTC 436
QY 719 TCCGCAATGTGCGCATGAGACCGAAGGGAGGACACTTGGAAATPACTGGGTTCAGTGT 778
DB 437 TCCGAGTGTATCCGATGAGACCGGCGGAGGACACTTGGAAATPACTGGGTTCAGTGT 496
QY 779 ATGCTTCAGCAAGGAATTAATCAGCTTGTATAGATTTTGGTTCTTAATTTT 838
DB 497 ATGCCACAGCAAGGAGCTGTGCTACGCTGCTGCTGCTTCTTCTCATCTCGG 556
QY 839 CCTCTTCTCTGCTATCTGTGGAAGAGATGCGCAATTAAGATTTTCTATATATGAG 898
DB 557 CCTCGTCTCTGCTATCTGTGGAAGAGGAGGAGCAACCTTTCAGCACTTACGCGG 616
QY 899 ATGCTCTGTGAGGCGACATTAATCACTATTTGGCTATGAGACAAACTCCCC 958
DB 617 ATGCACTGTGTGGGCGCTGATCAGCTGACACCATTTGCTACGCGGAGCAAGTACCC 676
QY 959 TAACCTTGTGAGAGATTCCTTTCAGAGGCTTTCGATCTCTTGGCATTTCTTTT 1018
DB 677 AGACCTGGAACGCAAGCTCTTTCGCGCAACTTCACTCATCGGTCTCTCTTTCG 736
QY 1019 CACTTCTCCGCGCATTTTGGCTCAGGTTTGCATTAAGAGTAAAGACAGAACACCGCC 1078
DB 737 CGCTGCTCTCAGGCACTTGTGGGCTGTGGGTTTCCCTGAAAGTTTCAGAGACAGCGC 796
QY 1079 AGAAACACTTTAGAAAGAGAACAGCACTGCAACCTCATTTCAATGTGTTGGGTA 1138
DB 797 AGAAGCACTTTAGAAAGAGGCGGAACCGGCAACAGGCTGATCCAGTCCGCTGAGAT 856
QY 1139 GTTACGC 1145
DB 857 TTACGC 863

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; Sequence 5, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Biana, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

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Query Match      15.2%; Score 420.6; DB 4; Length 900;
Best Local Similarity 68.7%; Pred. No. 2.0e-101;
Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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QY 309 GCGCAAGTCAAGTACCGCGGCGTGCAGACTACTTACAGCTGCTGGAGACCCG 368
DB 27 GCGCAAGCTTCTTACCGCAAGCTGAGATTTCTTACAGCTGATAGAGCGCCCG 86
QY 369 CGGCTGCGGCTTATACACGCTTCTGTTTCTCTCTGTTGTTGTTGTTGTTGTT 428
DB 87 CGGCTGCGGCTTATACACGCTTACACGCTTACGCTTCTTCTCTGTTGTTGTTGTT 146
QY 429 GTGAGTGTTCATACATCCCTGAGCAACAAATTTGCTCAAGTTGCTTGTATCT 488
DB 147 TTTGTTGTTTCCATCAGAGTACGAGAAAGCTGAGAGGGGCTTACATCTT 206
QY 489 GAGTTCGTGATGATGCTGCTTGTGAGTTTCATTCATTCATTCATTCATTCATTC 548
DB 207 GGAATTCGATGATGCTGCTGATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 266
QY 549 TTGCTGTTTCATATAGAGATGCAAGAGAGAGTGTGCTGCAAGCCCTTCTG 608
DB 267 CTGCTGTTGCGGTATCGAGGCTGAGGCGTCAAGTTGCGAGAAAGCTTCTG 326
QY 609 TGTATGATACCATTTGTTCTTATGCTTCAATAGAGATTTGTTGCAAAATCTGAG 668
DB 327 TGTATGATACCATTTGTTCTTATGCTTCAATAGAGATTTGTTGCAAAATCTGAG 386
QY 669 TAAATTTTGGCAGCTGCTGCACTGAGAGTCCCTTCTTCTTCTTCTTCTTCTTCT 728
DB 387 CAATCTTCTTGGCAGATCTGCGCTTGGAGCTTGGGTTCTTCAATCTTGGGATGAT 446
QY 729 GCGCATGACGCAAGGAGGACACTTGAATTAATCTGAGTTGCTGAGTTTATGCTCAG 788
DB 447 CCGTATGACCGGAGGAGGCTGACCTGGAAGCTTGGGATCGGTATGCTGACCTGAG 506
QY 789 CAAGGAATTAACAGAGTGTGATATAGATTTTGGTTGTTCTTATTTTCTGCTTCT 848
DB 507 CAAGGAGCTGAGCTGCTGATATAGATTTTGGTTGTTCTTATTTTCTGCTTCTTCT 566
QY 849 TGTATCTGTTGTAAGAGATGCAATTAAGATTTTCTATATGAGATCTGCTG 908
DB 567 GGTATCTTGGGAGAAAGGAGTGAATGACACTTTGACACTGAGATGACTG 626
QY 909 GTGGGCAATTAATGACACTTATGAGATTTGCTATGAGACAAACTCCCTTAATCTG 968
DB 627 GTGGGCTGTATCACCTTACAGCACTTGTGAGGAGTGAAGTACCTTACAGCTGAA 686

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QY 868 GATCCCAATATA-----GAGTTTCTACATATGAGATGCTCTGTGG 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1018 GAGCGGGGAAAGATGAGGCGGCGCTGAGTTGCGAGAGTACGAGATGCGTGTGG 1077
QY 913 GGCAAAATTACATTGACAACTATTGGCTATGAGACAAAATCCCTTAATTGGCTGGA 972
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1078 GGGGTGTGACAGTACACCATCGGCTATGAGGAGTCCGACAGTGGGTGGG 1137
QY 973 AGATGCTTTCGAGGCTTTCGACCTCTGCTTTCCTTTCGATTCCTGCGGCG 1032
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1138 AAGACATCGCTCTGCTTCTGCTTTCGATCTCTTTCGCTCCAGCGGG 1197
QY 1033 ATTCTGCTCAGGTTTTCATTAAGTACAAAGAACACCGGCAAACTTTGAG 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1198 ATTCTGCTCAGGTTTTCGCTTGAAGTGCAGGAGAACAGAGCACTTTCAAC 1257
QY 1093 AAAAGAAAGAACCCAGCTGCAACCTCATTCAGTGTGGCTAGTTAGCAAGCTGA 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1258 CGGAGATCCCGGCGGAGCCTCATCTCATTCAGACCGCATGAGAGTGTATGCGGA 1316

```

RESULT 17

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; Sequence 1, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Conners, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLDT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
US-09-135-010A-1

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Query Match 9.7%; Score 267.8; DB 4; Length 3181;
 Best Local Similarity 59.5%; Pred. No. 1.1e-60;
 Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

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QY 331 GTGCAAGACTACGCTACAGTGTGAGAGACCCCGGGGTGG---GCGTCACTAC 387
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Db 478 GTCCAGGGCCCGCTACAACTCTCTCGAGCTCCACCGGCTGGAAAGCTTCGTTAC 537
QY 388 CAGCGTTTCGTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 CACTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 597
QY 448 CTTGAGCAGACAAAATTGGCTCAAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 507
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 598 GAGCAGTATGCCCGCTGCGCACGGGAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 657

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QY 508 GTCCTTGGTTTGGAGTTCATCATTCGAATCTGGTCTGCGGGTTCGTTGCTGATATAGA 567
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Db 658 TTCTTCGAGAGAGATAGTGTGCTCCGCTGTGTCGCCGCGCTCCGAGCAAGATACGTG 717
QY 568 GGATGGCAAGAGACTGAGTGTGCTGGAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 GGGCTCTGGGGGCGGCTCCGCTTCCCGGAGGCCATTTCTCATCATGACCTCATCTG 777
QY 628 CTATCGCTTCATATAGAGTGTGTTTCGCAAAAACCTCGGGGAATATTTTTCGACGCT 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 778 GTCTGCTCTTCATGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837
QY 688 GCACTCAGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 GCATTCAGGGGCAATCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
QY 748 GGCATCTGGAATTAATCTGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 GGCACCTGAGAGGCTCTCTGCGCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 957
QY 808 TGTACATATAGATTTTGGTCTCTATTTTTCGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 958 CTGTACATCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
QY 868 GATCCCAATATA-----GAGTTTCTACATATGAGATGCTCTGTGG 912
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1018 GAGCGGGGAAAGATGAGGCGGCGCTGAGTTGCGAGAGTACGAGATGCGTGTGG 1077
QY 913 GGCAAAATTACATTGACAACTATTGGCTATGAGACAAAATCCCTTAATTGGCTGGA 972
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1078 GGGGTGTGACAGTACACCATCGGCTATGAGGAGTCCGACAGCTGATTAACCAAC 1137
QY 973 AGATGCTTTCGAGGCTTTCGACCTCTGCTTTCGATTCCTTTCGATTCCTGCGGCG 1032
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1138 AAGACATCGCTCTCTGCTTCTGCTTTCGATCTCTTTCGCTCCAGCGGG 1197
QY 1033 ATTCTGCTCAGGTTTTCATTAAGTACAAAGAACACCGGCAAACTTTGAG 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1198 ATTCTGCTCAGGTTTTCGCTTGAAGTGCAGGAGAACAGAGCACTTTCAAC 1257
QY 1093 AAAAGAAAGAACCCAGCTGCAACCTCATTCAGTGTGGCTAGTTAGCAAGCTGA 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1258 CGGAGATCCCGGCGGAGCCTCATCTCATTCAGACCGCATGAGAGTGTATGCGGA 1316

```

RESULT 18

```

; Sequence 1, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: US 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181

```



```

Db      1018 GAGCGGTGAACAGTCAAGCGCGCGGTGGAGTTGGCAGCTACGACAGATGCCCTGCGTGG 1077
Qy      913 GGCACATTTACATTTGACACTATTTGGCTATGAGACAAACTCCCTTACTTTGGCTGGGA 972
Db      1078 GGGGTGGTCACTACACCATCGCTATGGGACAAAGTGCCTCCACAGCTGGGTGGG 1137
Qy      973 AGATTGCTTCTGAGGCTTGGACCTCCCTGGCATTTCTTCTTGGCATTTCTCTGCGGC 1032
Db      1138 AAGACCATCGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
Qy      1033 ATTCTTGGCTCAGATTTTGGATTTAAAGTACAGACACACCCGACAGAACTTTGAG 1092
Db      1198 ATTCTTGGCTCAGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1257
Qy      1093 AAAAGAAGAACCCAGCTGCCACCTTATTCAGTGTGTTGGCTAGTTAGCAGCTGA 1151
Db      1258 CGCAGATGCCGGCGGCGCTCCTCATTCAGACCCGATGAGAGTGGCTATGCTGCGGA 1316

```

RESULT 20

```

US-09-444-295-1
; Sequence 1, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MIRK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
US-09-444-295-1

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Query Match      9.7%: Score 267.8; DB 4; Length 3181;
Best Local Similarity 59.5%: Pred. No. 1,1e-60;
Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

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Qy      331 GTGCAGAACTACCTGTACACGTGCTGAGAGACCCCGGCGCTG---GCGTTCACTTAC 387
Db      478 GTCCAGGGCCCGCTCTACACCTCTCGAGCGCTCCACCGCTGGAATGCTTGGTTTAC 537
Qy      388 CAGCCTTTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 447
Db      538 CACTTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 597
Qy      448 CCTGAGCAGACAAATGGCTCAAGTTGCTTGTGATCTGAGTTCGATGATGATGTC 507
Db      598 GAGCAGTATGCGCGCTGCGCAGCGGAGACTCTCTCTGATGATGATGATGATGATG 657
Qy      508 GTCTTTGGTTGAGTTCATTCATTCGAAATCTGCTGCGGCTGCTGTTGCTGATTAAGA 567

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Db      658 TTCTTGGGACGAGTACGTGTGTCGCGCTCTGTCGCGCGCGCTGCGCGCGCTGCGCGCTG 717
Qy      568 GATGAGCAAGAGACAGTGTGCTGCTGCAAGAGCCCTTCTGTGTATAGATTAACATTTGT 627
Db      718 GGGCTGTGGGGGGGCTGCGCTTTGGCCGGAAGCCATTTCATCATCGACTATGCTG 777
Qy      628 CTATGCTTCAATATACAGTGTGTTTGCAGAAACTCAGGAGTAATATTTTGGCAGCTCT 687
Db      778 GTGCTGGCTCCATGATGATGCTCTGCTGGGTGCCAAGGGGAGGTTGTTGCCACGTCG 837
Qy      688 GCACCTAGAAAGTCTCGCTTCTCTACAGATCTCCGCTATGTTGGCTATGACCGAGGGA 747
Db      838 GGCATCAGGGGGCATTCGCTTCTGCAAGATCTGAGATGCTACACGTCGACCGCAGGGA 897
Qy      748 GGCATGGAATATACGGGTTCAGGTCTTATGCTACAGACAGAAATTAATACAGCT 807
Db      898 GGCACCTGGAGGCTCTCGGCTCGTGCTCTTCTTACACCGCCAGGAGCTGATTAACACC 957
Qy      808 TGCTACATAGATTTTGTCTTCTTATTTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 867
Db      958 CTGTACATCGGCTTCCCTGGGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
Qy      868 GATGCCAATTA-----GAGTTTCTACATATGAGATGCTCTGCGG 912
Db      1018 GAGCGGTGAACAGTCAAGCGCGCGGTGGAGTTGGCAGCTACGACAGATGCCCTGGTGG 1077
Qy      913 GGCACATTTACATTTGACACTATTTGGCTATGAGACAAACTCCCTTACTTTGGCTGGGA 972
Db      1078 GGGGTGTCACTACACCATCGCTATGAGGACAAAGTGCCCGCAGCTGGGTGGG 1137
Qy      973 AGATTGCTTCTGAGGCTTGGACCTCTTGGCATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1032
Db      1138 AAGACCATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
Qy      1033 ATTCTTGGCTCAGATTTTGGATTTAAAGTACAAACAAACCCGCGCAAACTTTGAG 1092
Db      1198 ATTCTTGGCTCAGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 1257
Qy      1093 AAAAGAAGAACCCAGCTGCCACCTTATTCAGTGTGTTGGCTAGTTAGCAGCTGA 1151
Db      1258 CGCAGATGCCGGCGGCGCTCCTCATTCAGACCCGATGAGAGTGGCTATGCTGCGGA 1316

```

RESULT 21

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US-09-597-732-1
; Sequence 1, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,732
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181

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QY 866 AGGATGCCATATA-----GAGTTTCTACATATGACAGATGCTCTGTGT 910
 DB 656 AGGACCGCGGTGACAGACTAGCGCCGCGTGGAGTTGGCAGCTACGACATGGCTGTGT 715
 QY 911 GGGGCAATATACATATGACACTATGCTATGAGACAAACATCCCTTAATCTGGCTGTG 970
 DB 716 GGGGGGTGGTACAGTACCACTGCGCTATGGGACAAAGTGGCCACAGAGTGGGTGTG 775
 QY 971 GAAGATGCTTTTTCAGAGCTTTGACACTCTTGGCAATTTCTTTTTCACACTTCTGCG 1030
 DB 776 GGAAGACATGCGCT 835
 QY 1031 GCATTTCTGGCTCAGTTTTCATTAAGTACAAAGAACACACCGCCAGAGAACTTTG 1090
 DB 836 GGAATTTGGCTGGGGGTGGCTGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAG 895
 QY 1091 AGAAG 1150
 DB 896 ACCGGCAGATCCCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 955
 QY 1151 A 1151
 DB 956 A 956

RESULT 26
 US-09-135-021-5
 ; Sequence 5, Application US/09135021A
 ; Patent No. 6150104
 ; GENERAL INFORMATION:
 ; APPLICANT: Splawski, Igor
 ; APPLICANT: Keating, Mark T.
 ; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVL0T1 WHICH CAUSES JERVELL
 ; FILE REFERENCE: 2323-128
 ; CURRENT APPLICATION NUMBER: US/09/135,021A
 ; EARLIER FILING DATE: 1998-08-17
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/094,477
 ; EARLIER FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 3182
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (163)..(1011)
 ; FEATURE:
 ; NAME/KEY: mutation
 ; LOCATION: (730)
 ; OTHER INFORMATION: This base is an insertion as compared to the
 ; OTHER INFORMATION: wild-type.
 US-09-135-021-5

Query Match 9.3%; Score 258.4; DB 3; Length 3182;
 Best Local Similarity 59.5%; Pred. No. 3.3e-58;
 Matches 500; Conservative 0; Mismatches 321; Indels 19; Gaps 3;
 QY 331 GTGAGACATCCTGTACAGTGTGGAGAGACCCCGGGGGG--GCGTCACTTAC 387
 DB 478 GTCCAGGGGCGGCTTACAACTTCTCGAGCGTCCACCGGCTGGAATGCTTGTAC 537
 QY 388 CACGCTTCTGCTTCT 447
 DB 538 CACTTCGCGCT 597
 QY 448 CCTGAGCACACAAATTTGGCTCAAGTTGCTTGTATCTCTGAGTTCGATGATGTC 507
 DB 598 GAGCAGTATGCGCGCTGCGGAGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 657

QY 508 GTCTTTGGTTTGGAGTTTCATTCGANTCTGCTGCGGGTTGCTTTGTGATA-TAG 566
 DB 658 TTCTTTGGGAGGAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
 QY 567 AGGATGGCAAG 626
 DB 718 GGCCTCTGGGGGGGCGGCTGCGCTTGGCCGGAAGCCATTTCCATTCGACCTATCTGT 777
 QY 627 TCTTATCGCTTCATATGACATTTGTTTCTGCAAAAACAGAGGATATTTTGGCAGCTG 686
 DB 778 GGTGCGGCTCCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
 QY 687 TGCATCAGAGAGTCCGCTTCTACAGATCCCTGCGATGCTGCGCATGAGACCGAAGGG 746
 DB 838 GGCATCAGAGGAGATCCGCTTCTGCGAGATCCTAGAGATGCTACAGCTGACCGCAGAG 897
 QY 747 AGGCACTTGGAAATTAAGTGGGTTGAGTTTATGCTCAGACAGAGAAATTAATCAGAC 806
 DB 898 AGGCACTTGGAGGCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
 QY 807 TTGTTACATAGATTTTGTCTTATTTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 866
 DB 958 CCGTACATCGGCTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
 QY 867 GATAGCCATATA-----GAGTTTCTACATATGAGATGCTCTCTGTG 911
 DB 1018 GAGACGCGGTGAG 1077
 QY 912 GGGCACAATTAATTAAGCAACTATTTGCTATGAGACAAACATCCCTTAATCTGGCTG 971
 DB 1078 GGGGCTGTCAACATGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
 QY 972 AAGATTCCTTCTGACAGCTTTGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
 DB 1138 GAAGACCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
 QY 1032 CATCTTGGCTCAGAGTTTGCATTAAGTACAGAAACACCGCCAGAAACACTTTGA 1091
 DB 1198 GATTCCTTGGCTGCGGGGTTTGGCCTGAGAGTGCAGAGAGAGAGAGAGAGAGAGAG 1257
 QY 1092 GAAAAG 1151
 DB 1258 CCGGAGATCCCGCGGAGAGCTCCTCATTCAGACCGCAGAGAGAGAGAGAGAGAG 1317

RESULT 27
 US-09-177-650-102
 ; Sequence 102, Application US/09177650
 ; Patent No. 6413719
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Singh, Nanda
 ; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-134
 ; CURRENT APPLICATION NUMBER: US/09/177,650
 ; EARLIER FILING DATE: 1998-10-23
 ; EARLIER APPLICATION NUMBER: 60/063,147
 ; EARLIER FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 102
 ; LENGTH: 171
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-177-650-102

Query Match 3.5%; Score 95.8; DB 4; Length 171;
 Best Local Similarity 72.5%; Pred. No. 5.7e-16;
 Matches 124; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

RESULT 31
US-09-177-650-101
Sequence 101, Application US/0917765G
Patent No. 6413719
GENERAL INFORMATION:

APPLICANT: Lepeert, Mark F.
APPLICANT: Singh, Nanda
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 101
LENGTH: 204
TYPE: DNA
ORGANISM: Homo sapiens
US-09-177-650-101

Query Match 2.4%; Score 67; DB 4; Length 204;
Best Local Similarity 67.9%; Pred. No. 2.5e-08;
Matches 108; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 460 AAATGGCTCAAGTTGCTTGTGATCCTGAGATTCGTGATGATGTTGCTTGTGTTG 519
DB 8 AAGTGGCTCAGCTTCTC-CCTGCAAGAAATGATGATGATGTTGTTGCGCTG 66
QY 520 GAGTTCATCATTCGATTCGTGCTGGGCTGCTGTTGCTGATATAGAGAGTGGCAAGA 579
DB 67 GAGTACTCTGCTGGATCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126
QY 580 AGACTGAGTTGCTGCAAGCCCTTGTGTTATAGAT 618
DB 127 CGCTCAAGTTTCCCGGAACCGTTCTGTGATTTGTT 165

RESULT 32
US-09-177-650-115
Sequence 115, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepeert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 115
LENGTH: 245
TYPE: DNA
ORGANISM: Homo sapiens
US-09-177-650-115

Query Match 2.3%; Score 65; DB 4; Length 245;
Best Local Similarity 57.6%; Pred. No. 9.1e-08;
Matches 141; Conservative 0; Mismatches 95; Indels 9; Gaps 1;

QY 163 GCGACGCGCTCTACTGCTGGACACCCGCGGCGCAACCTGCTGGCGCGCGGCTGGC 222
DB 1 GCGACGCGCTGACCAATGCTTGGGCTGCGGCGCGGCGCAACCAAGCGGACCTG 60
QY 223 CTGAGGAGAGCGCGCGGCGCAAGCAAGCGGCGCGCGGCTGCTGCTGCTGCTGCTGCTG 282
DB 61 CTGCTGAGAGCGCGCGCGCGCAAGCAAGCGGCGCGGCTGCTGCTGCTGCTGCTGCTG 120
QY 283 TCTTACAGAGTAGCCAGAGCTGCC-----GGCGCAACGTCAAGTACCGCGGCGTG 333

DB 121 CTGCGCAAGACCCGCTGAGCGCCAGTCAAGAGAAACAGCCAGTACCGGCGCATC 180
QY 334 CAGACTACTCTGTACACGTGCTGAGAGAGACCCGCGGCTGCTGCTGCTGCTGCTGCTG 393
DB 181 CAACTTGTATCTACAGACGCCCTGAGAGACCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 394 TTGCT 398
DB 241 TTGCT 245

RESULT 33
US-09-177-650-110
Sequence 110, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepeert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 110
LENGTH: 211
TYPE: DNA
ORGANISM: Homo sapiens
US-09-177-650-110

Query Match 2.3%; Score 63.4; DB 4; Length 211;
Best Local Similarity 68.2%; Pred. No. 2.2e-07;
Matches 88; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1548 CAGATTTATGAATTTCTGTTGCAAAACGGAAGTTTAAGAAACATTACGTCATATGA 1607
DB 41 CAGTGTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 100
QY 1608 TGTAAAGATGCTGATTAACATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1667
DB 101 CGTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160
QY 1668 AAGCCTTCA 1676
DB 161 GAGCCTGCA 169

RESULT 34
US-09-177-650-117
Sequence 117, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepeert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 117
LENGTH: 859

Query Match 2.08; Score 55.2; DB 4; Length 318;

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;
;
FEATURE:
OTHER INFORMATION: CDC 1551
OUTPUT INFORMATION: "not bases at various positions throughout the sequence"
```

OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

query match	Score	DB	Length
1.98;	53.4;	DB 4;	4403765;

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Matches 120; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
```

37341194 AGCGGCAACGCTGGCGACGCCGGGCTGTCGGGAACGGCGCGCGGGGGGGCCGGGGCC 3734135

QY 81 GGGCGGGGCGCTTTGGCGAGCGGCATGAGGATGTGAGTCCGGCCGGGCCAGGTCCT 140
| | | | | | | | | | | | | | | | | |

DJ 5'34134 GCGGCGCCTCCCGGGAGTCAATTCACGTTGCTGCTGGGACCCCCGCGGCCAC

OY 141 GCCTGAATCGGGACCGCGCCAGGGGCGACGGCCCTGTACTGCTGGGACCCCCGCGGCCAC 200

Db 3734074 CGGAACCGCGCGCAACGCGCGCGCGGTTATTGCTTGGCAACGCGCGGCGCGCGG 3734015

[illegible]

РЕШЕНИЕ № 6

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Inventor: US 6904200

```

; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; ISSUING OFFICE:

```

APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.

TITLE OF INVENTION: TUBERCULOSIS
 FILE REFERENCE: 24366-20007.00

CORRECTION
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2

```

/ JOE FRANK, FUCHSBERG POLY, 201
/
/ SEQ ID NO 1
/
/ LENGTH: 441529

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;
; LIFE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
;

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Query Match	1.9%	Score 53.4	DB 4	length 4411529
US-09-103-840A-1				

Best Local Similarity 51.9%; Pred.No. 0.046;
Matches 120; Conservative 0; Mismatches 11; Indels 0;
Gaps 0;

21 AAGGAGAGACGGCGCGCGCGCGCGCTCGGGGTAAGAGCGCGGCGCACCGGCGCGCGCG 80

81 GGGCGGGGGCGCTTGGGCAAGCATGATGTGGAGTGGGCGGCGGAGGGTCTT 140

Db 374192 CCGGGGCTGCGGGGTCGCCCGGCTCAACGGGGGCCACGGCAGCGCGGCACGG 374189

Db 3741892 CGGACCGGGCGGCAACGGCGGGCGGGTATTGGTGGCAACGGCGGGCGGGCGG 3741893

201 GCTGCTGGCCGCGCGTGGCCCTGAGGGAGAGCCCGGGGGCAAGAGGG 251

REC'D 4/
US-09-177-650-105


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QY      6  CCGCCACACACCGGAGAGAGAGAGGCGCGCCCGGCTGTGGTGAAGAGCGGCG 65
Db      3054633  CGGCGCCACAGGCGCGCGGTCGCAACGGCGGTCGGCGGGGCTGTTCGGCGC 3054692
QY      66  AGCGCGCGCGCGCGCGCGCGCGGCGCTTGGGCAAGCGGCAWGAAGATGTGAGTCGGG 125
Db      3054693  CGGCGGTGCGCGCGCGCGCGCGCTTCAGCGACACCGGTGGACCGCGGCGG---CTGG 3054749
QY      126  CCGGGGCGAGGTGCTGTGAATCTGGCAAGCCGCAAGGGGCGACGGCTGTACTGTGGG 185
Db      3054750  CGGCGCGCGCGCGGCTGTTCGGCCCGGCGGCTCGGGCGCGCTTCGGCGA 3054809
QY      186  CAGCCGCGCGCGCACGCTCGGTGGCGCGCGGCTGTAGGAGAGAGCGCGCGGCGG 243
Db      3054810  CACCGGTGGGACCGCGCGCGACGGCGGCGAGCGCGGCTGTTCGGCTGTGGCGGCGGCG 3054867

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Search completed: June 19, 2003, 11:25:11
 Job time : 192 secs


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80 129.8 4.7 461 9 A1347525 A1347525 q098e02.x
C 81 129.2 4.7 411 12 BF414224 BF414224 UI-R-BJ2-
C 82 128.8 4.6 267 12 BG185740 BG185740 RST4692 A
C 83 128.2 4.6 226 9 A1705051 A1705051 UI-R-GO-u
C 84 128.2 4.6 330 10 AM533367 AM533367 UI-R-BUO-
C 85 128 4.6 239 10 AM122800 AM122800 UI-M-BH2.
C 86 124.6 4.5 650 13 B1228823 B1228823 RCE90B05.x
C 87 124.6 4.5 493 9 A1439544 A1439544 rc26b05.x
C 88 124.2 4.5 1068 12 BF311176 BF311176 60189648
C 89 124 4.5 335 12 BG218030 BG218030 RST37756
C 90 123.8 4.5 545 12 BE753839 BE753839 207018 MA
C 91 123.4 4.5 344 13 B1049443 B1049443 CM2-GN029
C 92 119 4.3 631 10 BE159001 BE159001 MR0-HT040
C 93 114 4.1 334 9 AA091374 AA091374 111297.se
C 94 113.6 4.1 425 10 BE648243 BE648243 UI-M-BH2.
C 95 113.2 4.1 311 14 H23702 H23702 yP72g11.s1
C 96 112.8 4.1 443 9 A1871417 A1871417 w18h11.x
C 97 112.4 4.1 530 12 BE721570 BE721570 189148 MA
C 98 110 4.0 539 12 AM135705 AM135705 UI-H-B11-
C 99 109.6 4.0 160 12 BE959223 BE959223 QV2-NN004
C 100 108.4 3.9 899 17 CNS024X7 CNS024X7 Tetracodon
C 101 107.2 3.9 442 9 A1769029 A1769029 wg31h01.x
C 102 107.2 3.9 1087 17 CNS05CVN CNS05CVN Tetracodon
C 103 106.8 3.9 442 12 BG979542 BG979542 CM4-CN006
C 104 106.8 3.9 812 12 BG328061 BG328061 602427108
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C 136 80 2.9 994 17 CNS028EF CNS028EF Tetracodon
C 137 80 2.9 1009 17 CNS036DE CNS036DE Tetracodon
C 138 79.6 2.9 776 17 CNS010RY CNS010RY Tetracodon
C 139 77.6 2.8 903 17 CNS022P4 CNS022P4 Tetracodon
C 140 77.4 2.8 271 12 BF415113 BF415113 UI-R-BJ2-
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ALIGNMENTS

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LOCUS BE158938 658 bp mRNA linear EST 21-JUN-2000
DEFINITION MK0-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE158938
VERSION BE158938
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 658)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=st2-MR0-HT0404-210
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High quality sequence stop: 657.
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/dev_stage="Adult"
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Site_2: Smat; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196/716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 181 a 175 c 153 g 149 t
ORIGIN

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Query Match

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Best local Similarity 99.5%; Pred. No. 3,6e-138;
Matches 639; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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996 ACTCCCTGACATTTCTTTCTTTCGACCTTCTCCGGGACATTTGGCTAGGTTTGCAAT 1055
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1056 AAAAGTACAAAGACACACCGCAGAAACCTTGGAGAAAGAGAACCCAGCTGCCAA 1115
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137 AAAAGTACAAAGACACACCGCAGAAACCTTGGAGAAAGAGAACCCAGCTGCCAA 196
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1116 CCTCATTCAGTGTGTTGGCGGTAGTTACGACGATGAGAAATCTGTTGCATTCGACAC 1175
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O	y		1236	TAAAGAGCCGAGTGCAGCTAGGCTAGCCCCAGGGGCGACAAGTATTAAAGAGCCGACAAGCTC	1295
D	b		317	TAAAGAGCCGAGTGCAGCTAGGCTAGCCCCAGGGGCGACAAGTATTAAAGAGCCGACAAGCTC	376
O	y		1296	AGTAGGTGACAGAGAGTCCCACAGCACCGACATCACAAGCCGAGGGCAGTCCCACCAAAGT	1355
D	b		377	AGTAGGTGACAGAGAGTCCCACAGCACCGACATCACAAGCCGAGGGCAGTCCCACCAAAGT	436
O	y		1356	GCGAAGAGGTGGAGCTTCAACGACGACACCCGTTCCGGCCCGGCTGGCGCTCCAAG	1415
D	b		437	GCGAAGAGGTGGAGCTTCAACGACGACACCCGTTCCGGCCCGGCTGGCGCTCCAAG	496
O	y		1416	TTCCTCAGCCAAAACCACTGATAGATGCTGACACACGCCCTTGCGACTGATGATATGA	1475
D	b		497	TTCCTCAGCCAAAACCACTGATAGATGCTGACACACGCCCTTGCGACTGATGATATGA	556
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D	b		557	TGAAAAAGGATGCCAGTGTGATGTATCATGTGGAGAGACTTCAACCCACACCTTAATAACGT	616
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LOCUS			602565103P1 NIH_MGC_61	Homo sapiens cDNA clone IMAGE:4699776 5'	
DEFINITION			mRNA sequence.		
ACCESSION			BG532543		
VERSION			BG532543.1	GI:13524082	
KEYWORDS			EST.		
SOURCE			human.		
ORGANISM			Homo sapiens		
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			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			1 (bases 1 to 734)		
AUTHORS			NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL			National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT			Unpublished (1999)		
			Contact: Robert Strausberg, Ph.D.		
			Email: cgapbs-r@mail.nih.gov		
			Tissue Procurement: ATCC		
			cDNA Library Preparation: CLONETECH Laboratories, Inc.		
			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)		
			DNA sequencing by: Incyte Genomics, Inc.		
			Clone distribution: MGC clone distribution information can be		
			found through the I.M.A.G.E. Consortium/ILNI at:		
			http://image.llnl.gov		
			Plate: LICM1532 row: f column: 01		
			High quality sequence stop: 699.		
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  and 3' adaptors were used in cloning as follows: 5'
  adaptor sequence: 5'-CACGGCCATTTGGCC-3' and 3' adaptor
  sequence: 5'-ATTCTAGAGGCCGACGGCCGCCACCATG-AT(30)BN-3'
  (where B = A, C, or G and N = A, C, G, or T). Average

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[illegible]

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1CM1034 row: b column: 14
 High quality sequence stop: 615.
 Location/Qualifiers
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 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccatcggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATATGACC-3' and 3' adaptor (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
 BASE COUNT 263 a 229 c 217 g 199 t
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 Best Local Similarity 92.48; Pident. No. 3,1e-111;
 Matches 628; Conservative 0; Mismatches 40; Indels 12; Gaps 7;
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 121 CCCACCTCCCTCCAGCCATCAAGCATCTGCCAGGCCAGAACTCTCACCCTAACCC 179
 2283 TGCAGGCTTAACAGAAAGCATTTCTGACGTCACCACTGCTGTGCTCCAGAGAAA 2242
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 420 GTCAGTGGCTCCAGAGGCAAG-CAAGATTTTACCCCAATGAGAGGAATCCAAATTTG 478
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Db 479 TTTATTAAGTGAAGAGTGGGTCGCCGAGAGACAGACAGACACACTTTTATGATGCC 538
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 539 GCACAGAGTTCGCCCGGAGAAAGCTGCTTTGATTCAGAAATCTTAAGAGTGAAGGTC 598
 2697 AGCATATCTCAGAGCATTTTGTAAAGCAGAGAGA--AAGTACAGATGCC--TCAGCTTGC 2752
 599 AGCATATCTCAGAGCATTTTGTAAAGCAGAGAGACAGATGATGATGCTTCAGATGCC 658
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 VERSION AM049888
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 SOURCE EST.
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 Mus musculus.
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 1 (bases 1 to 584)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 JOURNAL
 MEDLINE
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: MEST@mail.nih.gov
 Oligo-dT track not found. Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 37-71, >GC-rich#low_complexity
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 POLYA=NO.
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 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M.S2 library is a subtracted library derived from NIH_BMAP_M.S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, ganglia bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.
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TAG: TISSUE=corpus-striatum
 TAG_SRO=ACGGC
 BASE COUNT 107 a 151 c 174 g 152 t
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 Best Local Similarity 93.0%; Pred. No. 2,1e-110;
 Matches 543; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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 QY 272 GGAAGCGGCTCTCTTACAGCAGTACAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGG 331
 121 GGAAGCGGCTCTCTTACAGCAGTACAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGG 180
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 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 506)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.G.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&st=2-QV2-NN0045-
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 High quality sequence stop: 506.
 Location/Qualifiers
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 /clone_lib="NN0045"
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 site: 2; Smal: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 125 a 108 c 104 g 168 t 1 others
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 Best Local Similarity 98.0%; Pred. No. 6.5e-104;
 Matches 496; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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 QY 1938 TGACTATCAAGCCCTGAGATAGA 1963
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 LOCUS BB624101

AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Breniani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
 20202663
COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?rl-QV2&rl2-QV2-NN0045-031200-511-003&rl3-2000-12-03&rl4-1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 491.
 location/Qualifiers

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 /clone_id="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous_normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
 165 a 105 c 107 g 114 t

ORIGIN

Query Match 17.2%; Score 477.2; DB 12; Length 491;
 Best Local Similarity 99.4%; Pred. No. 8.8e-101;
 Matches 479; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1369 AGCTTCACGACGACGACCCGCTCCGCGCCCTCCGCTCAAAAGTCTCAGCCAAA 1428
 10 AGGCTCAACGACGACCCGCTCCGCGCCCTCCGCTCAAAAGTCTCAGCCAAA 69
 1429 CCACTGATAGATGCTGACACAGCCCTTGGCACTGATGATATGATGAAGAGATGC 1488
 70 CCACTGATAGATGCTGACACAGCCCTTGGCACTGATGATATGATGAAGAGATGC 129
 1489 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548
 130 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189
 1549 AGAATTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1608
 190 AGAATTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 249
 1609 GTAAAGATGTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1668
 250 GTAAAGATGTCATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 309
 1669 AGCCTTCAAAACGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1728
 310 AGCCTTCAAAACGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 369
 1729 AGCCGAGAGAAATTAACAGAGACATGACACAGAGATGCTGATGCTGCTGCTGCTGCTG 1788
 370 AGCCGAGAGAAATTAACAGAGACATGACACAGAGATGCTGATGCTGCTGCTGCTGCTG 429
 1789 GTGCTCAAGGTTGAAAAACAGGTACAGTCCATGAAATCCAAAGCTGACCTGCTACTAGAC 1848

Db
 430 GTGCTCAAGGTTGAAAAACAGGTACAGTCCATGAAATCCAAAGCTGACTGACTACTAGAC 489

QY
 1849 AT 1850
 490 AT 491

RESULT 11
 BB609854
 LOCUS
 DEFINITION
 BB609854 RIKEN full-length enriched, adult male lung Mus musculus
 CDNA clone 1200002p22 5', mRNA sequence.
 BB609854
 VERSION
 BB609854.1 GI:15390457
 KEYWORDS
 EST.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1 (bases 1 to 997)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,U., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>,
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,U., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, L72-L86 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES
 source
 1. 997
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_id="1200002p22"
 /clone_lib="RIKEN full-length enriched, adult male lung"
 /sex="male"
 /tissue_type="lung"
 /dev_stage="adult"

Db 315 GTTGTGTAGATTAAAGCCTTCAACACGCTGTTGATCAATTTCTTGAAAAAGGCCAAT 256

QY 1713 CACATTCAGTAAAGAGCCGAGAGAAAATACAGCAGAACATGAGACACAGCATCT 1772

Db 255 CACATTCAGTAAAGAGCCGAGAGAAAATACAGCAGAACATGAGACACAGCATCT 196

QY 1773 CAGTATGCTCGGCTGGCTGCTCAAGTTGAAAAACAGTACATCATAGATCCAAAGCT 1832

Db 195 CAGTATGCTCGGCTGGCTGCTCAAGTTGAAAAACAGTACATCATAGATCCAAAGCT 136

QY 1833 GCACTCCCTACTAGATCATCAACAGTCTCTCGAAAAAGCTCTGCTCAGCCCTGCG 1892

Db 135 GCACTCCCTACTAGATCATCAACAGTCTCTCGAAAAAGCTCTGCTCAGCCCTGCG 76

QY 1893 TTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCTGATCAAAAGCC 1951

Db 75 TTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCTGATCAAAAGCC 17

RESULT 13
BE103175 469 bp mRNA linear EST 13-JUN-2000

LOCUS UI-R-BT1-axq-h-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone

DEFINITION UI-R-BT1-axq-h-11-0-UI 3', mRNA sequence.

ACCESSION BE103175

VERSION BE103175.1 GI:8495314

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 469)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: mscares@blue.weeg.uiowa.edu

Oligo-dt track not found, Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com) The following repetitive

elements were found in this cDNA sequence: 1-71,

>C_richlow_complexity

Seq primer: M13 Forward

POLYA-No.

FEATURES

SOURCE

Location/Qualifiers

1..469

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-BT1-axq-h-11-0-UI"

/clone_1db="UI-R-BT1"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pUT3D-Pac (Pharmacia) with a modified

polylinker. Site_1: Not I; Site_2: Eco RI; The library

UI-R-BT1 is a subtracted library derived from a mixture of

the following tissues: hippocampus, thalamus, mid-brain,

medulla, corpus striatum, cerebral cortex and testis. For

a detailed description of the library from which this

clone was derived, please visit our web site at

ratseq.eng.uiowa.edu. The subtraction has been previously

described in (Bonaldo, Lennon and Soares, Genome Research

6:791-806, 1996)

TAG_SEQ=None found"

BASE COUNT 79 a 120 c 152 g 118 t

ORIGIN

Query Match 15.0%; Score 416.2; DB 10; Length 469;

Best Local Similarity 93.0%; Pred. No. 1,6e-86;

Matches 436; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 152 CAGCCGCCAGGGGCGAGCGGCTGCTGCTGCGGCAACCCGCGGCGCAGCTGCGTGGC 211

Db 1 CGGCGCGCCAGGGGCGAGCGGCTGCTGCTGCGGCAACCCGCGGCGCAGCTGCGTGGC 60

QY 212 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271

Db 61 GCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 272 GGAAGCCGCTCTCTTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGT 331

Db 121 GGAAGCCGCTCTCTTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGTACAGAGT 180

QY 332 TGAGAACTACCTGTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391

Db 181 TGAGAACTACCTGTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 392 CTTTCCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451

Db 241 CGTTGCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 452 AGCACAACAATATGCGCTCAAGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511

Db 301 AGCACAACAATATGCGCTCAAGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 512 TTGGTTGGAGTTCATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 571

Db 361 TTGGTTGGAGTTCATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 420

QY 572 GGCAGAGAGACGTAGGTTGCTCGAAAGCCCTTCTGTATAGATAC 620

Db 421 GGCAGAGAGACGTAGGTTGCTCGAAAGCCCTTCTGTATAGATAC 469

RESULT 14

BF954375 517 bp mRNA linear EST 22-JAN-2001

LOCUS QV2-NN0045-131100-414-f08 NN0045 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF954375

ACCESSION BF954375

VERSION BF954375.1 GI:12371650

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 517)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 517)

Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.R., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?rl-QV2-NN0045-

QY 1896 GCCTTCATTCAGATCCAC 1915
 DB 549 GGCTTCATTCAGATCCAC 568

RESULT 16
 A2443500/c 477 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0238H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0238H18 R, DNA sequence.
 ACCESSION A2443500
 VERSION A2443500.1 GI:10591541
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 477)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0238 row: H column: 18
 SEQ PRIMER: CACACAGCAACAGCTAGTACACC
 CLASS: plasmid ends
 HIGH QUALITY SEQUENCE STOP: 477.
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 1..477
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0238H18"
 /clove.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (91473211419b1AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance.

BASE COUNT 100 a 98 c 150 g 129 t
 ORIGIN

Query Match 13.7%; Score 378.4; DB 17; Length 477;
 Best Local Similarity 87.2%; Pred. No. 1.1e-77;
 Matches 415; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1981 GCACAAACAGTGGCTGTATCCAGTCACTAGTGCACAACTTCGAGAGGCGTCAG 2040
 DB 476 GCACAAACAGGCGCTGTAAAGAGTGCAGCCAGTCCAAATCTCAAGAGGCGTCAG 417
 QY 2041 TTCATTCTGACGGCAATATGATGATGAGTCCAGACTTTCAGCGCTTACCGCTACATG 2100
 DB 416 TTCATCTTAACACCAATATGATGATGATGAGTCCAGACTTTCAGCGCTTACCGCTACATG 357
 QY 2101 CACAGTCACGACACACAGTGCACATTTATGTCACAAAGCATGGCTGAGAGTGGACGCC 2160
 DB 356 CACAGCCAGCTACCCAGTACCATGATGTCACAAATACGCTCTCCGTGGTGGACCC 297
 QY 2161 AACACCATTCGCAACCAATATATATACGACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2220
 DB 296 AATTAATTTCCAAACCAATATATATACGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 237
 QY 2221 ATCCACCTCTCTCTCCAGCCATTCACATGCTGCTCCAGCCAGCCAGCCAGCCAGCCAGCC 2280
 DB 236 ATCCCT 177
 QY 2281 CCTGACGGCTTACAGGAAGCATTTCTGAGCTGACGTCACACCTCTCTCTCTCTCTCTCTCTCTCT 2340
 DB 176 CCACAGCGCTTACAGAGAGATTTCTGATGTCACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 117
 QY 2341 AATGTCAGGTTGACAGTCAATCTCACCAGGACCGTCTATGAGGAAAGCTTTGAC 2400
 DB 116 AGTGTTCAGTTTGACAGTCAATCTCACCAGGACCGTCTCTCTCTCTCTCTCTCTCTCTCTCT 57
 QY 2401 ATGGGAGGAAACTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2456
 DB 56 ATGGGAGGAAACTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1

RESULT 17
 BI290441/c 434 bp mRNA linear EST 19-JUL-2001
 LOCUS UI-R-DK0-cfw-c-12-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone
 DEFINITION UI-R-DK0-cfw-c-12-0-UI 3', mRNA sequence.
 ACCESSION BI290441
 VERSION BI290441.1 GI:14949018
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 434)
 Bonaldo, M.F., Lennon, G., and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE
 COMMENT 97044477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mesoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized rat brain pool library cDNA library Preparation: M.B.
 Soares lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.
 Location/Qualifiers
 1..434
 /organism="Rattus norvegicus"

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QY	1727	AGAGCCGAGAGAAA	1740
Db	14	AAAAAAAAAAAAA	1
RESULT	18		
LOCUS	Bg732557	528 bp	mRNA
DEFINITION	Bg732557	33306 MARC IPig Sus scrofa cDNA 5', mRNA sequence.	EST 11-MAY-2001
VERSION	Bg732557.1	GI:14018840	
KEYWORDS	EST.		
SOURCE	Pig.		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
	1 (bases 1 to 528)		
	Fahrenkrug,S.C., Fekling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,		
	Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.		
	and Keele,J.W.		
TITLE	Design and use of two pooled tissue normalized cDNA libraries for		
JOURNAL	EST discovery in swine		
COMMENT	Unpublished (2000)		
	Contact: Smith TPL		
	USDA, ARS, US Meat Animal Research Center		
	PO Box 166, Clay Center, NE 68933-0166, USA		
	Tel: 402 762 4366		
	Fax: 402 762 4390		
	Email: smith@email.marc.usda.gov		
	Single pass sequencing. Bases called and alt-trimmed with phred		
	v0.980904.e. Vector identified by cross-match with the -minscore 18		
	and -mismatch 12 options.		
	PCR Primers		
	FORWARD: AGGAACAGCTATGACCAT		
	BACKWARD: GTTTCGCCAGTCACGACG		
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	Seq primer: ATTATGCTGACCTCATG.		
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	/clone_lib="MARC IPig"		
	/tissue_type="pooled"		
	/lab_host="DH10B"		
	/note="Vector: pCMV SPORT6; site_1: NotI; site_2: SalI;		
	library made from pooled tissue from day 11, 13, 15, 20,		
	and 30 embryos."		
BASE COUNT	112 a 197 c 135 g 84 t		
ORIGIN			
Query Match	12.3%;	Score 339.8;	DB 12; Length 528;
Best Local Similarity	79.4%;	Pred. No. 1.2e-68;	
Matches 436; Conservative	0;	Mismatches 92;	Indels 21; Gaps 2;
QY	1961	GCAAGATCTTTCCGGGTCGGGCAAAACAGTGGCTGCTTATCGATGACACTAGTGCCA	2020
Db	1	GCAAAAGACTGTGTCAGCTCCGACAAACAGCGGCTGCTGTCCGATCAGCCAGTGCCA	60
QY	2021	ACATCTGAGAGAGCGCTGACGTTTCATTTCTGACGCCAAATGATTCAGTGCAGCACTTCT	2080
Db	61	ACATCTCCCGAGGCGCTGACGCTCATCTTGACCCCAATGATTCAGGCGCCAGACTTCT	120
QY	2081	ACGGGCTTAGCGCTTACTATGACACAGTCACAGCAGCAGGTCGCCAATTAAGTAAAGCGCATG	2140
Db	121	ACGGGCTTAG--TCTTATGACACAGTCACAGCAGCAGGTCGCCGAGTCTAAAGCGCAGC	177
QY	2141	GCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAATTAATACGGACCCCAAGCCAG	2200

Db	178	GCCCAGCGGGGGGGTACCCACGACATGCGACACCAAAATAAACGGCCGTCGAAGCCCG	237
QY	2201	CAGCCCCAACACTTTACAGATCCACCTCTCTCCAGCCATCAGCATCTGCCAAGC	2260
Db	238	CGGCCCCAGGCACCTTTGCAGATCCCGCTCTCTCCCGCCCTCAACACCTGGCC-----	292
QY	2261	CAGAAACTCTGCACCCCTAACCCCTGCAGGCGTTACGAGAAAGCATTTCTGAGGTCACCACT	2320
Db	293	-----CCCCACCCCGTGGCCCTGCAGGAGAGCATTTCCGAGGTCACCACT	339
QY	2321	GCGTTGTTCCTCCAGAAATAATGTTAGGTTGCACAGTCATAATCTACCAAGAGACGTT	2380
Db	340	GCGTTGTTCCTCCAGAGAGATTTTGGGCTGGCGAGCAAACTCGAACCAAGACGCT	399
QY	2381	CTATGAGAAAAGCTTTGACATGCGAGAGAGAAACTCTGTTCTCTCTGTCCATGTCG	2440
Db	400	CTTTGGCCCAAGAGCTTGACCTGGGCGGAGAAAGCGCTGCTCCGTCGCCCCGGGTAC	459
QY	2441	CGAAGGACTTGGGAAATCTTGTCTGTGCAAAACCTGATCAGGTCGACGAGGAACCTGA	2500
Db	460	CCAAGGACCTGGGGAAGTCTCTGTGTGCAAAAACCTGATCCGATCGACGGAGGAACCTGA	519
QY	2501	ATTATCAAC	2509
Db	520	ATTACACAGC	528

RESULT 19	427 bp	linear	EST 11-DEC-2000
BF523361/c			
LOCUS	BF523361		
DEFINITION	UT-R-60-ug-h-09-0-UT.1	UT-R-C0	Rattus norvegicus
	UT-R-60-ug-h-09-0-UT 5'		cDNA sequence.

ACCESSION	B#5233561	GI:11631328
VERSION	B#523361.1	
KEYWORDS	EST.	
SOURCE	Norway rat.	
ORGANISM	Rattus norvegicus	

REFERENCE	1 (bases 1 to 427)
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium
LLNL (info@imgc.llnl.gov). IMAGE ID= 1794020
Seq primer: M3 Forward.

FEATURES	Location/Qualifiers
source	1. .427

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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-GO-ug-h-09-0-UI"
/clone_lib="UI-R-GO"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the

```

oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806

Query Match	11.2%;	Score 310.8;	DB 12;	Length 427;
Best Local Similarity	92.4%;	Pred. No. 6,9e-62;		
Matches 327;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;

QY 772 GTGGTTTATGCTCAGCAGCAAGAAATTAATACACAGCTTGGTACAAAGAAATTTTGGTCTT 831

Db 426 GTGTTTAAGCTCAGCAGCAAGAAATTAATACACAGCCTGGTACATTGGATTTCTGGTCTT 367

OY 832 ATTTTTCGCTCTCCCTGTCTCATCTGATGGCAAAAGATGCACATAAAGAATTCTCACA 891
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 366 ATTITTTCATCTCTCCTGTCTCATCTTGCGAAAAAGATGCCAATAAAGAGTTTTTCACA 307
 |||

QY 892 TATGAGATTGCCTCTGGTGGGGACCAATTCATTCATGACAACCATTTGGCTATGTGAACAAA 951
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 TATGGGAGTCTCTCTGGTGGGGACCAATTACACTGACACCAATTTGGCTATGTGAACAAA 247

QY 952 ACTCCCCAACCTTGGCTGGGAAGATTGCTTTCTCAGGCTTGCGACTCCCTGGCAATTCCT
|| |||||||
Dd 246 ACACCCCCTAAGTGGCTGGGAAGATTGCCTCTCTGCAAGCTTGCCCTCTTGGTATTCT 187

Qy 1012 TTCTTTGACCTTCGCGGACATTTGGCTAGGTTTTCATTAAGTAAACAAACAA 107
 |||||
 Db 186 TTCTTTGACCTTCGCGGACATTTGGCTAGGTTTTCATTAAGTAAACAAACAA 127

QY	1072 CACCGCCAGAAACACTTTGAGAAAAGAAGAACCCAGTCGCACCTCAATTCAG 1125
Db	126 CACCGCCAGAACATTGTGAGAAAAGAAGAACCCAGTCGCCAACCCTCATCCAG 73

RESULT 20	
BF962769	
LOCUS	515 bp
BF962769	mRNA
	1 linear
	EST 22-JAN-2001

DEFINITION	QV2-NN0045-181200-560-b10 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF962769
VERSION	BF962769.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 515)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., *et al.* 2003. A genome map of *Trachinotus* sp. M. A. Bordin, S. Costa, F. F. *et al.*

TITLE	JOURNAL	COMMENT
Sequence sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
20202663	Contact: Simpson A.J.G. Laboratory of Cancer Genetics	

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICor Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scicraps/gethtml2.pl?tl=qv2&tc=qv2-NN0045>)
181200-560-b10&t3=3000-12-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 73.

FEATURES	Location/Qualifiers
source	1. .515

OY 442 ACCATCCCTGACACACAAATTTGGCTTCAAGTTCCTTCACTGAGTTGATG 501
 DB 133 ACCATCCGAGGACACACAGACTTGCACACGAGTGTCTCTTATCTTGATTCGATG 192
 OY 502 ATTTGCGATTTGGTGGATTCATCATTCGAATCTGGCTGGGATTCCTGTCGA 561
 DB 193 ATTTGCGATTTGGTGGATTCATCATTCGAATCTGGCTGGGATTCCTGTCGA 252
 OY 562 TATAGAGATGACAGAAAGACTGAGTTGTCTGCAAAAGCCCTTGTGTATAGATACC 621
 DB 253 TACAGAGATGACAGAGAGCTTTGCTTGGCAGAAACCTTGTGTATAGATACC 312
 OY 622 ATTTGCTTATGCTTCAATAGCAGTTGTTGCAAAAATCAGGTAATTTTGGC 681
 DB 313 ATCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
 OY 682 ACCTGTCACAGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
 DB 373 ACTTCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
 OY 742 AGGGAGGACACTTGGAAATTTACTGGG-TTCAGTGTGTTATGTCACAGCAAGCAATTAT 800
 DB 433 CGAGGTGACCTGGAATGTTGGGAAATCCGCGTCTATGTCACAGTGAAGCTGAT 492
 OY 801 CACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 DB 493 CACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 OY 860 TGGAAAGG 868
 DB 553 CTGAAGAG 561

RESULT 25
 LOCUS BQ219245 1004 bp mRNA linear EST 02-MAY-2002
 DEFINITION AGENCOURT 7506202 NIH_MGC_70 Homo sapiens cdna clone IMAGE:6017909
 5' mRNA sequence.
 ACCESSION BQ219245
 VERSION BQ219245.1 GI:20400645
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1004)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM13217 row: p column: 06
 High quality sequence stop: 413.
 Location/Qualifiers
 1.1004
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NIH_MGC_70"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1; Nci:
 Site-2; Salt: Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

BASE COUNT 201 a 323 c 263 g 216 t 1 others

ORIGIN

Query Match 9.7%; Score 270.2; DB 14; Length 1004;
 Best Local Similarity 68.0%; Pred. No. 2,3e-52;
 Matches 391; Conservative 0; Mismatches 183; Indels 1; Gaps 1;

OY 542 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 DB 1 CCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 OY 602 CTTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 661
 DB 61 GTTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 120
 OY 662 CTCAGGATATATTTTGGCAGCTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 721
 DB 121 CCCAGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 OY 722 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
 DB 181 GATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 OY 782 CTCACAGCAAGATATATGATATGATATGATATGATATGATATGATATGATATGAT 841
 DB 241 CCCACAGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 OY 842 CTTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 901
 DB 301 GTTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 360
 OY 902 CTTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 961
 DB 361 CACTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 420
 OY 962 CTTGCTGGAAGATATGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAG 1021
 DB 421 CTTGCTGGAAGATATGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAG 480
 OY 1022 TTTCTGCTGGAAGATATGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAG 1081
 DB 481 TTTCTGCTGGAAGATATGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAGCTTTCGCAAG 540
 OY 1082 AACACT-TTGAGAAAGAAAGAAAGCAAGCTGCCA 1115
 DB 541 AGCACTCTTGAAGAAAGAGGCGGAACCCGCAAGAA 575
 RESULT 26
 LOCUS BF317072 920 bp mRNA linear EST 21-NOV-2000
 DEFINITION BF317072 601903470F1 NIH_MGC_19 Homo sapiens cdna clone IMAGE:4136200 5'
 mRNA sequence.
 ACCESSION BF317072
 VERSION BF317072
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 920)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov
 Plate: LLM1041 row: k column: 17
 High quality sequence stop: 714.

Db 184 CGAAGAGCTCTGCTCAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGATGT 243

OY 1927 GAACAGATCTGACTATCAAG 1949
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Db 244 GAACAGATCTGACTATCAAG 266

RESULT 28
AI968605
LOCUS
DEFINITION
w90e010.x1 NCI_CGAP.GC6 Homo sapiens CDNA clone IMAGE:2514762 3'
similar to TR:Q99454 Q99454 HNSPC.; mRNA sequence.
AI968605
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D., Bento Soares, Ph.D., M. Fatima
Bonaldio, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/db/tp/image/image.html
Insert Length: 1029 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 382.
Location/Qualifiers
1. 541
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2514762"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldio. "
BASE COUNT 84 a 157 c 173 g 127 t
ORIGIN

Query Match 9 3%; Score 256.8; DB 9; Length 541;
Best Local Similarity 67.2%; Pred. No. 3e-49;
Matches 363; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

OY 418 TGCCTGATTTTGTCTGTTTCTACATCCCTGAGCAGACAAATTTGGCTCAAGTGC 477
|||||

Db 2 TGCCTGCTGCTGCTGCTGCTTTCACCATCAAGAGACTATGAGAGAGCTGGAGGGGCC 61
|||||

OY 478 CTCTGATCTCGAGATCGATGATGTCTCTTCTTTGGAGTTCAATTCGATC 537
|||||

Db 62 CTCTGATCTCGAGATCGATGATGTCTCTTCTTTGGAGTTCAATTCGATC 537
|||||

OY 538 TGGTCTGGGGTCTGCTGTTTGTGATATGAGATGAGAGAACTGAGGTTGCTCA 597
|||||

Db 122 TGGGCGCAGAGCTGCTGCTGCTGCTGCTGCTGAGAGGGGGGCTCAAGTTTGCCGG 181
|||||

OY 598 AAGCCCTTCTGTTATAGATACCATTTCTTATCCGTTCAATAGACATTTCTGCA 657
|||||

Db 182 AAGCCCTTCTGTTATAGATACCATTTCTTATCCGTTCAATAGACATTTCTGCA 657
|||||

OY 658 AAACTCAGGGTAAATATTTTGGCAGCTGCTGCTCAGAGCTCTGCTTCTCAGATC 717
|||||

Db 242 GGCCTCCAGGAGCAAGCTTCTTCCACATCTCGCTCCGAGACCTGCTTCTCAGATC 301
|||||

OY 718 CTCCGATGTTGGCCATGAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 777
|||||

Db 302 CTGCGATGATGATCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361
|||||

OY 778 TATGCTCAGCAGCAATTAATATCAAGCTTGTATGATAGATTTTGTCTTATTTT 837
|||||

Db 362 TATGCTCAGCAGCAATTAATATCAAGCTTGTATGATAGATTTTGTCTTATTTT 837
|||||

OY 838 TCGTCTTCTGCTGCTATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 897
|||||

Db 422 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
|||||

OY 898 GATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
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Db 482 GATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
|||||

RESULT 29
BB635544
LOCUS
DEFINITION
BB635544 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus CDNA clone AA30075J21 5', mRNA sequence.
BB635544
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 626)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haru, A.,
Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koude,
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Sakai,
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Tsurumatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
url: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a


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Db      87  TTAATGAATTTTCAGTTCAGAAACGGAAGTTAA-GAAACATTACGTCATATGATGATA 29
QY      1613 AAGATGTCATTGACA 1628
        |||
Db      28  AAGATGTCATTGACA 13

RESULT 31
A1517016      771 bp      mRNA      linear      EST 19-APR-2001
LOCUS      GH27636.5prime GH Drosophila melanogaster head pot2 Drosophila
DEFINITION      A1517016
ACCESSION      A1517016
VERSION      A1517016.1 GI:4420116
KEYWORDS      EST
SOURCE      fruit fly
ORGANISM      Drosophila melanogaster
REFERENCE      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
              1 (bases 1 to 771)
              Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
              Lewis, S. and Rubin, G.M.
              BDGP/HMT Drosophila EST Project
              Unpublished (2001)
              Contact: Stapleton, M.
              BDGP
              Lawrence Berkeley National Lab
              One Cyclotron Rd, Berkeley, CA 94720, USA
              Fax: 510 486 6798
              Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
              hit genomic sequence AC005974
              Plate: 276 row: C column: 12
              High quality sequence stop: 553.
              Location/Qualifiers
                1..771
                /organism="Drosophila melanogaster"
                /db_xref="taxon:7227"
                /clone_lib="GH Drosophila melanogaster head pot2"
                /sex="male and female"
                /dev_stage="adult"
                /lab_host="DH5 - alpha"
                /note="Organ: head; Vector: pOT2; Site 1: EcoRI; Site 2:
                XhoI; Sized fractionated cDNAs were directly ligated into
                pOT2. Plasmid cDNA library."
BASE COUNT      163 a      200 c      213 g      194 t      1 others
ORIGIN
Query Match      8.7%; Score 241; DB 9; Length 771;
Best Local Similarity 61.9%; Pred. No. 1.5e-45;
Matches 415; Conservative 0; Mismatches 251; Indels 4; Gaps 2;

QY      295 AGCCAGAGCTGCACGCGCAACGTCAGTACGCGGCGTGACAGACTACCTGTACACGTCG 354
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Db      103 AACCGCGCACACCGCGCGATGTCGTCACCGCGCCCTCCACAGATCGCTTACACATTC 162
QY      355 CTGAGAGAGACCCCGCGCTG---CGCTTCATCTACACAGCTTTCCTTCCTCTGTC 411
        |||
Db      163 CTGAGAGGCGCGCGCTCACCGCCATCTTCTACCATGTAGTATTCCTGATGAGTCG 222
QY      412 TTTCGTTGCTTGTGTCAGTGTGTTCTTCTACCATCCCGAGACACAAATTTGGCCTCA 471
        |||
Db      223 TTTCACCTGCTGCGCGCTCAGTGTGTTCTTCCACCATCAAGAGATACCAAGACGCCGTC 282
QY      472 AGTTGCTCTTGATCTGAGTTCGTGATGATGTGCTCTTTGTTGGAGTTTCATCATT 531
        |||
Db      283 TACATTCGTTCCGATGAGATCCTGCGTATCTGTTCTGATCAACATGAGTTTGAAGCT 342
QY      532 CGAATCTGCTGCGCGCTTGTGCTGTGTCATATAGAGATGCGCAAGAGATGAGAGTTT 591
        |||
Db      343 CGACTCTGCTCATGCGCTCGCATCGCATACAGGAGATGCTGGTGGTGCAGCTGAGAGTT 402

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QY      592 GCTCGAAGACCCCTCTGTTATAGATACCATGTTCTTATCGCTTACATAGACATGTT 651
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Db      403 GTGAGGACCATCTTCTATATATATATATGATATGTCACACATTTTACGCTCATTTGATATA 462
QY      652 TCTGCAAAAACCTCAGGCTAATATTTTGGCAGCTGTCACATCAGAAAGTCTCGTTCTCTA 711
        |||
Db      463 GGAATGGGACCTTCGGCGCCAGGCTGTCGCGACAGAGATGTTTACGGCTCGGCTTCCTT 522
QY      712 CAGATCTCTCCGATGCTGCGCATGATGACCGAAGGAGGAGGACCTTGGAAATTTACTGGCTCA 771
        |||
Db      523 CAGATCTCTTGGAGAGCGCGCATGATGATCGCGGAGGACCTGGAACCTGCTCGGCTCG 582
QY      772 GTGTTTATCTCTCAGCAAGAAATTAATACACACTTGTACATATGATTTTGGCTCTT 831
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Db      583 GTTGTATACGCACATACAGAGAACTGATACACACATGATACATGATGATGATGATGAT 642
QY      832 ATTTTTCGTTCTTCTGTTCTATCTGTTGGAAGAAAGATGCCAATTAAGATTTTCTACA 891
        |||
Db      643 ATCTTTCATCATCTCTGTTCTATGTTGAGAGAGACGTCATGATGATGATGATGATGAT 702
QY      892 TATGCAATGCTCTCTGTTGCGGACATATGATGATGATGATGATGATGATGATGATGAT 951
        |||
Db      703 TTGCGCCAGCCCTCTGTTGAGG--TGATACACTCTGACGCTGCTATGAGAGACATG 761
QY      952 ACTCCCTTAA 961
        |||
Db      762 GTGCCCATCA 771

RESULT 32
A1418222      502 bp      mRNA      linear      EST 30-MAR-1999
LOCUS      t77403.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2104972 3'
DEFINITION      similar to TR:Q99454 Q99454 HNSPC.; mRNA sequence.
ACCESSION      A1418222
VERSION      A1418222.1 GI:4264153
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 502)
              NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute / National Institute of Neurological
              Disorders and Stroke, Brain Tumor Genome Anatomy Project
              (CGAP/BrCAP), Tumor Gene Index
              Unpublished (1998)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
              Ph.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
              Bonaldo, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA sequencing by: Washington University Genome Sequencing Center
              clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/ILNI at:
              www-bio.llnl.gov/bbrp/image/image.html
              Insert Length: 1080 Std Error: 0.00
              Seq primer: -400P from Gibco
              High quality sequence stop: 322.
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                /db_xref="taxon:9606"
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                /clone_lib="NCI CGAP Brn23"
                /tissue_type="gliblastoma (pooled)"
                /lab_host="DH10B"
                /note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
                modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'

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SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 469)
JOURNAL	NCBI/NINIS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BNGAP), Tumor Gene Index Unpublished (1998)
	Contact: Robert Strausberg, Ph.D. Email: cgaps-rt@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfield M.D., Ph.D.
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
	cDNA Library Arrayed by: Greg Lennon, Ph.D.
	DNA Sequencing by: Washington University Genome Sequencing Center
	Clone distribution: NCIC-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html
	Insert Length: 1048 Std Error: 0.00
	Seq primer: -400P from Gluco
	High quality sequence stop: 454.
FEATURES	location/Qualifiers
SOURCE	1..469
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	/db_xref="taxon:9606"
	/clone="IMAGE:2428714"
	/clone_1lb="NCI CGAP Brn25"
	/tissue.type="neoplastic oligodendrogloma"
	/lab_host="DH10B"
	/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGTTACCACTGTGAAGGGGCGGCATGATTGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	64 a 136 c 148 g 121 t
ORIGIN	
Query Match	7.9%; Score 217.8; DB 9; Length 469;
Best Local Similarity	69.3%; Pred. No. 3.8e-40;
Matches 325:	Conservative 0; Mismatches 142; Indels 2; Gaps 2;
OY	364 CCCCCGGCGTCATCATCACACGCCCTTGTTTCCTGTCCTTGTCCTG 423
Db	1 CCGCCGGCGTGGCGTTTCATCTACCATCTCCATCGTTCCTCCTGTCCTC 60
OY	424 ATTTTGTGAGTTTCTACCATCCCAGAGCACAAATAATGGCCATGGCCCTTG 483
Db	61 GTGCTGTCTGTTTTTCCACATCACAAGAGATATAGAAGAGCTCGAGGGGCCCTTCAC 120
OY	484 ATCTGAGTTTCTGATGATTTGTCGTTTGGTTTGAAGTTCATTCGAATCTGCTGT 543
Db	121 ATCTGGAATTCGTACTATCGTGGTGTGGCGTGGAGTAGTACTGTGGGATCTGGGCC 180
OY	544 GCGGTTCTGTTCATATAGAGATGCGAAGAGACGTGAGTTGCTGGAAGCCC 603
Db	181 GCAGGCTCTGTCGCGGTACCGTGGCTGAGAGGGGGCGGCTCAAGTTGCCGGAACCG 240
OY	604 TTCTGTGTAATGATACATTTGTTCTTATGCTTCATATAGAGATGTTTCTGCAAAAAC 663
Db	241 TTCTGTGATGATGACATCATGTGCTCATGCGCTCCATTTGCGGTCTGAGCCGCGCTCC 300
OY	664 CAGGTAATATTTTGGCACGTCGACATCAGAAGTCTCCGTTTCTACAGATCTCCGC 723
Db	301 CAGGGCAACGCTTTGGCACATCTGGGCTCGGAGCGCTGCGCTTCTGCAAGTTCTGGCG 360
OY	724 ATGTTGGCATGAGACCAGAGGGAGGCGACTTGGAAATTAATCTGGGTC-AGTGGTTTATGC 782

[illegible]

Db	535	CGGGTTCCTTTGTGTCATCTCGGCGCTGGTTCCTGTGTACTTGGCAGAGAAAGGGGAGAA	476
QY	876	TAAAGACTTTTCTACATATGCAGATGCTCTCTGTGTGGGCGACAATTACATTGACACTAT	935
Db	475	CGACCACTTTTGACACCTACGCGGGATGCACTCTGTGTGGGGCCTGATCAACGCGACCAACAT	416
QY	936	TGGCTATGGAGACAAACTCCCTCAACTTGGCTGGGAAGATTGGTTTCTGAGGCTTTGC	995
Db	415	TGGTTACGGGGACACAGATACCCCGACACTGGAAACGGCAGGTCCTTGGCGCAACCTTAC	356
QY	996	ACTCCCTTGGCAATTTCTTCTTTTGGCACTTCCTGCGGCAATTTCTGCTCAGGTTTTGCATT	1055
Db	355	CCCTATCGGTGTCTCTTTTTCGGCTGCGCTGACGAGCACTTTGGGGTCTGGGTTGGCCCT	296
QY	1056	AAAAGTACAGAACAAACCGCGCCAGAAAACATTGAGAAAAAAGAAAGAAACCGACTGCCAA	1115
Db	295	GAAAGTTTCAGGAGGACAGCAGGCAAGAACACTTTGAGAAAAAGGCGAACCAGGACAGG	236
QY	1116	CCCTATTCAGTGTGTTTGGCGCTAGCTTAACG	1145
Db	235	CCCTATTCAGTGTGCGCTGGAGATTTTTACG	206

Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco.
Location/Qualifiers
1. 438

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5781976"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1:
NotI; Site:2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1910, Fax: 314-747-2692."

BASE COUNT

61 a 125 c 138 g 114 t

ORIGIN

Query Match 7.7%; Score 214.8; DB 14; Length 438;
Best Local Similarity 68.4%; Pred. No. 1.9e-39;
Matches 297; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

400 TTCTCCCTGCTCTGCTGCTGATTTGTCAGTGTTCCTACATCCCTGACACACA 459
1 TTCTCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
460 AATGAGCTCAAGTTGCTGATCCGAGATTCGATGATGCTGCTGCTGCTGCTGCTG 519
61 AAGAGTTGGAGGGGCTGATCCTGAGAAATGCTGATGCTGCTGCTGCTGCTGCTG 120
520 GAGTTCATCATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 579
121 GAGTTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
580 AGAGTTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639
181 CGGCTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
640 ATACAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
241 ATTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
700 CTGCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
301 CTGCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
760 TTACTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
361 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
820 TTTTGGTTCTTAT 833
421 TTCTTGTCTCAT 434

RESULT 39
BF954374 224 bp mRNA linear EST 22-JAN-2001
LOCUS BF954374
DEFINITION OY2-NN0045-131100-414-C02 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF954374
VERSION BF954374.1 GI:12371649
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=OY2-NN0045-
131100-414-C02&f3=2000-11-13&f4=1)
Seq primer: puc 18 forward
High quality sequence stop: 224.

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous-normal; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORSTS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT

69 a 58 c 46 g 51 t

ORIGIN

Query Match 7.5%; Score 207.4; DB 12; Length 224;
Best Local Similarity 99.5%; Pred. No. 9.6e-38;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1373 TCACGACCGAAGCCGCTTCCGCGCTGCGCTCAAAAGTTTCAGCCAAACAG 1432
16 TCACGACCGAAGCCGCTTCCGCGCTGCGCTCAAAAGTTTCAGCCAAACAG 75
1433 TGATGATCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATG 1492
76 TGATGATCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATG 135
1493 GTGATGATCAGTGAAGACCTGACCCACACCTTAAGCTGATTCAGACTATCAGAA 1552
136 GTGATGATCAGTGAAGACCTGACCCACACCTTAAGCTGATTCAGACTATCAGAA 195
1553 TTATGAATTCATGTTGCAAAACGAG 1581
196 TTATGAATTCATGTTGCAAAACGAG 224

RESULT 40
BM640404 698 bp mRNA linear EST 26-FEB-2002
LOCUS BM640404
DEFINITION 17000687765888 A.Gam.ad.cdna1 Anopheles gambiae cDNA clone
ACCESSION BM640404
VERSION BM640404.1 GI:18939915
KEYWORDS EST.
SOURCE African malaria mosquito.

ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 698)
REFERENCE Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C., and Hoffman, S.L.
Cclera Anopheles gambiae EST project
Unpublished (2002)
JOURNAL COMMENT Contact: Holt R.A.
Cclera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@cclera.com
Place: ND01004B12 row: H column: 24
Seq primer: M13 Reverse.
FEATURES
source
1. 698
Location/Qualifiers
/organism="Anopheles gambiae"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="1960049622026"
/clone_1lb="A.Gam.ad.cdna1"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cdna inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)"
BASE COUNT 139 a 203 c 206 g 150 t
ORIGIN
Query Match 7.4%; Score 206.4; DB 13; Length 698;
Best Local Similarity 61.8%; Pred. No. 1.8e-37;
Matches 346; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
OY 632 TCGCTTCATAGCAGTGTTCGCAAAACTCAGGTAATATTTTCCACAGTCTGCAC 691
DB 9 TCCGCTCCATAGTGTCTCGTATGGGACATCCGCGGAGTGTTCACACAGTGCAC 68
OY 692 TCGAATCTCCGCTTCACAGATCCCTCCGATGTCGATGAGGAGGAGGA 751
DB 69 TCGAGGGCTCCGCTTCCTCCAAATCCGCGATGCGATGAGCGCGCTGCAGCA 128
OY 752 CTGGAATTTACTGCTTCAAGTGTTCATGCTACAGCAGGAAATTAATCAGCTTGT 811
DB 129 CGTGAAGAGCTCGGAGAGTGTCTACAGCTCACAGACAGAAATTAATTAACCTTGT 188
OY 812 ACATAGATTTTGGTCTTATTTTTCGTCCTTCCTCTATCTGTGGAAGAGATG 871
DB 189 ATATAGGTTTTCGCGCTTATTTTTCGCTGTTTATGTAATTAATGAGAAGATG 248
OY 872 CCA--ATTAAGATTTTCTCATATGAGATGCTCTGTGGGGGACAAATTAATCA 928
DB 249 TAAGGGAGACCAATGTAATCTTGTGCTCAAGCTTGTGGGGGTGATAGAGCTT 308
OY 929 CAATATTTGCTATGAGACAAACTCCCTTAATCTGCTGGAGAGATTTGCTTGACG 988
DB 309 GCAGGCTGGGTATGCGGATATGTCGCGGAGAGCTGCGCAAGCAAAATTAATGATCGT 368
OY 989 GCTTGCATCTCTTGCAATTTCTTTTTCGATCTCTGCGGCAATTTGCTCAGTGT 1048
DB 369 TCTCGCGCTCTGAGGATCTCTCTTCGCACTCCGCGGGGTATCCGCGAGGCGGT 428
OY 1049 TTGATATAAAGTACAGAAACACACCGCCGAAGAACTTTGAGAAAGAAAGAACCCAG 1108
DB 429 TCGCGCTGAAAGTACAGCAGACGCGCCAGAAACATGATCCGCGCCGCAACCGG 488
OY 1109 CTGCAACCTTCATTCAGTGTGTGGCTAGTTAGCAGCTGATGAGAAATCTGTTTCA 1168

DB 489 CCGGACGCTGATATACAGTCTGCTGAGAGATTTAGCGCGGACAGACACTGATGCCG 548
OY 1169 TTGCAACTGGAAGCCACAC 1188
DB 549 AGCGACGCTGGAATATCCAC 568
RESULT 41
A1871198
LOCUS
DEFINITION w170906.x1 NCI-CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2430298 3'
similar to TR:099454 Q99454 HNSPC.; mRNA sequence.
ACCESSION A1871198
VERSION A1871198.1 GI:5545166
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 407)
REFERENCE NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert length: 1097 Std Error: 0.00
Seq primer: -400P from Glibco
High quality sequence stop: 384.
FEATURES
source
1. 407
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2430298"
/clone_1lb="NCI-CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cdna was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAGTGGGAGCGCGGACATAGGTTTATTTTATTTTATTTT
T 3']; double-stranded cdna was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 60 a 115 c 134 g 97 t 1 others
ORIGIN
Query Match 7.4%; Score 205.6; DB 9; Length 407;
Best Local Similarity 69.3%; Pred. No. 2.7e-37;
Matches 280; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
OY 418 TGGTGAATTTTGTAGGTTTCTTACCAATCCCTGACACACAAATTTGGCTCAAGTTCG 477
DB 2 TGGCTCGTGTGCTGTGCTGTTTCCACCATCAGAGATGAGAGAGCTCGAGAGGCGC 61
OY 478 CTCTGATTCGCGAGGTGCGATGATGCTGCTTTGGTTGAGTTTCATCATTCGATTC 537
DB 62 CTCTACATCCCTGGAATATGATCATCTGCTGTTTGGCTGAGATCTTCTGCGGATC 121
OY 538 TGGTTCGCGGGTGTGCTGTTCGATATAGAGATGAGCAAGAGAACTGAGTTTGTCTGA 597

Db	122	TGGGCGCGAGCTGCTGCTGCCGGTACCGTGGCTGAGAGGGGGGGGCTCAAGTTTGGCCG	181
QY	598	AAGCCCTTCGTGTATATGATACCATTTCTTATACGCTTCAATATAGCAATTTCTTCTGA	657
Db	182	AAACCGTTCTGTGTATGATGACATCATCTGCTCATCGCTTCATATGCGGTGCTGGCGGC	241
QY	658	AAAACCTAGGGTAATATTTTTGGCCAGTCTGCACATCAGAAAGTCTCGTTTCTACAGATC	717
Db	242	GGCTCCAGGGCAACGTCCTTGGCCACATCTGCGCTCCGAGGCTTCGCTTCTCGAGATT	301
QY	718	CTCCGCATGTGTGCATGATGACCGAAGGGGAGGACATTTGAAATTCATGGGTTCAAGGTT	777
Db	302	CTGGGATGTATCCGATCTGACCGGGGGGGAAGACACTGGAAGCTCTGTGGCTCTGTGGTC	361
QY	778	TATCTCAGACAGAGAAATTAATACAGCTTGTATCATAGATTT	821
Db	362	TATGCCACACAGAGAGCTGTGTCTCTCTCGATATCATGGGCTT	405

RESULT 42	AV838434/c	448 bp	mRNA	linear	EST 07-NOV-2001
LOCUS	AV838434				
DEFINITION	AV838434 NotI Setoh unpublished cDNA library, egg Ciona				
	intestinalis cDNA clone rcleg03115, mRNA sequence.				
ACCESSION	AV838434				

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VERSION      AV838434.1  GI:16782585
KEYWORDS     EST.
SOURCE       Clona intestinalis.
ORGANISM     Clona intestinalis

```

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 448)	Satoh, N., Satou, Y., Kohara, Y. and Shino, T.	Expressed genes in <i>Clona intestinalis</i>	Unpublished (2000)	Contact: Nori Satoh

Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.

FEATURES	Location/Qualifiers
source	1. .448

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organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="rcleg03115"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/note="Vector: pBluescript SK"
BASE COUNT
132 a 110 c 81 g 125 t

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Query Match 7.3%; Score 202; DB 10; Length 448;
Best Local Similarity 68.2%; Pred. No. 1.9e-36;
Matches 29; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 726 GGTGGCATTGACCGAAGGGAGAGGCACCTTGGAAATTACTGGTTCAGTGGTTTAGCTCA 785
 ||| | ||||| ||||| ||||| | ||| ||||| |||||
 Db 434 GGTAAATGTGACAGAAGAGAGCATCATGCAAGTGTATTCTCTGTGTGTTACAGCTCA 375

OY 786 CAGCAAGAATTATCATCAGCTTGTCACATAGGATTTTGGTCTGTATTTTTGCCTCTTT 845
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 CAGTTAAAGACTTATCATCACGACATGTAATTGCGCTTCCTGGCCCTCATATTTTGCCCTGGT 315

QY 846 CCTGCTATCCTGTGAAAAAGATG---CCAAATAAGAGTTTTCATCATATGCAGATGC 902
||||| | | |||| | | | |||| | | | |||| |
DB 314 TCTTGCTATCAAGCAGAAAAAGATGAACAACAGCAAGAATTTCAAACTTTGCCGATGC 255

003

303 TCCTGGTGGGCAATTACATTGACACTATTGGCTATGAGACAAACTCCCTTAC 962

Db	254	CTTATGCTGGGGATTGATTAA	CCCTGACACACATCGGTACGAGAAAGAGTCCGATCAC	195
QY	963	TTGGCTGGGAGATTGCTTTCT	TGCAGGCTTTGCACCTCTGGCATTCTTCTTTTGCAC	1022
Db	194	ATGGCGGGGTCGCTCTAATAG	CAAGTGTATTTCGAATCTTGGAAATTTCAATTTTGGCTCT	135
QY	1023	TCCTGCGGCGATCTTGCTGCT	CAGTTTGGATTTGAATTAACAGAAACAAACCGCCGAGAA	1082
Db	134	ACCAGCCGGAATTTCTGGGTT	CAGGATTTGCTTTAAATTTCAAGAAACAAACCGTCAGAA	75
QY	1083	ACACTTTGAAGAAAGAGAAC	CAACCGCTGCCAACCCTCATTCAGATGTGTTTGGCGTATGTA	1142
Db	74	GCATTTTCGCTCGCAGAGAG	AATGCGCGCCCTATTATTATACAGTATATGTGCGGATGTA	15
QY	1143	CGCAGCTGATGAGA	1156	
Db	14	TGCTGCGGATTAATAA	1	

	622 bp	mRNA	linear	EST J3-JUL-2000
LOCUS				
DEFINITION	601108867F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349625 , mRNA sequence.			
ACCESSION	BE257127			

VERSION	BE25/17.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

AND EXTENDED	1 (bases 1 to 622)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccranbs-remail@nih.gov

Tissue Procurement: ATCC
CNA Library Preparation: Ling Hong/Rubin Laboratory
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Plate: LLCM144 row: e column: 18
High quality sequence ston: 621

```

FEATURES
Source
Location/Qualifiers
1. .622
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3349625"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"

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7/00ec Organ. eye; vector: pGB1; site-1: amino; site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

ORIGIN					
Query Match	7.2%	Score 200.8;	DB 10;	Length 622;	
Best Local Similarity	61.1%;	Pred. No. 3.7e-36;			
Matches 325;	Conservative	0. Mismatches 207;	Totals	0;	0;

Accession	Conserved	0	Mismatches	20	Indels	0	Gaps	20
169	GGCCTGCTACTGCTGGGACCCGCGGGGACAGCCTGGTGGCGCGGCGGTGGGCTGTAGG	228						
OY								
Db	91 GGGCTTCGGGGAGCTGAGCCCCGCGCGCCGACCTACCCCGGGAGCGGGGCGCTGTGATC	150						

229 GAGAGCCGCCCGGGGCAAGCAGGGGGGCCCGGATGAGCCCTGGGGAAGCCGCTCTTTAC 288

[illegible]

```

RESULT 44
AL588359
LOCUS AL588359 555 bp mRNA linear EST 02-MAR-2001
DEFINITION AL588359, BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION ROS071C08, mRNA sequence.
VERSION AL588359
KEYWORDS AL588359.1 GI:13193393
SOURCE EBF.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 555)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel.: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTT TTTT TTTT TTTT 3' POLY A RNA purchased from Clontech
(*6854-
Seq primer: T7.
FEATURES
SOURCE
Location/Qualifiers
1..555
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS071C08"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site1: NotI; Site2: SalI; Cloned
unirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACATCGAG 3' , 3' adaptor sequence: 5'
GCGCGCGCTTTT TTTT TTTT TTTT 3' POLY A RNA purchased from
Clontech (*6854-1)"

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BASE COUNT	106 a	133 c	175 g	139 t	2 others
ORIGIN					
Query Match	7.1%	Score 197.2;	DB 9;	Length 555;	
Best Local Similarity	62.5%;	Pred. No. 2.5e-35;			
Matches 345;	Conservative	0;	Mismatches 195;	Indels 12;	Gaps 2;
QY	204	CGGTGGGGGGGGGGGGTGGCCCTGAGGAGAGAGCCCGGGGAGAGAGAGGGGGCCCGGATGAG	263		
Db	7	CGATCGGGAGACGGGACGGCTGCTGCGAAGGGGGGGGAGAGAGAGAGAGAGAGCGGAG	66		
QY	264	CCGTCTGGGGGAGGCGCGCTCTTACAGAGATGAGCAGAGCTGCC-----GAGCGAA	314		
Db	67	CCCTCCGGGGGTTGGGGGCTGTGTGGGAGAGACCCCTTGAGCCGCCCGGCTGAAGAGGAACCA	126		
QY	315	CGTCAGATACCGGCGGTGTCAGAACTACCTGACAGCTGCTGAGAGAGACCCCGGCTG	374		
Db	127	CGCGAAGATGCGCGGAGATCCAACTTTGATCTACGAGCGCCCTGGAGAGACCCCGGCTG	186		
QY	375	GGCGTTACATCACCACGCTTGGTTTTCTCTCTTGTCTTTGGTTGCTTGAATTTGTCACT	434		
Db	187	GGCGCTGCTCTACACAGCGCTGCTGTTTCTGATTTGGGTTGTTGATCTTACGCTGT	246		
QY	435	GTTTTCTACCATCCCTGAGCAGCAAAATGGCCTCAAGTGGCTCTTGATCTCGAGGT	494		
Db	247	CCTGACAACTTTCAAGGAGTGAACCGTTGGGGTGATCGGCTTCTTTGCTGGAAC	306		
QY	495	CGTATGATGTTCGCTCTTTGGAGTTCATATTCGATTCGATTCGCTGGGTTGCTG	554		
Db	307	CTTTGGCATTTTCACTTTTGGAGCAGAGATTTGCTTAAGATCTGCGGTGCTGGGTGTG	366		
QY	555	TTTGCATATATGAGATGCGCAAGAGAGACTGAGTTGCTCGAAAGCCCTTCTGTATT	614		
Db	367	CTGCGTTACAAAGATGAGAGAGAGAGACTGAGTTGCTCGAAAGCCCTTCTGTATT	426		
QY	615	AGATACCATTTTCTTATCGCTTAAATAGCAGTGTCTTCTCAAAAACCTCAGGGTAAT	674		
Db	427	AGATATCTTTTGTGATGCTTCAAGTCCAGTGCTGCTTGGGAAACGAGGCAATGT	486		
QY	675	TTTTGGCCGCTGCTGACACAGATGCTCCGTTCTACAGATTCCTCGCATGTGCGCAT	734		
Db	487	TCTGGCCACAT---CGCTCANAGACCTTCCCTTCTTCAAGTCTCGAGATGCTCCNAAT	543		
QY	735	GGACCGAAGGGG	746		
Db	544	GGATAGAGAGAGG	555		
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DEFINITION	UT-M-ALL-ahk-e-04-0-UI.r1 NIH BMP-MCO.N Mus musculus cDNA clone				
ACCESSION	BE860721				
VERSION	BE860721.1	GI:10377952			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	Bonaldi,M.F., Lennon,G. and Soares,M.B.				
JOURNAL	Normalization and subtraction: two approaches to facilitate gene				
MEDLINE	discovery				
COMMENT	Genome Res. 6 (9), 791-806 (1996)				
	97044477				
	Contact: Chin, H				
	National Institute of Mental Health				
	6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD				
	20892-9643, USA				
	Tel: 301 443 1706				
	Fax: 301 443 9890				
	Email: mbs@mail.nih.gov				

Search completed: June 19, 2003, 11:07:39
Job time : 3488 secs

ACCESSION BO340041
VERSION BO340041.1 GI:21000357
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 297)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&tl2-QV2-NN0045-
261200-569-b11&tl3-2000-12-26&tl4-1)
Seq primer: puc 18 forward
High quality sequence stop: 50.
Location/Qualifiers
1. 297
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0045"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 82 a 73 c 69 g 73 t
ORIGIN
Query Match 6.7%; Score 185.4; DB 14; Length 297;
Best Local Similarity 82.1%; Pred. No. 1.4e-32;
Matches 239; Conservative 0; Mismatches 46; Indels 6; Gaps 2;
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DB 61 AGCCGAGAGAGCATGACTGCGAAGAGAGAGCCCAAAATATCTCAGAGATGCCAGTCC 120
QY 1788 GGTGGTCAAGGTGGAAGAAAGAGTACAGTCCATGAAATCCAAAGTGGAGCTGCTACTAGA 1847
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QY 1848 CATCTATCAACAGAGTCTTGGAAGAGCTGCTCAGCCCTCGCTTGGCTTCATTCCA 1907
DB 181 CATCTATCAACAGAGTCTTGGAAGAGCTGCTCAGCCCTCGCTTGGCTTCATTCCA 240
QY 1908 GATCCCACTTTTGAATGTGAACAGACATGACTATCAAGCCCTGTGA 1958
DB 241 GATCCCACTTTTGAATGTGAACAGACATGACTATCAAGCCCTGTGA 291

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84	54.6	2.0	1337	24	ABQ68452	Listeria monocytrog
85	54.2	2.0	1459	21	AAK02528	Human colon cancer
86	53.6	1.9	11495	20	AAK53451	Human adenosine A1
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88	53.6	1.9	237	21	AAAB1807	N. meningitidis pa
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92	53.4	1.9	4403765	22	AAI99683	Mycobacterium tub
93	53.4	1.9	4411529	22	AAI99682	Mycobacterium tub
94	52.8	1.9	238	20	AAK57154	Mycobacterium tub
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96	52.8	1.9	712	24	ABQ40858	Oligonucleotide fo
97	52.8	1.9	1000	21	AAK02484	Oligonucleotide fo
98	52.8	1.9	3218	23	ABL01914	Human colon cancer
99	52.8	1.9	3339	23	ABL20762	Drosophila melanog
100	52.8	1.9	3339	23	ABL01915	Drosophila melanog
101	52.8	1.9	3441	23	ABL20763	Drosophila melanog
102	52.6	1.9	6031	22	ABAI5148	Human nervous syst
103	52.6	1.9	584	24	ABO51928	Human nervous syst
104	52.6	1.9	584	24	ABO51928	Oligonucleotide fo
105	52.6	1.9	1127	21	AAK02477	Oligonucleotide fo
106	52.6	1.9	4176	22	AAI57831	Human colon cancer
107	52.4	1.9	241	20	AAK57153	Human polynucleoti
108	52.4	1.9	3188	20	AAK02974	Human KCMQ2 introg
109	52.4	1.9	4411529	20	AAK02974	Human IL-1ra BAC c
110	52.4	1.9	1126	22	AAI99682	Mycobacterium tub
111	51.8	1.9	998	22	AAK02538	Human colon cancer
112	51.8	1.9	998	22	ABAA3164	Human breast cell
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114	51.8	1.9	998	22	ABA23338	Probe #1804 for ge
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147	51.4	1.9	36778	21	AAZ87318	S. venezuelae ptx
148	51.4	1.9	37948	21	AAZ87285	S. venezuelae pik
149	51.4	1.9	38506	21	AAZ57633	Nucleotide sequenc
150	51	1.8	38506	21	AAZ56001	Recombinant cosmid
			1326	22	AAH44336	Human GATM4 nucleo

ALIGNMENTS

XX	AAH43633	standard; cDNA, 2772 BP.
XX	AAH43633;	
XX	21-JAN-2002	(first entry)
XX		Human ion-channel forming protein ORF.
XX		Ion-channel forming protein; voltage-gated potassium channel;
KW		fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX	Homo sapiens.	
OS		
PN	WO200175108-A1.	
PD	11-OCT-2001.	
PF	03-APR-2001; 2001WO-US10875.	
PR	03-APR-2000; 2000US-194255P.	
PA	(LEXI-) LEXICON GENETICS INC.	
PI	Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B,	
P1	Sands AT;	
XX	WPi: 2001-656987/75.	
DR	P-PsDB: AAB47678.	
PT	New human ion channel protein and polynucleotides encoding the protein,	
PP	useful in diagnosing or treating diseases, in drug screening, and in	
XX	clinical trial monitoring -	
PS	Claim 1: Page 34-35; 41pp; English.	
XX	The sequences in AAH43633-34 encode a novel ion-channel forming protein.	
CC	The protein shares structural similarity with mammalian ion channel	
CC	proteins, particularly voltage-gated potassium channel proteins. The	
CC	protein is expressed in many human cell lines including fetal brain,	
CC	brain, thymus, prostate, heart and skeletal muscle. The novel protein	
CC	can be used in the diagnosis or treatment of diseases, in drug	
CC	screening, and in clinical trial monitoring. The oligonucleotides may	
CC	be used as hybridization probes for screening libraries, and assessing	
CC	gene expression patterns (particularly using a micro array or high	
CC	throughput chip format). The nucleic acids and novel protein can also be	
CC	used in the identification, selection and validation of novel molecular	
CC	targets for drug discovery, to screen collections of genetic material	
CC	from patients who have a particular medical condition, to identify	
CC	mutations associated with a particular disease, as a diagnostic or	
CC	prognostic assay, and to screen for drugs which can be used to treat	
CC	symptomatic or phenotypic manifestations of perturbing the normal	
CC	function of novel human protein. The polypeptides are further used in	
CC	generating antibodies.	
XX		
SQ	Sequence 2772 BP: 715 A; 700 C; 713 G; 644 T; 0 other:	
	Query Match 100.0%; Score 2772; DB 22; Length 2772;	
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301 AGCTGCGGGCGGACCTCAAGTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
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Dd		2521	GAGTCAAGTGGCTTCAGAGGAGCCAGATTTTAACCCCAATGAGAGGAATCCAAATG	2580
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Dd		2581	TTTTATACGATGATGAGAGGTGGGTCCGAAAGACAGACAGACACTTTTGATGCCGA	2640
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Dd		2641	CCGACACCTGCCAGGGAAGCTGCCCTTTCATCAGACTCTTAAGACTGGAAAGTCAGA	2700
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Dd		2701	TGATCTCAGAGCACTTTGTAAGGAGAGAGAAATACAGATGCCCCAAGCTTGCCATGTC	2760
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RESULT 2				
XX	ID	AAH43634	standard; cDNA; 3111 BP.	
XX	AAH43634;			
XX	21-JAN-2002	(first entry)		
DE		Human ion-channel forming protein coding sequence.		
KW		Ion-channel forming protein; voltage-gated potassium channel;		
XX		fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.		
OS		Homo sapiens.		
XX	Key	Location/Qualifiers		
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FN		WO200175108-A1.		
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XX		03-APR-2001; 2001WO-US10875.		
PF		03-APR-2000; 2000US-194255P.		
PR		(LEXI-) LEXICON GENETICS INC.		
PA		Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;		
PI		Sands AT;		
DR		MP1: 2001-656987/75.		
XX		P-PDB; AAB47678.		
PT		New human ion channel protein and polynucleotides encoding the protein,		
PT		useful in diagnosing or treating diseases, in drug screening, and in		
XX		clinical trial monitoring		
SS		Disclosure: Page 37-38; 41pp; English.		

Query Match	Best Local Similarity	100.0%	Score 2772	DB 22	Length 3111
Matches 2772	Conservative	0	Mismatches	0	Indels
					Gaps
XX	The sequences in AAAH3633-34 encode a novel ion-channel forming protein.				
CC	The protein shares structural similarity with mammalian ion channel				
CC	proteins, particularly voltage-gated potassium channel proteins. The				
CC	protein is expressed in many human cell lines including fetal brain,				
CC	brain, thymus, prostate, heart and skeletal muscle. The novel protein				
CC	can be used in the diagnosis or treatment of diseases. The novel				
CC	screening, and in clinical trial monitoring. The oligonucleotides may				
CC	be used as hybridization probes for screening libraries, and assessing				
CC	gene expression patterns (particularly using a micro array or high				
CC	throughput chip format). The nucleic acids and novel protein can also be				
CC	used in the identification, selection and validation of novel molecular				
CC	targets for drug discovery, to screen collections of genetic material				
CC	from patients who have a particular medical condition, to identify				
CC	mutations associated with a particular disease, as a diagnostic or				
CC	prognostic assay, and to screen for drugs which can be used to treat				
CC	symptomatic or phenotypic manifestations of perturbing the normal				
CC	function of novel human protein. The polypeptides are further used in				
CC	generating antibodies.				
XX					
SO	Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 other;				
QY	1 ATGCCCCGACACACGAGGGAAGAGAGGCGCGCGCGGCTGGGTGAAGAC	60			
DB	60 ATGCCCCGACACACGAGGGAAGAGAGGCGCGCGGCTGGGTGAAGAC	119			
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DB	120 GCGCAGCGCGCGCGCGCGCGCGCGCTTGGCAGCGCATGAAGATGTGAG	179			
QY	121 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTACTG	180			
DB	180 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTACTG	239			
QY	181 CTGGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240			
DB	240 CTGGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	299			
QY	241 GCGAAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300			
DB	300 GCGAAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	359			
QY	301 AGTCG	360			
DB	360 AGTCG	419			
QY	361 AGACCCG	420			
DB	420 AGACCCG	479			
QY	421 TTGATTTTGTACGATTTTGTACATCCGTAGACACAAATTTGGCTCAAGTTC	480			
DB	480 TTGATTTTGTACGATTTTGTACATCCGTAGACACAAATTTGGCTCAAGTTC	539			
QY	481 TTGATTCGTGAGTTTGTGATGATTTGTGCTTTTGTGAGTTTCATTCATTCG	540			
DB	540 TTGATTCGTGAGTTTGTGATGATTTGTGCTTTTGTGAGTTTCATTCATTCG	599			
QY	541 TTTGCGGCGGTGCTTTGTGCTATTAAGAGATGCAAGAGACGAGTTTGTGAA	600			
DB	600 TTTGCGGCGGTGCTTTGTGCTATTAAGAGATGCAAGAGACGAGTTTGTGAA	659			
QY	601 CCGTTTGTGTTATAGATACCATTTTGTTCCTCAATTAAGAGATTTTGTGCAAA	660			
DB	660 CCGTTTGTGTTATAGATACCATTTTGTTCCTCAATTAAGAGATTTTGTGCAAA	719			
QY	661 ACTCAGGTAATATTTTTCGACGTGCACTCAAGAGTCTCGTTTCTTACAGATCTC	720			
DB	720 ACTCAGGTAATATTTTTCGACGTGCACTCAAGAGTCTCGTTTCTTACAGATCTC	779			

QY 721 CGCATGTTGGGCATGAGCCGAGGGAGGCACTTGGAAATTACTGGGTTTCACTGAGTTTAT 780
DB 780 CGCATGTTGGGCATGAGCCGAGGGAGGCACTTGGAAATTACTGGGTTTCACTGAGTTTAT 839
QY 781 GCTCACAGCAAGAAATTAATCAAGCTTGGTACATAGAGATTTTGGTTCTTAATTTTTCG 840
DB 840 GCTCACAGCAAGAAATTAATCAAGCTTGGTACATAGAGATTTTGGTTCTTAATTTTTCG 899
QY 841 TCTTTCTGCTATCTGCTGGAAAAGATGCAATTAAGAGTTTCTTCAATATGAGAT 900
DB 900 TCTTTCTGCTATCTGCTGGAAAAGATGCAATTAAGAGTTTCTTCAATATGAGAT 959
QY 901 GCTCTGCTGGGGGACAAATTAATGCAACTATTTGGTATGGAGACAAACTCCCTTA 960
DB 960 GCTCTGCTGGGGGACAAATTAATGCAACTATTTGGTATGGAGACAAACTCCCTTA 1019
QY 961 ACTTGGCTGGGAGAAATCTTCTGACAGCTTGGCACTTCTTGGCATTTCTTCTTGGCA 1020
DB 1020 ACTTGGCTGGGAGAAATCTTCTGACAGCTTGGCACTTCTTGGCATTTCTTCTTGGCA 1079
QY 1021 CTTCCTGCGGCATCTTGGCTCAGGTTTGGCATTAAGTACAGACACACCCGAC 1080
DB 1080 CTTCCTGCGGCATCTTGGCTCAGGTTTGGCATTAAGTACAGACACACCCGAC 1139
QY 1081 AAACACTTGAAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAGTGTGTTGGCTAGT 1140
DB 1140 AAACACTTGAAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAGTGTGTTGGCTAGT 1199
QY 1141 TACGAGCTGATGAGAAATCTGTTCCATTGGCACTTGGAGCCACACTTGAAGGCTTG 1200
DB 1200 TACGAGCTGATGAGAAATCTGTTCCATTGGCACTTGGAGCCACACTTGAAGGCTTG 1259
QY 1201 CACACCTGACGCTTACCAATAGAGAGTAAAGTTTAAAGAGAGAGTGGCCATGGCTAGC 1260
DB 1260 CACACCTGACGCTTACCAATAGAGAGTAAAGTTTAAAGAGAGAGTGGCCATGGCTAGC 1319
QY 1261 CCCAGGGGCGAGATTAATTAAGACCGCAGACCTCAGTAGGTGACAGAGAGTCCCAAGC 1320
DB 1320 CCCAGGGGCGAGATTAATTAAGACCGCAGACCTCAGTAGGTGACAGAGAGTCCCAAGC 1379
QY 1321 ACCGACATCACAGCCGAGGGAGTCCCAACCAAGTCCAGAGAGCTGAGCTTACAGAC 1380
DB 1380 ACCGACATCACAGCCGAGGGAGTCCCAACCAAGTCCAGAGAGCTGAGCTTACAGAC 1439
QY 1381 CGAACCCTGTCGGGCTCGCTGGCGCTCAAAAGTTTTCAGGCCAAACAGATGATGAT 1440
DB 1440 CGAACCCTGTCGGGCTCGCTGGCGCTCAAAAGTTTTCAGGCCAAACAGATGATGAT 1499
QY 1441 GCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1500 GCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1559
QY 1501 TTAGAGGAAGACCTCACCCACCACTTAAACCTGCTATGAGCTATACAGATTAAGAA 1560
DB 1560 TTAGAGGAAGACCTCACCCACCACTTAAACCTGCTATGAGCTATACAGATTAAGAA 1619
QY 1561 TTTTCATGTTGCAAAAGGAAGTTTAAAGAAACATTAAGCTCATATGATTAAGATGTC 1620
DB 1620 TTTTCATGTTGCAAAAGGAAGTTTAAAGAAACATTAAGCTCATATGATTAAGATGTC 1679
QY 1621 ATTGAACAATATTTCTGCTGCTATGAGACATGTTGTAGATTAAGACCTTCAACA 1680
DB 1680 ATTGAACAATATTTCTGCTGCTATGAGACATGTTGTAGATTAAGACCTTCAACA 1739
QY 1681 CGTGTGATCAAAATTTGGAAGAGGCAATACATCAGATTAAGAGAGCGAGAGAA 1740
DB 1740 CGTGTGATCAAAATTTGGAAGAGGCAATACATCAGATTAAGAGAGCGAGAGAA 1799
QY 1741 ATTAACAGCAAGACATGAGACAGACGATCTCAGTATGCTCGGTTGCTCAAGGTT 1800
DB 1800 ATTAACAGCAAGACATGAGACAGACGATCTCAGTATGCTCGGTTGCTCAAGGTT 1859

QY 1801 GAAAAACAGGTACAGTCCATAGAAATCCAGAGTGCCTGACTTACATGATCTATCAACAG 1860
DB 1860 GAAAAACAGGTACAGTCCATAGAAATCCAGAGTGCCTGACTTACATGATCTATCAACAG 1919
QY 1861 GTCTTTGGAAAGCTCTGCTCCAGCCCTGCTTGGTCAATTCACATCCACCTTTT 1920
DB 1920 GTCTTTGGAAAGCTCTGCTCCAGCCCTGCTTGGTCAATTCACATCCACCTTTT 1979
QY 1921 GAATGTACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 1980
DB 1980 GAATGTACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 2039
QY 1981 GCACAAAACAGTGCCTGTTATCCAGATCAAACTAGTCCCAATCTCGAGAGCCCTGACG 2040
DB 2040 GCACAAAACAGTGCCTGTTATCCAGATCAAACTAGTCCCAATCTCGAGAGCCCTGACG 2099
QY 2041 TTCAATTCGAGCCCAAAAGATTTACAGTCCCAAGTCTTCTAGGCTTACGCTTACTATG 2100
DB 2100 TTCAATTCGAGCCCAAAAGATTTACAGTCCCAAGTCTTCTAGGCTTACGCTTACTATG 2159
QY 2101 CACAGTCAAGACACAGGTGCCAATATGTCMAAGCGATGCTCAGCACTGCGACGACCC 2160
DB 2160 CACAGTCAAGACACAGGTGCCAATATGTCMAAGCGATGCTCAGCACTGCGACGACCC 2219
QY 2161 AACACCAATTCGAAACCAATATATAGGCAACCCAGCCAGACGCCCAACCTTTACAG 2220
DB 2220 AACACCAATTCGAAACCAATATATAGGCAACCCAGCCAGACGCCCAACCTTTACAG 2279
QY 2221 ATCCCACTCTCTCCGACCATCAAGATCTGCCAGCCAGCAACCTGCTGCTTCAAGAA 2280
DB 2280 ATCCCACTCTCTCCGACCATCAAGATCTGCCAGCCAGCAACCTGCTGCTTCAAGAA 2339
QY 2281 CCTGAGGCTTACAGAAAGCATTTCTGACGTACACACCTGCTGCTGCTTCAAGAA 2340
DB 2340 CCTGAGGCTTACAGAAAGCATTTCTGACGTACACACCTGCTGCTGCTTCAAGAA 2399
QY 2341 AATGTTCAAGTTGTCACAGTCAAAATCTCAGCAAGACCTGTTATAGGAAAGCTTGGAC 2400
DB 2400 AATGTTCAAGTTGTCACAGTCAAAATCTCAGCAAGACCTGTTATAGGAAAGCTTGGAC 2459
QY 2401 ATGGAGAGAGAAACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
DB 2460 ATGGAGAGAGAAACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2519
QY 2461 TTGTTCTGCAAAACCTGATCAGTGCAGCGAGGAAGTAAATTAACACTTTTACGAGAT 2520
DB 2520 TTGTTCTGCAAAACCTGATCAGTGCAGCGAGGAAGTAAATTAACACTTTTACGAGAT 2579
QY 2521 GAGTCAAGTGGCTCCAGAGGCAAGCAAGTTTTTACCACAAATGGAGGGAATCCAAATG 2580
DB 2580 GAGTCAAGTGGCTCCAGAGGCAAGCAAGTTTTTACCACAAATGGAGGGAATCCAAATG 2639
QY 2581 TTTATTAATGATGAAGAGTGGGTCCGGAAGACAGAGACAGACACTTTTGTATGCCGA 2640
DB 2640 TTTATTAATGATGAAGAGTGGGTCCGGAAGACAGAGACAGACACTTTTGTATGCCGA 2699
QY 2641 CCGCAGCTGCGCAGGAGAGCTGCTTTCATCAGATCTCTTAAGGACTGGAAGTCCAGCA 2700
DB 2700 CCGCAGCTGCGCAGGAGAGCTGCTTTCATCAGATCTCTTAAGGACTGGAAGTCCAGCA 2759
QY 2701 TCATGTCAGAGCATTTGTAAGGAGAGGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2760
DB 2760 TCATGTCAGAGCATTTGTAAGGAGAGGAAAGTACAGATCCCTCAGCTTGCCTCATGTC 2819
QY 2761 AAACCTGAATAA 2772
DB 2820 AAACCTGAATAA 2831

RESULT 3
AAH49499
ID AAH49499 standard; DNA; 3074 BP.
XX

QY	1294	TCAGTTAGTACAGGAGGTCCTCCCAAGACCGACATACACACCGAGGGCACTCCACAAA	1353
Db	1430	TCAGTTAGTACAGGAGGTCCTCCCAAGACCGACATACACACCGAGGGCACTCCACAAA	1489
QY	1354	GTCACAGAAAGAGCTGAGAGCTTCAACGACCGAACCGGCTCCGGGCGCTCGCCCTCAAA	1413
Db	1490	GTCACAGAAAGAGCTGAGAGCTTCAACGACCGAACCGGCTCCGGGCGCTCGCCCTCAAA	1549
QY	1414	AGTTCTCAGCCAAACACAGTATAGATGCTGACACAGACCCCTTGACACTGATGATATAT	1473
Db	1550	AGTTCTCAGCCAAACACAGTATAGATGCTGACACAGACCCCTTGACACTGATGATATAT	1609
QY	1474	GATGAAAAAAGATGCCAGTGTGATGTTTCAGGTGAGAGACCTCCACCCACACTTAAACT	1533
Db	1610	GATGAAAAAAGATGCCAGTGTGATGTTTCAGGTGAGAGACCTCCACCCACACTTAAACT	1669
QY	1534	GTCATTCGACCTATACAGAAATATGAAATTCATGTTCCAAACAGGAGTTTAAGGAACA	1593
Db	1670	GTCATTCGACCTATACAGAAATATGAAATTCATGTTCCAAACAGGAGTTTAAGGAACA	1729
QY	1594	TTACGTCATATGATGTAAAGATGTCATTGAACATATTTCTGCTGTCATCTTGACATG	1653
Db	1730	TTACGTCATATGATGTAAAGATGTCATTGAACATATTTCTGCTGTCATCTTGACATG	1789
QY	1654	TTGGTGTGAATTTAAACCCCTTCAACACGCGTTGATCCAAATTCGTGGAAAAAGGCAATC	1713
Db	1790	TTGGTGTGAATTTAAACCCCTTCAACACGCGTTGATCCAAATTCGTGGAAAAAGGCAATC	1849
QY	1714	ACATCAGATTAAGAAAGACCGACAGAAATAATTAACAGCAGACATGAGACCACAGAGATCTC	1773
Db	1850	ACATCAGATTAAGAAAGACCGACAGAAATAATTAACAGCAGACATGAGACCACAGAGATCTC	1909
QY	1774	AGTATGCTCGGTGGGTGTCGAAGTTGAAAAACAGGTACAGTGCATAGATCCAAAGCTG	1833
Db	1910	AGTATGCTCGGTGGGTGTCGAAGTTGAAAAACAGGTACAGTGCATAGATCCAAAGCTG	1969
QY	1834	GACGCGCTACTAGACATCTATCAACAGAGCTCTTGGAAGAGCTGCGCTACAGCCCTGCT	1893
Db	1970	GACGCGCTACTAGACATCTATCAACAGAGCTCTTGGAAGAGCTGCGCTACAGCCCTGCT	2029
QY	1894	TTGGCTTCATTCGACGATCCGACCTTTTGAATGTAAACAGACATCTGCATTCAAAGCCCT	1953
Db	2030	TTGGCTTCATTCGACGATCCGACCTTTTGAATGTAAACAGACATCTGCATTCAAAGCCCT	2089
QY	1954	GTCGATAGCAAAAGATCTTTCGGGTTCCGCAACAAAACAGTGGCTGTTATCCAGATCACT	2013
Db	2090	GTCGATAGCAAAAGATCTTTCGGGTTCCGCAACAAAACAGTGGCTGTTATCCAGATCACT	2149
QY	2014	AGTCCCAACATCTGAGABAGGCTCTGCACTTCTTGCAGCCAAATGAGTTGAGTGGCCAG	2073
Db	2150	AGTCCCAACATCTGAGABAGGCTCTGCACTTCTTGCAGCCAAATGAGTTGAGTGGCCAG	2209
QY	2074	ACTTCTACGGGGCTTAGCCCTACTACTATGCACAGTAAAGCAACACAGGGGCCAATTAGTCAA	2133
Db	2210	ACTTCTACGGGGCTTAGCCCTACTACTATGCACAGTAAAGCAACACAGGGGCCAATTAGTCAA	2269
QY	2134	AGCGATGGCTCAGCAGTGGCAGCCACCAACACACTTGCCAAAACCAATTAATATACGGCACCC	2193
Db	2270	AGCGATGGCTCAGCAGTGGCAGCCACCAACACACTTGCCAAAACCAATTAATATACGGCACCC	2329
QY	2194	AAGCCACAGCCCCCAACAATTTACAGATCCCACTCTCTCCCAAGCATTAAGCATCTG	2253
Db	2330	AAGCCACAGCCCCCAACAATTTACAGATCCCACTCTCTCCCAAGCATTAAGCATCTG	2389
QY	2254	CCGAGGGCAGAAAATCTGACACCCCTTAACCCCTGACAGGTTACAGGAAAGCATTTCTGACGTC	2313
Db	2390	CCGAGGGCAGAAAATCTGACACCCCTTAACCCCTGACAGGTTACAGGAAAGCATTTCTGACGTC	2449
QY	2314	ACCACTGCTCTTTGTGCTCCCAAGGAAATGTTGAGTTGCACAGTCAAAATCTCACCAAG	2373
Db	2450	ACCACTGCTCTTTGTGCTCCCAAGGAAATGTTGAGTTGCACAGTCAAAATCTCACCAAG	2509
QY	2374	GACCGTCTTATAGAGAAAAGCTTTGACATGGGAGAGAAACTCTGTGTCTGTCTCC	2433

Db	2510	GACCGTTCTATGAGGAAAGAGCTTTGACATGGGAGAGAACTCGTGTGTCTGCC	2569
QY	2434	ATGGTGGCGAAGAGACTTGGGCAATCTTTTGTCTGTGCAAAACCTGATCAGTGCACCGAG	2493
Db	2570	ATGCTGGCGAAGGAGCTTGGGCAAACTCTTGTCTGTGCAAAACCTGATCAGTGCACCGAG	2629
QY	2494	GAATGGAATATACAACTTTCAGGAGAGAGCAAGTGGCTCCAGAGGAGCAGAAATTTT	2553
Db	2630	GAACTGAAATATACAACTTTCAGGAGAGTATGCAAAAGTGGCTCCAGAGGAGCAGAAATTTT	2689
QY	2554	TACCCCAAAATGGAGGGAATCCAAATTTGTTTAACTGATGAGAAGTGGTGTCGCGAAG	2613
Db	2690	TACCCCAAAATGGAGGGAATCCAAATTTGTTTAACTGATGAGAAGTGGTGTCGCGAAG	2749
QY	2614	ACAGAGACAGACATTTTGAATGGCGACACCGAGCTGGCAGAGGAAGTGCCTTTCATCA	2673
Db	2750	ACAGAGACAGACATTTTGAATGGCGACACCGAGCTGGCAGAGGAAGTGCCTTTCATCA	2809
QY	2674	GACTCTCTAAAGAGCTGGAAGGTCAAGATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGT	2733
Db	2810	GACTCTCTAAAGAGCTGGAAGGTCAAGATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGT	2865
QY	2734	ACAGATGCGCTCAGCTTGCCCTCAATGTCAAACTGAATTA	2772
Db	2870	ACAGATGCGCTCAGCTTGCCCTCAATGTCAAACTGAATTA	2908

RESULT 4	
AA014653	
ID	AA014653 standard; cDNA; 2667 BP.
XX	
AC	AA014653;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
XX	
KW	Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW	cerebroprotective; neurotropic; analgesic; vision disorder;
KW	central nervous system disorder; epilepsy; migraine; hearing disorder
KW	psychotic disorder; seizure; learning disorder; memory disorder;
XX	stroke; pain; gene therapy; splice variant.
OS	Homo sapiens.
XX	
EH	Key
FT	Location/Qualifiers
FT	1..2967
FT	/*tag= a
FT	/product= "hKCNQ5-2"
XX	
PN	W0200170759-A1.
XX	
PD	27-SEP-2001.
XX	
PF	20-MAR-2001; 2001MO-US09328.
XX	
PR	21-MAR-2000; 2000US-190954P.
XX	
PA	(ICAG-) ICAGEN INC.
XX	
PI	Jeg1a TJ;
XX	
DR	WPI; 2001-611467/70.
XX	
DR	P-PSDB; AA009021.
XX	
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX	identifying a compound modulating ion flux in eukaryotic cell or cell
PT	membrane expressing the protein, comprises KCNQ alpha
XX	subunits -
XX	
PS	Claim 5; Page 63-64; 78bp; English.
XX	

CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-2.

CC XX Sequence 2667 BP: 701 A: 667 C: 660 G: 639 T: 0 other;

Query Match 96.0%: Score 2662.2: DB 22: Length 2667;

Best Local Similarity 99.9%: Pred. No. 0: Matches 2664: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 106 ATGAAGATGTGGAGTGGGCGGCGGAGGCTGCTGAATCGGAGCGCCGAGGGC 165
 Db 1 ATGAAGATGTGGAGTGGGCGGCGGAGGCTGCTGAATCGGAGCGCCGAGGGC 60
 QY 166 GAGGCGCTGCTAGCTGCTGGGACCGCGGCGGCGCTGGTGGCGGCGGCGGCTG 225
 Db 61 GAGGCGCTGCTAGCTGCTGGGACCGCGGCGGCGCTGGTGGCGGCGGCGGCTG 120
 QY 226 AGGAGAGACCCCGGCGGAGAGGAGGCGCGGAGTGGCTGGGAGAGCGCTCT 285
 Db 121 AGGAGAGACCCCGGCGGAGAGGAGGCGCGGAGTGGCTGGGAGAGCGCTCT 180
 QY 286 TACACGATGACCCAGAGCTGCGGCGGAGAGTACCGGCGGCTGCAAACTACCT 345
 Db 181 TACACGATGACCCAGAGCTGCGGCGGAGAGTACCGGCGGCTGCAAACTACCT 240
 QY 346 TACAACGTGTGAGAGAGACCCCGGCTGGGCTGATACACGCTTTGTTTTCTC 405
 Db 241 TACAACGTGTGAGAGAGACCCCGGCTGGGCTGATACACGCTTTGTTTTCTC 300
 QY 406 CTGTGCTTTGGTCTGATTTTGTCACTGTTTTCACATCCCTGAGCACAAATTTG 465
 Db 301 CTGTGCTTTGGTCTGATTTTGTCACTGTTTTCACATCCCTGAGCACAAATTTG 360
 QY 466 GCCCAGATGCTGCTGATCTGAGATTCGATGATTTGCTTTGTTGGAGTTC 525
 Db 361 GCCCAGATGCTGCTGATCTGAGATTCGATGATTTGCTTTGTTGGAGTTC 420
 QY 526 ATCATTCGAATCTGCTGCGGCTGCTGTTTCGATATAGAGATGAGCAAGAGACT 585
 Db 421 ATCATTCGAATCTGCTGCGGCTGCTGTTTCGATATAGAGATGAGCAAGAGACT 480
 QY 586 AGGTTTCTCGAAGACCCCTTCTGTATTATAGATACATTTGTTCTATCCCTCAATAGCA 645
 Db 481 AGGTTTCTCGAAGACCCCTTCTGTATTATAGATACATTTGTTCTATCCCTCAATAGCA 540
 QY 646 GTTGTCTTCGAAGAACTCAGAGGTAATTTTGGCAGCTTCGACCTCAAGTCTCCGT 705
 Db 541 GTTGTCTTCGAAGAACTCAGAGGTAATTTTGGCAGCTTCGACCTCAAGTCTCCGT 600
 QY 706 TTCTCAGATGCTCCGATGCTGCGATGAGACGAGGAGGAGCACTGGAAATTAAGT 765
 Db 601 TTCTCAGATGCTCCGATGCTGCGATGAGACGAGGAGGAGCACTGGAAATTAAGT 660

QY 766 GTTTCAGTGTATTATGCTCAGCAGAGGAATTAATCACAGCTGTGTACATAGATTTC 825
 Db 661 GTTTCAGTGTATTATGCTCAGCAGAGGAATTAATCACAGCTGTGTACATAGATTTC 720
 QY 826 GTTCTATTATTTTTCGCTTCTTCTGCTATCTGCTGAGAAAGAGATTAAGAGTTT 885
 Db 721 GTTCTATTATTTTTCGCTTCTTCTGCTATCTGCTGAGAAAGAGATTAAGAGTTT 780
 QY 886 TCTACATATGCAATATGCTCTGCTGCTGAGCAATTTACATTGACATTAATGCTATGGA 945
 Db 781 TCTACATATGCAATATGCTCTGCTGCTGAGCAATTTACATTGACATTAATGCTATGGA 840
 QY 946 GACAAATCCCTTAATCTGCTGAGAGATTTGTTTCTGAGGCTTGTGACCTCTGTC 1005
 Db 841 GACAAATCCCTTAATCTGCTGAGAGATTTGTTTCTGAGGCTTGTGACCTCTGTC 900
 QY 1006 ATTTCTTTCTTTCACCTTCTGCGGCAATTCCTGCTCAGGTTTTCATTAAGTACAA 1065
 Db 901 ATTTCTTTCTTTCACCTTCTGCGGCAATTCCTGCTCAGGTTTTCATTAAGTACAA 960
 QY 1066 GAACAAACACCGCCAGAAACACTTTGAGAAAAAGAAACCAAGCTGCCAATTCAG 1125
 Db 961 GAACAAACACCGCCAGAAACACTTTGAGAAAAAGAAACCAAGCTGCCAATTCAG 1020
 QY 1126 TGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCA 1185
 Db 1021 TGTGTTTGGGATGTTACGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCA 1080
 QY 1186 CACTTGAAGGCTTTGACACACCTGACAGCCCTACCAATCAGAACTTAATTTTAAGAGCGCA 1245
 Db 1081 CACTTGAAGGCTTTGACACACCTGACAGCCCTACCAATCAGAACTTAATTTTAAGAGCGCA 1140
 QY 1246 GTGCGATAGGCTAGCCCGAGGCGCAGAGTATTAAAGCCGCAAGCTCAGTAGTAC 1305
 Db 1141 GTGCGATAGGCTAGCCCGAGGCGCAGAGTATTAAAGCCGCAAGCTCAGTAGTAC 1200
 QY 1306 AGGAGTCCCAAGACCCGACATCACAGCCGAGGAGCTCCACCAAAAGTCAGAAAGC 1365
 Db 1201 AGGAGTCCCAAGACCCGACATCACAGCCGAGGAGCTCCACCAAAAGTCAGAAAGC 1260
 QY 1366 TGGAGCTTCAAGCAGCCGAAACCGCTTCGCGCTGCTGCGCTCAAAAGTTCAGCCA 1425
 Db 1261 TGGAGCTTCAAGCAGCCGAAACCGCTTCGCGCTGCTGCGCTCAAAAGTTCAGCCA 1320
 QY 1426 AAACCAATATGATGCTGACACAGCCCTTGGACATGATATATGATGAAGAAAGGA 1485
 Db 1321 AAACCAATATGATGCTGACACAGCCCTTGGACATGATATATGATGAAGAAAGGA 1380
 QY 1486 TGCCAGTGTATGATGATGATGAGAGCTTCCACCACTTAATTAACCTGATTCAGACT 1545
 Db 1381 TGCCAGTGTATGATGATGATGAGAGCTTCCACCACTTAATTAACCTGATTCAGACT 1440
 QY 1546 ATCAGAAATTAATTAATTTATGTTGCAAAAGGAAAGTTTAAGCAATTAAGTCAATAT 1605
 Db 1441 ATCAGAAATTAATTAATTTATGTTGCAAAAGGAAAGTTTAAGCAATTAAGTCAATAT 1500
 QY 1606 GATGTAAAAAGATGCTTGAACAAATATTCGCTGCTGATGCTGATGCTGATGAT 1665
 Db 1501 GATGTAAAAAGATGCTTGAACAAATATTCGCTGCTGATGCTGATGCTGATGAT 1560
 QY 1666 AAAAGCTTCAAAACAGTGTGATCAAAATTCCTGGAAGAAAGGCAAAATCACATCAGATTAAG 1725
 Db 1561 AAAAGCTTCAAAACAGTGTGATCAAAATTCCTGGAAGAAAGGCAAAATCACATCAGATTAAG 1620
 QY 1726 AAGAGCCGAGAGAAATTAACAGCAGAAATGAGACCAAGATCTCAGTATGCTCGGT 1785
 Db 1621 AAGAGCCGAGAGAAATTAACAGCAGAAATGAGACCAAGATCTCAGTATGCTCGGT 1680
 QY 1786 CGGCTGTCAGAGGTTGAAGAAAGAGTACAGTCCATGAATCCAAAGCTGAGCTGCTACTA 1845
 Db 1681 CGGCTGTCAGAGGTTGAAGAAAGAGTACAGTCCATGAATCCAAAGCTGAGCTGCTACTA 1740

QY	1846	GACATCTATCAACAGGTCCTTGGAAAAGGCTGCGCCACACCCCGGTTTGGCTTCAATC	1905
Db	1741	GACATCTATCAACAGGTCCTTGGAAAAGGCTGCGCCACACCCCGGTTTGGCTTCAATC	1800
QY	1906	CAGATCCACACCTTTTGAATGTGAACAGACATCTGACATATCAAAAGCCCTGTGATAGCAAA	1965
Db	1801	CAGATCCACACCTTTTGAATGTGAACAGACATCTGACATATCAAAAGCCCTGTGATAGCAAA	1860
QY	1966	GATCTTTTGGGGTTCCGCACAAAACAGTGGCTGCTTATTCAGATCAACTAGTGGCCACATC	2025
Db	1861	GATCTTTTGGGGTTCCGCACAAAACAGTGGCTGCTTATTCAGATCAACTAGTGGCCACATC	1920
QY	2026	TCCGAGAGCCCTGCAGTTCATCTTGACGCCCAAAATGATTCAGTGGCCGACCTTCTACGC	2085
Db	1921	TCCGAGAGCCCTGCAGTTCATCTTGACGCCCAAAATGATTCAGTGGCCGACCTTCTACGC	1980
QY	2086	CTTAGCCCTACTATGTCACAGTCAAGCAACACAGGTGGCAATTAATGATCAAGCGATGGCTCA	2145
Db	1981	CTTAGCCCTACTATGTCACAGTCAAGCAACACAGGTGGCAATTAATGATCAAGCGATGGCTCA	2040
QY	2146	GCACTGGCAGCCACCAACACACCTTTCGAACCCAAATTAATACGGCAGCCCAAGCCAGCAGCC	2205
Db	2041	GCACTGGCAGCCACCAACACACCTTTCGAACCCAAATTAATACGGCAGCCCAAGCCAGCAGCC	2100
QY	2206	CCAAACAATTTACAGATTCGCCACCTCTCTCTCCAGCATTCAAGCATCTGCCCCAGGCCAGAA	2265
Db	2101	CCAAACAATTTACAGATTCGCCACCTCTCTCTCCAGCATTCAAGCATCTGCCCCAGGCCAGAA	2160
QY	2266	ACTCTGCACCCCTAACCCCTGCAGGGCTTACAGAAAGCATTTTCTGACAGTCACACCTGGCCTT	2335
Db	2161	ACTCTGCACCCCTAACCCCTGCAGGGCTTACAGAAAGCATTTTCTGACAGTCACACCTGGCCTT	2220
QY	2336	GTTTGCCTTCCAAAGAAAAATGTTTCAGGTTCACACATCAAAATCTCACCAAGAGACCGTTCTATG	2385
Db	2221	GTTTGCCTTCCAAAGAAAAATGTTTCAGGTTCACACATCAAAATCTCACCAAGAGACCGTTCTATG	2280
QY	2386	AGGAAAAAGCTTTGACATGAGGAGGAAAACTGTGTCTGTCTGTCTGCCATGGTGCCAGAG	2445
Db	2281	AGGAAAAAGCTTTGACATGAGGAGGAAAACTGTGTCTGTCTGTCTGCCATGGTGCCAGAG	2340
QY	2446	GACTTGGGCAAAATCTTTGTCTGTGTCTCAAAAACCTGATCAGGTGAGCCGAGAACTGAATTA	2505
Db	2341	GACTTGGGCAAAATCTTTGTCTGTGTCTCAAAAACCTGATCAGGTGAGCCGAGAACTGAATTA	2400
QY	2506	CAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACAGCCAAGATTTTTCACCCCAATGG	2565
Db	2401	CAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACAGCCAAGATTTTTCACCCCAATGG	2460
QY	2566	AGGGAATCCAAATTTGTTATTAATCATGATGAAGAAGTGGTCCCCGAAAGACACAGACAGAC	2625
Db	2461	AGGGAATCCAAATTTGTTATTAATCATGATGAAGAAGTGGTCCCCGAAAGACACAGACAGAC	2520
QY	2626	ACTTTTGTATGCGCGACCGCAGCCTGCGCCAGGAGAGGTGGCTTGTGATCAGACTCTCTAAGG	2685
Db	2521	ACTTTTGTATGCGCGACCGCAGCCTGCGCCAGGAGAGGTGGCTTGTGATCAGACTCTCTAAGG	2580
QY	2686	ACTGGAAGTCAAGCATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTC	2745
Db	2581	ACTGGAAGTCAAGCATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTC	2640
QY	2746	AGCTTGGCTCATGTCAAACTGAATAA 2772	
Db	2641	AGCTTGGCTCATGTCAAACTGAATAA 2667	
RESULT 5			
AAS14651			
ID	AAS14651 standard; cDNA; 3071 BP.		
XX	AAS14651;		
AC			
XX			
DT	18-DEC-2001 (first entry)		
XX			

DE	Human cDNA for voltage gated potassium channel hKCNQ5.
XX	
KM	Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KM	cerebroprotective; neurotrophic; analgesic; vision disorder;
KW	central nervous system disorder; epilepsy; migraine; hearing disorder;
KW	psychotic disorder; seizure; learning disorder; memory disorder;
KW	stroke; pain; gene therapy.
XX	
OS	Homo sapiens.
PN	WO200170759-A1.
PD	27-SEP-2001.
XX	
PF	20-MAR-2001; 2001WO-US09328.
PR	21-MAR-2000; 2000US-190954P.
XX	
PA	(ICAGEN-) ICAGEN INC.
PI	Jegla TJ;
XX	
DR	WPI; 2001-611467/70.
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT	identifying a compound modulating ion flux in eukaryotic cell or cell
PT	membrane expressing the protein, comprises KCNQ alpha
PT	subunits -
XX	
PS	Claim 5; Page 61-62; 78pp; English.
XX	
CC	The invention relates to an isolated polypeptide comprising an
CC	alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC	65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC	sequence and forms a KCNQ potassium channel having the characteristic of
CC	voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC	included in the scope of the invention are the nucleic acids encoding
CC	hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC	expression vectors encoding them, antibodies against them, the use of
CC	3-dimensional computer modelling to identify molecules that bind to a
CC	KCNQ containing potassium channel and modulate ion flux through the
CC	channel. The KCNQ polypeptide is useful for identifying a compound that
CC	increases or decreases ion flux through a potassium channel expressed in
CC	an eukaryotic host cell or cell membrane. The compound (and the
CC	KCNQ nucleic acid when used in gene therapy)is useful as
CC	a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC	such as disorders of the central nervous system, such as epilepsy,
CC	migraines, hearing and vision problems, psychotic disorders, seizures,
CC	learning and memory disorders, stroke and pain. The antibodies are
CC	useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC	use of a nucleotide sequence of KCNQ5 to search computer databases to
CC	find variants of the sequence which are associated with disease states,
CC	is useful for screening mutations of KCNQ5. The present sequence is
CC	a representative cDNA for hKCNQ5.
XX	
SQ	Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other;
	Query Match 95.1%; Score 2635.4; DB 22; Length 3071;
	Best Local Similarity 98.9%; Pred. No. 0;
	Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1
OY	97 GCACGCGCATGAAGATGTGGAGTCGGGCAGCGGCGAGGGTCTGCTGAACTCGGCAGCC 156
DB	1 GGCAAGCGCATGAAGATGTGGAGTCGGGCAGCGGCGAGGGTCTGCTGAACTCGGCAGCC 60
OY	157 GCCAGGGGCGACGCCCTGCTACTGCTGGGCACCCGCGGCGCACAGCTCGGTGGCGGGCC 216
DB	61 GCCAGGGGCGACGCCCTGCTACTGCTGGGCACCCGCGGCGCACAGCTTGTTGGCGGGCC 120
OY	217 GGGGGGCTTAGGGAGAGCGCGCGGGACAAGGGGGCCCGGATGAGCCTGCTGGGGAAAG 276
DB	121 GGGGGGCTTAGGGAGAGCGCGCGGGACAAGGGGGCCCGGATGAGCCTGCTGGGGAAAG 180

QY	277	CCGCTCTCTTACACGATGACCGACAGCTGCCGGCGCACTGCAATGACCGCGGGTGCAG	336
Db	181	CCGGCTCTTACACGATGACCGACAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAG	240
QY	337	AACACTCGTACACGCTGCTGGAGAACCCCGGGCTGGGGGTCATCTACCAAGCTTAC	396
Db	241	AACACTCGTACACGCTGCTGGAGAACCCCGGGCTGGGGGTCATCTACCAAGCTTTC	300
QY	397	GTTTTTCTCTGTCTTTGGTTCGTTGATTTTGTCACTGTTTTCTACATCCCTGAGAC	456
Db	301	GTTTTTCTCTGTCTTTGGTTCGTTGATTTTGTCACTGTTTTCTACATCCCTGAGAC	360
QY	457	ACAAATATGGCCCTCAAGTGGCCCTTGATCTGGAGTTCGGATGATGTCTGTTGGT	516
Db	361	ACAAATATGGCCCTCAAGTGGCCCTTGATCTGGAGTTCGGATGATGTCTGTTGGT	420
QY	517	TTGAGTTCATTCATTGCAATCTGCTGCGGGTGTGCTGTCTGCATATAGAGATGGCA	576
Db	421	TTGAGTTCATTCATTGCAATCTGCTGCGGGTGTGCTGTCTGCATATAGAGATGGCA	480
QY	577	GGAGACTGAGGTTTGGTCGAAAGCCCTCTGTATATATACATACCATTTGTTTATCGT	636
Db	481	GGAGACTGAGGTTTGGTCGAAAGCCCTCTGTATATATATACATACCATTTGTTTATCGT	540
QY	637	TCAATACAGTGTGTTTCGCAAAAATCTCAGGGGTAAATTTTTCACAGTCTGCACCTACA	696
Db	541	TCAATACAGTGTGTTTCGCAAAAATCTCAGGGGTAAATTTTTCACAGTCTGCACCTACA	600
QY	697	AGATCCGGTTCCTACACATCCCTCCGCAATGTCGCATGGACGACGAAAGGGAGCACTTGG	756
Db	601	AGATCCGGTTCCTACACATCCCTCCGCAATGTCGCATGGACGACGAAAGGGAGCACTTGG	660
QY	757	AAATTAAGTGGTTCAGTGGTTATATGCTCAGCAGCAAGAAATTAATCACAGTGTGCATATA	816
Db	661	AAATTAAGTGGTTCAGTGGTTATATGCTCAGCAGCAAGAAATTAATCACAGTGTGCATATA	720
QY	817	GGATTTTGGTTCCTATTTTTCGCTTTCCTTGTCTATCTGGTGGAAAGAGATGCCAAT	876
Db	721	GGATTTTGGTTCCTATTTTTCGCTTTCCTTGTCTATCTGGTGGAAAGAGATGCCAAT	780
QY	877	AAAGAGTTTCTACATATGACAGATCTCTCTGGTGGGGCAAAATTAATTAATTAACAATCTAT	936
Db	781	AAAGAGTTTCTACATATGACAGATCTCTCTGGTGGGGCAAAATTAATTAATTAACAATCTAT	840
QY	937	GGCTATGGAGACAAACCTCCCTAACTTGGCTGGAGAAATGCTTCTTGCAGGCTTTGCA	996
Db	841	GGCTATGGAGACAAACCTCCCTAACTTGGCTGGAGAAATGCTTCTTGCAGGCTTTGCA	900
QY	997	CTCCTTGGCAATTTCTTTCTTGGCACCTCTCGCGCGGATCTTGGCTCAGGTTTGCATTA	1056
Db	901	CTCCTTGGCAATTTCTTTCTTGGCACCTCTCGCGCGGATCTTGGCTCAGGTTTGCATTA	960
QY	1057	AAAGTACAGACACACACCGCCAGAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAAC	1116
Db	961	AAAGTACAGACACACACCGCCAGAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAAC	1020
QY	1117	CTATTCAGTGTGTTGGCGTAGTAAACGAGTGATGAGAAATCTGTTTCATTTGCATCC	1176
Db	1021	CTATTCAGTGTGTTGGCGTAGTAAACGAGTGATGAGAAATCTGTTTCATTTGCATCC	1080
QY	1177	TGGAGCCACACTTGAAGGCGTTCGACACCTTGACAGCCCTTACCA-----1220	1220
Db	1081	TGGAGCCACACTTGAAGGCGTTCGACACCTTGACAGCCCTTACCA-----1220	1140
QY	1221	-----TAGAGCTTAAGTTTAAAGAGCGAGTCCGATGGCTAAGCCCGAGGGGC	1286
Db	1141	GCATCAAGCAGTCAAGAGCTTAAGTTTAAAGAGCGAGTCCGATGGCTAAGCCCGAGGGGC	1200
QY	1270	CAGAGTATTAAGAGCCGACAGACCTCTCACTAGTGTGACAGAGAGTCCCAACACCGACATTC	1329
Db	1201	CAGAGTATTAAGAGCCGACAGACCTCTCACTAGTGTGACAGAGAGTCCCAACACCGACATTC	1260
QY	1330	ACAGCGAGGCGACGTCCACCAAAAGTGCAGAGAGACTGAGCTTCAACGACGAAACCGC	1389

Db	1261	ACAGCCGAGGGCAGTCCACCAAAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGC	1320
QY	1390	TTGGGGCCCTGGCTGGCGCTCAAAAGTCTCAGCCCAAAACCAAGTATGATGCTGCACACA	1443
Db	1321	TTCCGGCCCTGGCTGGCGCTCAAAAGTCTCAGCCCAAAACCAAGTATGATGCTGCACACA	1380
QY	1450	GCCCTTGGCACTGATGATGATATGATGAAAAAGATGGCAGTGTGATGATCAGTGAA	1509
Db	1381	GCCCTTGGCACTGATGATGATATGATGAAAAAGATGGCAGTGTGATGATGATCAGTGAA	1440
QY	1510	GACCTCACCCCACTTAAAACTGTCAATTCAGCTATGAGAATATGAAATTTCAATGT	1569
Db	1441	GACCTCACCCCACTTAAAACTGTCAATTCAGCTATGAGAATATGAAATTTCAATGT	1500
QY	1570	GCAAAACGAGATTAAAGAAACCTACCTCATATGATGATGAAAGATGATGAAACAA	1629
Db	1501	GCAAAACGAGATTAAAGAAACCTACCTCATATGATGATGAAAGATGATGAAACAA	1560
QY	1630	TATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAACAGCTGTGAT	1689
Db	1561	TATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAACAGCTGTGAT	1620
QY	1690	CAAAATTTGGAAAAAGGCAATCATCATCAGTAAGAAAGCCGAGAGAAATTAACGCA	1749
Db	1621	CAAAATTTGGAAAAAGGCAATCATCATCAGTAAGAAAGCCGAGAGAAATTAACGCA	1680
QY	1750	GAACATGAGACACAGACGATCTCAGTATGCTGGTGGGTGAGTGAAGAAACAG	1809
Db	1681	GAACATGAGACACAGACGATCTCAGTATGCTGGTGGGTGAGTGAAGAAACAG	1740
QY	1810	GTCAGTGCATAGAAATCCAAAGCTGGACAGCTGACTAGATCATATCAACAGTCCCTGG	1869
Db	1741	GTCAGTGCATAGAAATCCAAAGCTGGACAGCTGACTAGATCATATCAACAGTCCCTGG	1800
QY	1870	AAAGGCTCTGCTTCAAGCCCTTGGCTTGGCTTCATTCAGATCCACCTTTTGAATGAA	1929
Db	1801	AAAGGCTCTGCTTCAAGCCCTTGGCTTGGCTTCATTCAGATCCACCTTTTGAATGAA	1860
QY	1930	CAACATCTGACTATCAAAAGCCCTGGATAGCAAAAGTCTTCCGGGTTCCGACAAAC	1989
Db	1861	CAACATCTGACTATCAAAAGCCCTGGATAGCAAAAGTCTTCCGGGTTCCGACAAAC	1920
QY	1990	AGTGGCTCTTATTCAGATCAACTAGTGGCAACATCTGGAGAGGCTGCAAGTTCATTTG	2049
Db	1921	AGTGGCTCTTATTCAGATCAACTAGTGGCAACATCTGGAGAGGCTGCAAGTTCATTTG	1980
QY	2050	AGCCCAAAATGATTCAGTGGCCCAACTTTCTACGGGCTTACGCCCTACTATGCACAGTCAA	2109
Db	1981	AGCCCAAAATGATTCAGTGGCCCAACTTTCTACGGGCTTACGCCCTACTATGCACAGTCAA	2040
QY	2110	GCAACACAGTGGCAATTAGTCAAAAGGATGGCTCAGAGTGGAGGCCACCAACACCAT	2169
Db	2041	GCAACACAGTGGCAATTAGTCAAAAGGATGGCTCAGAGTGGAGGCCACCAACACCAT	2100
QY	2170	GCAACCAAAATAATACGGACCCCAAGCCACAGCCCAACACTTTACAGATCCACCT	2229
Db	2101	GCAACCAAAATAATACGGACCCCAAGCCCAAGCCCAACACTTTACAGATCCACCT	2160
QY	2230	CCCTTCCCAAGCATCAAGCATCTGCCAGAGGCAGAAACTGTGCACCCCTAACCTGCAGGC	2289
Db	2161	CCCTTCCCAAGCATCAAGCATCTGCCAGAGGCAGAAACTGTGCACCCCTAACCTGCAGGC	2220
QY	2290	TTACAGGAAAGCATTTCTGACGTCCACACCTGCTTTGGCTCCAGAGAAATGTTTCAG	2349
Db	2221	TTACAGGAAAGCATTTCTGACGTCCACACCTGCTTTGGCTCCAGAGAAATGTTTCAG	2280
QY	2350	GTTGCACAGTCAAAATCTACCAAGAGACGTTCTATAGGAAAGAGCTTTGACATGGAGAGA	2409
Db	2281	GTTGCACAGTCAAAATCTACCAAGAGACGTTCTATAGGAAAGAGCTTTGACATGGAGAGA	2340
QY	2410	GAACCTGTGTGTCTGTCTGTCCATGAGTGCAGAGACTTGGGCAAAATCTTGTCTGTG	2469

CC as KCM05 and nucleic acid molecules encoding such polypeptides. KCM05
 CC polypeptides are useful for identifying compounds that modulate their
 CC biological activity. The compounds identified and KCM05 polynucleotides
 CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for treating neurophysiological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCM05 polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease
 CC tissues or cells. The present sequence is human KCM05 cDNA.

SO Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 94.7%; Score 2625.2; DB 24; Length 2694;

Best Local Similarity 96.9%; Pred. No. 0; Mismatches 3; Indels 27; Gaps 1;

Matches 2664; Conservative 0;

106 ATGAAAGATGTGAGTGGGCGGCGGAGGCTGTGCTGAACCTCGGACGCCAGGGGC 165
 1 ATGAAAGATGTGAGTGGGCGGCGGAGGCTGTGCTGAACCTCGGACGCCAGGGGC 60
 166 GAGCGCTGCTACTGCTGGGCAACCGCGGCGACGCTGCGGCGGCGGCGGCTG 225
 61 GAGCGCTGCTACTGCTGGGCAACCGCGGCGACGCTGCGGCGGCGGCGGCTG 120
 226 AGGAGAGCGCGCGGCGGCAACGAGGCGGCGGAGTGTGCTGCGGAGGCGGCTG 285
 121 AGGAGAGCGCGCGGCGGCAACGAGGCGGCGGAGTGTGCTGCGGAGGCGGCTG 180
 286 TACACGAGTACGACGAGTGGCGGCGCAACGTCACAGTACCGGCGGCGGAGT 345
 181 TACACGAGTACGACGAGTGGCGGCGCAACGTCACAGTACCGGCGGCGGAGT 240
 346 TACACGAGTGGGAGAGACCGCGGCGGCGGCTGCTACACGCTTTCGTTTTC 405
 241 TACACGAGTGGGAGAGACCGCGGCGGCGGCTGCTACACGCTTTCGTTTTC 300
 406 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465
 301 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 466 GCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
 361 GCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 526 ATCAATGCAATCGTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
 421 ATCAATGCAATCGTGGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 586 AGTTTGGTGGCAAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
 481 AGTTTGGTGGCAAGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 646 GTTGTGCTGCAAAAATCAGAGGTATATATTTTGCACGCTGCTGCTGCTGCT 705
 541 GTTGTGCTGCAAAAATCAGAGGTATATATTTTGCACGCTGCTGCTGCTGCT 600
 706 TTCTCAGATGCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
 601 TTCTCAGATGCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 766 GCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 825
 661 GCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 720
 826 GTTCTATATTTTTCGCTTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885

DB 721 GTTCTATATTTTTCGCTTTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 886 TCTACATATGCAATGCTCTCTGCTGGGCGACATTTACATTTGACAACTATGCTATGGA 945
 781 TCTACATATGCAATGCTCTCTGCTGGGCGACATTTACATTTGACAACTATGCTATGGA 840
 946 GACAAATCTCCCTAACCTTGGCTGGAGATTTGCTTCTGACGCTTTCACCTCTTGGC 1005
 841 GACAAATCTCCCTAACCTTGGCTGGAGATTTGCTTCTGACGCTTTCACCTCTTGGC 900
 1006 ATTTCTTTCTTGGCACTTCTGCGGCAATCTTGGCTGCTGCTGCTGCTGCTGCT 1065
 901 ATTTCTTTCTTGGCACTTCTGCGGCAATCTTGGCTGCTGCTGCTGCTGCTGCT 960
 1066 GAACACACCGCGGCGGAGAACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1125
 961 GAACACACCGCGGCGGAGAACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
 1126 TGTGTTGGGCTAGTACGAGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCA 1185
 1021 TGTGTTGGGCTAGTACGAGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCA 1080
 1186 CACTTGAAGGCTTGCACACCTGCAACCTTACCA----- 1220
 1081 CACTTGAAGGCTTGCACACCTGCAACCTTACCAAGAAAGAAAGAAAGAAAGAAAGCA 1140
 1221 --TCAGAAAGCTAAGTTTAAAGGAGCGAGTGGCGATGCTAGCCCGAGGGCGAGTATT 1278
 1141 AGTCAGAAAGCTAAGTTTAAAGGAGCGAGTGGCGATGCTAGCCCGAGGGCGAGTATT 1200
 1279 AAGAGCCGACAAAGCTAGTACGAGAGTGGCGATGCTAGCCCGAGGGCGAGTATT 1338
 1201 AAGAGCCGACAAAGCTAGTACGAGAGTGGCGATGCTAGCCCGAGGGCGAGTATT 1260
 1339 GGCAGTCCCAACAAAGTGGCAAGAGTGGAGTTCACAGCAACCGGCTTCCGGGCC 1398
 1261 GGCAGTCCCAACAAAGTGGCAAGAGTGGAGTTCACAGCAACCGGCTTCCGGGCC 1320
 1399 TCGCTGGCGCTCAAAAGTTCACAGCAACCAAGTATGATGCTGACACAGCCCTTGGC 1458
 1321 TCGCTGGCGCTCAAAAGTTCACAGCAACCAAGTATGATGCTGACACAGCCCTTGGC 1380
 1459 ACTGATGATGATATGATGATAAAGAGATCCAGTGTATGATGATGATGATGATGAT 1518
 1381 ACTGATGATGATATGATGATAAAGAGATCCAGTGTATGATGATGATGATGATGAT 1440
 1519 CCACCACTTAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
 1441 CCACCACTTAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1579 AAGTTTAAAGAAATATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1638
 1501 AAGTTTAAAGAAATATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 1639 GGTCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1698
 1561 GGTCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 1699 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1758
 1621 GGAAGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 1759 ACCACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1818
 1681 ACCACAGAGATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
 1819 ATGATATCAAGTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1878
 1741 ATGATATCAAGTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 1879 GCTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1938

Db 1801 GCGTCAGCCCTGCGTTGGCTTCATTCAGATCCACCTTTTGAATGAAACAGACATCT 1860
 QY 1939 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGTGGCTGC 1998
 Db 1861 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGTGGCTGC 1920
 QY 1999 TTATTCAGATCAACTAGTGGCAACATCTGAGAGGCTGAGTTCATCTGAGCCCAAT 2058
 Db 1921 TTATTCAGATCAACTAGTGGCAACATCTGAGAGGCTGAGTTCATCTGAGCCCAAT 1980
 QY 2059 GAGTTCAGTGGCCCAACTTTTACGGCTTACGGCTTACTAGTGCACAGTCAACACACAG 2118
 Db 1981 GAGTTCAGTGGCCCAACTTTTACGGCTTACTAGTGCACAGTCAACACACAG 2040
 QY 2119 GTGCCAATTAAGTCAAAAGGATGGCTCAGCAGTGGCCACCAACACCATTTGCAACCAA 2178
 Db 2041 GTGCCAATTAAGTCAAAAGGATGGCTCAGCAGTGGCCACCAACACCATTTGCAACCAA 2100
 QY 2179 ATAAATAGGCAACCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2238
 Db 2101 ATAAATAGGCAACCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
 QY 2239 GCCATCAAGCATCTGCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2298
 Db 2161 GCCATCAAGCATCTGCCAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2220
 QY 2299 AGCATTTCTGACGTACACCACTGCTTGTGCTCCCAAGAAATGTTGAGTGGACAG 2358
 Db 2221 AGCATTTCTGACGTACACCACTGCTTGTGCTCCCAAGAAATGTTGAGTGGACAG 2280
 QY 2359 TCAATATCTACCAAGAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAAACTCTG 2418
 Db 2281 TCAATATCTACCAAGAGACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAAACTCTG 2340
 QY 2419 TTGCTCTGCTGCTCCATGCTGCGGCAAGACTTTGGCAATCTTTGCTGTCGCAAAACTG 2478
 Db 2341 TTGCTCTGCTGCTCCATGCTGCGGCAAGACTTTGGCAATCTTTGCTGTCGCAAAACTG 2400
 QY 2479 ATCAGGTGCAACCGAGAACTGATATACAACTTTCAGAGAGTGAAGTGCCTCCAGA 2538
 Db 2401 ATCAGGTGCAACCGAGAACTGATATACAACTTTCAGAGAGTGAAGTGCCTCCAGA 2460
 QY 2539 GGGAGCCCAAGATTTTATCCCAATGGAGGAATCCAAATTTTATTAACGTATGAAAGAG 2598
 Db 2461 GGGAGCCCAAGATTTTATCCCAATGGAGGAATCCAAATTTTATTAACGTATGAAAGAG 2520
 QY 2599 GTGGGTCGCCAAGAGAGACAGACACTTTTGTATGCGCAGCCGAGGCTGCGCAGGAA 2658
 Db 2521 GTGGGTCGCCAAGAGAGACAGACACTTTTGTATGCGCAGCCGAGGCTGCGCAGGAA 2580
 QY 2659 GCTGCTTTGCTGATGACACTCTCTAAGAGACTGGAAGGTCAAGATCTTCAGAGCATTTGT 2718
 Db 2581 GCTGCTTTGCTGATGACACTCTCTAAGAGACTGGAAGGTCAAGATCTTCAGAGCATTTGT 2640
 QY 2719 AAGGCAAGAGAAAGTACAGATGCGCTGAGTTCATGTCATGCAACTGAAATTA 2772
 Db 2641 AAGGCAAGAGAAAGTACAGATGCGCTGAGTTCATGTCATGCAACTGAAATTA 2694
 RESULT 9
 AAC64371
 ID AAC64371 standard; cDNA; 3718 BP.
 XX
 AC AAC64371:
 DT 07-FEB-2001 (first entry)
 XX
 DE Human KCNQ5 (KCN6q) cDNA sequence SFO ID NO:2.
 XX
 KW Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;

KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; ss.
 OS Homo sapiens.
 PN WO20061606-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000MO-US09587.
 XX
 PR 14-APR-1999; 99US-0129274.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Petrukhin K, Caskey CT, Li W, Metzker ML.
 XX
 DR WPI: 2000-647417/62.
 XX
 DR P-PSDB: AAB24241.
 XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Claim 3; Fig 2; 99pp; English.
 XX
 CC The present sequence encodes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.
 XX
 SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
 Query Match 91.0%; Score 2523.2; DB 21; Length 3718;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 2562; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
 QY 208 GCGGCGCGGCTGCTGAGGAGAGCCCGGCGCAAGCAGAGGCGCCGAGTGGCTG 267
 Db 87 GACTGCGCGGCTGCTGAGGAGAGCCCGGCGCAAGCAGAGGCGCCGAGTGGCTG 146
 QY 268 CTGGGGAAGCGCTCTTACACAGATGACAGAGTGGCGGCAACGTCAGTACCGG 327
 Db 147 CTGGGGAAGCGCTCTTACACAGATGACAGAGTGGCGGCAACGTCAGTACCGG 206
 QY 328 CGGCTGCAAACTACCTGTACAAAGTGTGAGAGAGACCCGCGGCTGAGGCTATAC 387
 Db 207 CGGCTGCAAACTACCTGTACAAAGTGTGAGAGAGACCCGCGGCTGAGGCTATAC 266
 QY 388 CACGCTTGGTTTCTCCTTCTCTTGTGCTGCTGATTTTGTGATGTTTCTACATC 447
 Db 267 CACGCTTGGTTTCTCCTTCTCTTGTGCTGCTGATTTTGTGATGTTTCTACATC 326
 QY 448 CCTGAGCACAATAATGGCTCAAGTGGCTCTTGTATCTGAGTTCGATGATGTC 507
 Db 327 CCTGAGCACAATAATGGCTCAAGTGGCTCTTGTATCTGAGTTCGATGATGTC 386
 QY 508 GTCTTTGGTTTGGATTCATTCATTCGAATCTGCTGCGGTTGCTGTTGCTATATAGA 567
 Db 387 GTCTTTGGTTTGGATTCATTCATTCGAATCTGCTGCGGTTGCTGTTGCTATATAGA 446
 QY 568 GGATGGCAAGAGAAAGTGGTTCCTGGAAGCCCTTCTGTTATGATACATTTGTT 627
 Db 447 GGATGGCAAGAGAAAGTGGTTCCTGGAAGCCCTTCTGTTATGATACATTTGTT 506

QY	628	CTATGCGCTTCATPAGAGTGTGTTCTCTCAAAAACTCAGGGTAAATATTTTGGCAGCTCT	687
Db	507	CTATGCGCTTCATPAGAGTGTGTTCTCAAAAACTCAGGGTAAATATTTTGGCAGCTCT	566
QY	688	GCACCTAGAAAGTCTCCGTTTCTCAGAGATCCCGCATGCTGCGATGGAACCGAAGGGGA	747
Db	567	GCACCTAGAAAGTCTCCGTTTCTCAGAGATCCCGCATGCTGCGATGGAACCGAAGGGGA	626
QY	748	GGCATTGGAAATTTACTGGGTTCACTAGTGGTTATGCTCACAGCAGGAATTTAATCACAGCT	807
Db	627	GGCATTGGAAATTTACTGGGTTCACTAGTGGTTATGCTCACAGCAGGAATTTAATCACAGCT	686
QY	808	TGGTACATAGGATTTTGGTCTTAATTTTTCGTTTCCCTGCTCATCTGCGTGGGAAG	867
Db	687	TGGTACATAGGATTTTGGTCTTAATTTTTCGTTTCCCTGCTCATCTGCGTGGGAAG	746
QY	868	GATGCCAATAAAGATTTTCTACATATGACAGATGCTCTCTGCTGGGGACAATTTACTATTC	927
Db	747	GATGCCAATAAAGATTTTCTACATATGACAGATGCTCTCTGCTGGGGACAATTTACTATTC	806
QY	928	ACAACATTTGGCTATGAGACAAAACCTCCCTAACCTGGCTGGGAAGATTGCTTTCTGCA	987
Db	807	ACAACATTTGGCTATGAGACAAAACCTCCCTAACCTGGCTGGGAAGATTGCTTTCTGCA	866
QY	988	GGCTTGGCACTCCTTGGCAATTTCTTTCTTTCGACTTCCCGCGGCAATTCCTGGCTCAGGT	1047
Db	867	GGCTTGGCACTCCTTGGCAATTTCTTTCTTTCGACTTCCCGCGGCAATTCCTGGCTCAGGT	926
QY	1048	TTTGCATTTAAAGTACAGAACAACCCGCCAGAAAACCTTTGAGAAAAAGAAAGAACCA	1107
Db	927	TTTGCATTTAAAGTACAGAACAACCCGCCAGAAAACCTTTGAGAAAAAGAAAGAACCA	986
QY	1108	GGCGCAACCTCAFTTCAGTGTGTTGGGTGTGTTGGCAGCTGANTGAGAAATCTGTTTCC	1167
Db	987	GGCGCAACCTCAFTTCAGTGTGTTGGGTGTGTTGGCAGCTGANTGAGAAATCTGTTTCC	1046
QY	1168	ATTGCAACCTGGAAGCCACACTTGAAGGCTTTGCACACTGCAAGCCCTTACCA	1220
Db	1047	ATTGCAACCTGGAAGCCACACTTGAAGGCTTTGCACACTGCAAGCCCTTACCAAGAAAGA	1106
QY	1221	-----TCAGAGCTAAAGTTTAAAGAGCAGTGGCCATGCGTAGC	1280
Db	1107	CAGGGGAAGCATCAACAGCTCAAAAGCTAAAGTTTAAAGAGCAGTGGCCATGCGTAGC	1166
QY	1261	CCCAGGGGCCAGAGTATTAAAGGCGCAGCAGCCTCAGTAGGAGACGGAGGTCGCCAAGC	1320
Db	1167	CCCAGGGGCCAGAGTATTAAAGGCGCAGCAGCCTCAGTAGGAGACGGAGGTCGCCAAGC	1226
QY	1321	ACCGACATCAGACCCGAGGGCAGTCCCAACCAAGTGCAAGMAAGCTGGAGCTTCAAGAC	1380
Db	1227	ACCGACATCAGACCCGAGGGCAGTCCCAACCAAGTGCAAGMAAGCTGGAGCTTCAAGAC	1286
QY	1381	CGAACCCTGCTCGGGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTAGAT	1440
Db	1287	CGAACCCTGCTCGGGCCCTGCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTAGAT	1346
QY	1441	GGTGACACAGCCCTTGGCAGCTGATGATGTATATGTAGAAAAAGAGTGGCAGTGTGATGA	1500
Db	1347	GGTGACACAGCCCTTGGCAGCTGATGATGTATATGTAGAAAAAGAGTGGCAGTGTGATGA	1406
QY	1501	TCAGTGGAAAGACCTCACCACCACTTAAAACTGTCATTCGAGCTATCAGAAATTATGAAA	1560
Db	1407	TCAGTGGAAAGACCTCACCACCACTTAAAACTGTCATTCGAGCTATCAGAAATTATGAAA	1466
QY	1561	TTTTCAATGTTGCAAAAAGGAAGTTTAAAGAAACATTAGCTCCATATGATGTAAAAAGATGC	1620
Db	1467	TTTTCAATGTTGCAAAAAGGAAGTTTAAAGAAACATTAGCTCCATATGATGTAAAAAGATGC	1526
QY	1621	ATTGAACAATATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAAAAGCCTTCAACA	1680
Db	1527	ATTGAACAATATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAAAAGCCTTCAACA	1586

QY	168	CGGTTGATCAAAATCTTGAAAAAGGGCAAAATCACATCGAGTAPGAAGAGCCGAGATAA	1740
Db	1587	CGGTTGATCAAAATCTTGAAAAAGGGCAAAATCACATCGAGTAPGAAGAGCCGAGATAA	1646
QY	1741	ATACAGCAAAACATGAGACACAGACATCTCAGTATGCTCGGTGGGTGATCAAGTT	1800
Db	1647	ATAACAGCAAAACATGAGACACAGACATCTCAGTATGCTCGGTGGGTGATCAAGTT	1706
QY	1801	GAAAAACAGGTACAGTCCATGAAATCCAAAGCTGGACCTGCTACTAAGCATCTATCAACG	1860
Db	1707	GAAAAACAGGTACAGTCCATGAAATCCAAAGCTGGACCTGCTACTAAGCATCTATCAACG	1766
QY	1861	GTCCTTCGAAAAAGCTCTGCCTCAGCCCTCGCTTGGCTTCATCTCAGATCCCACTTTT	1920
Db	1767	GTCCTTCGAAAAAGCTCTGCCTCAGCCCTCGCTTGGCTTCATCTCAGATCCCACTTTT	1826
QY	1921	GAAATGACAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTGGGGTTCC	1980
Db	1827	GAAATGACAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTGGGGTTCC	1886
QY	1981	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAAATCCTCGAAGGCTCTCAG	2040
Db	1887	GCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAAATCCTCGAAGGCTCTCAG	1946
QY	2041	TTGATTCCTGAGCCCAATGAGTTCAAGTCCGACACTTCTTAAGCGCTTAAGCCCTACTATG	2100
Db	1947	TTGATTCCTGAGCCCAATGAGTTCAAGTCCGACACTTCTTAAGCGCTTAAGCCCTACTATG	2006
QY	2101	CACAGTCACACACACAGGTGCCCCAATTAAGTCAACAGAGTGGCTCAGACAGTGGGACCCAC	2160
Db	2007	CACAGTCACACACACAGGTGCCCCAATTAAGTCAACAGAGTGGCTCAGACAGTGGGACCCAC	2066
QY	2161	AACACCATTCGAAAACCAATTAATATAGCGCACCCCAAGCCAGACAGCCCAACACTTTACG	2220
Db	2067	AACACCATTCGAAAACCAATTAATATAGCGCACCCCAAGCCAGACAGCCCAACACTTTACG	2126
QY	2221	ATGCCAACCTCCTCTCCCAAGCCATCAAGATCTGCCAGGCCAGAAACTCTGACCCCTAAC	2280
Db	2127	ATGCCAACCTCCTCTCCCAAGCCATCAAGATCTGCCAGGCCAGAAACTCTGACCCCTAAC	2186
QY	2281	CCGCGAGGCTTACAGSAAAGCATTTCTACGTCACACACTGCACTTGTGCTTCACAAAGAA	2340
Db	2187	CCGCGAGGCTTACAGSAAAGCATTTCTACGTCACACACTGCACTTGTGCTTCACAAAGAA	2246
QY	2341	AATGTTCAAGTTGACACATCAAAATCTCACCAAAGACCTTTATATGAGAAAAGCTTTGAC	2400
Db	2247	AATGTTCAAGTTGACACATCAAAATCTCACCAAAGACCTTTATATGAGAAAAGCTTTGAC	2306
QY	2401	ATGGGAGGAAAACTCTGTTGCTGCTGTCGCCATGAGTGGCCGGAAGACTTGGGCAATCT	2460
Db	2307	ATGGGAGGAAAACTCTGTTGCTGCTGTCGCCATGAGTGGCCGGAAGACTTGGGCAATCT	2366
QY	2461	TTGCTCTGTGAAAAACCTGATCAGGTGCAACGAGAACTGAATATACAACTTTCAGGGAGT	2520
Db	2367	TTGCTCTGTGAAAAACCTGATCAGGTGCAACGAGAACTGAATATACAACTTTCAGGGAGT	2426
QY	2521	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTATCCCAATTGGAGGGAAATCCAAATG	2580
Db	2427	GAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTATCCCAATTGGAGGGAAATCCAAATG	2486
QY	2581	TTTATTAAGTATGAGAGGTGGTGGCCCAAGAGACAGAGACACTTTTGTATGGCGCA	2640
Db	2487	TTTATTAAGTATGAGAGGTGGTGGCCCAAGAGAGACAGAGACACTTTTGTATGGCGCA	2546
QY	2641	CCGCGACCTGCGCAGGGAAGCTGCTTTGCACTACACTCTTAAGGACTGGAAAGTCACGA	2700
Db	2547	CCGCGACCTGCGCAGGGAAGCTGCTTTGCACTACACTCTTAAGGACTGGAAAGTCACGA	2606
QY	2701	TCATCTCAGAGCACTTTGTAAGGCGAGGAAGTACAGATGCCCTCAGCTTGGCTCAATGTC	2760
Db	2607	TCATCTCAGAGCACTTTGTAAGGCGAGGAAGTACAGATGCCCTCAGCTTGGCTCAATGTC	2666
QY	2761	AAACTGAATAAA 2772	

Db 2667 AACCTGAATAA 2678

RESULT 10
AAC64370
ID AAC64370 standard; DNA; 125910 BP.

AC AAC64370;
XX 07-FEB-2001 (first entry)
DT

XX Human KCNQ5 (KCNBq) gene sequence SEQ ID NO:1.
DE
XX Human: KCNQ5; KCNBq; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioclastic; anticonvulsant; gastrointestinal; muscular atrophy;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ds.

XX Homo sapiens.
OS
XX WO200061606-A1.
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000MO-US09587.
PE
XX 14-APR-1999; 9905-0129274.
PR
XX (MERI) MERCK & CO INC.
PA
XX Petrukhin K, Caskey CT, Li W, Metzker ML;
PI
XX WPI; 2000-647417/62.
DR
XX P-PSDB; AAB24241.
DR

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
PT
XX Claim 3; Fig 1; 99pp; English.

XX The present sequence represents the human KCNQ5 (also called KCNBq) gene,
XX which encodes a voltage-gated potassium channel protein. Human KCNQ5
XX has ophthalmological, auditory, central nervous system (CNS),
XX cardioclastic, anticonvulsant, gastrointestinal and muscular active
XX activities. Sequences and methods from the present invention are useful
XX for identifying activators or inhibitors of KCNQ5 protein. These
XX activators and inhibitors are useful for treating Stargardt-like macular
XX dystrophy, cone-rod dystrophy, Salla disease, age-related macular
XX degeneration, other forms of macular degeneration, deafness, epilepsy,
XX and different forms of neuropsychiatric, heart, gastrointestinal, and
XX muscle disorders. Stargardt-like macular dystrophy and cone-rod
XX dystrophies are located at chromosome 6q.

XX Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 72 other;

Query Match 34.8%; Score 965; DB 21; Length 125910;
Best Local Similarity 100.0%; Pred. No. 3.2e-243;
Matches 965; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 AGGTACAGTCCATAGATCCAGCTGACCTGCTACATGACATATCAAGAGTCCCTC 1867
DB 123624 AGGTACAGTCCATAGATCCAGCTGACCTGCTACATGACATATCAAGAGTCCCTC 123683

QY 1868 GGAAGGCTCTGCTGAGCCCTGCTTGGCTTCATCCAGATCCACCTTTGAATGTG 1927
DB 123664 GGAAGGCTCTGCTGAGCCCTGCTTGGCTTCATCCAGATCCACCTTTGAATGTG 123743

QY 1928 AACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAA 1987

Db 123744 AACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTGGGTTCCGACAAA 123803

QY 1988 ACAAGTGGCTCTTATTCAGATCAACTAGTGGCCAAATCTCCAGAGAGCCCTGACATCTTC 2047
DB 123804 ACAAGTGGCTCTTATTCAGATCAACTAGTGGCCAAATCTCCAGAGAGCCCTGACATCTTC 123863

QY 2048 TGACGCCAAATGATTCAGTCCAGATCTTCTACGCGCTTAAGCCCTACTATGACAGATC 2107
DB 123864 TGACGCCAAATGATTCAGTCCAGATCTTCTACGCGCTTAAGCCCTACTATGACAGATC 123923

QY 2108 AACCAACACAGTGGCCATTAATGATCAAAAGCGATGGCTGACAGTGGCCAGCCACCAACCA 2167
DB 123924 AACCAACACAGTGGCCATTAATGATCAAAAGCGATGGCTGACAGTGGCCAGCCACCAACCA 123983

QY 2168 TTGCAAAACCAATTAATTAAGCCGACCCAGCCAGCCGACCCCAACCACTTACAGATCCAC 2227
DB 123984 TTGCAAAACCAATTAATTAAGCCGACCCAGCCAGCCGACCCCAACCACTTACAGATCCAC 124043

QY 2228 CTCCTCTCCAGCCATCAAGCATCTGCCAGCCGCAAAACTCTGCAACCTTAACCCCTGCAG 2287
DB 124044 CTCCTCTCCAGCCATCAAGCATCTGCCAGCCGCAAAACTCTGCAACCTTAACCCCTGCAG 124103

QY 2288 GCTTTACAGGAAGCATTTTGTGAGCTCACACCTGCTTGTGCTCCAGGAATGTTTC 2347
DB 124104 GCTTTACAGGAAGCATTTTGTGAGCTCACACCTGCTTGTGCTCCAGGAATGTTTC 124163

QY 2348 AGGTGACAGTCAATCTGACCAAGGACGCTTGTATGAGGAAGAAAGCTTTGACATGGGAG 2407
DB 124164 AGGTGACAGTCAATCTGACCAAGGACGCTTGTATGAGGAAGAAAGCTTTGACATGGGAG 124223

QY 2408 GAGAAACTCTGTTGTCTGTCTGTCCATGATGCGGAAGGACTTGGCAAACTTGTCTG 2467
DB 124224 GAGAAACTCTGTTGTCTGTCTGTCCATGATGCGGAAGGACTTGGCAAACTTGTCTG 124283

QY 2468 TGCAAAACCTGATCAGTCCGACCGAGGACCTGATATACACTTTCAGGAGTGAATCA 2527
DB 124284 TGCAAAACCTGATCAGTCCGACCGAGGACCTGATATACACTTTCAGGAGTGAATCA 124343

QY 2528 GTGGCTCCAGAGGAGGACCAAGATTTTACCCCAATGAGGAAATCCAAATGTTTATTA 2587
DB 124344 GTGGCTCCAGAGGAGGACCAAGATTTTACCCCAATGAGGAAATCCAAATGTTTATTA 124403

QY 2588 CTGATGAAGAGTGGGTCCCGAAGAGACAGACACTTTTATGATGGCCGACCGCAGC 2647
DB 124404 CTGATGAAGAGTGGGTCCCGAAGAGACAGACACTTTTATGATGGCCGACCGCAGC 124463

QY 2648 CTGCCAGGGAAGCTGCTTGTGATCAGACTCTCTAAGAGCTGGAAGTTCAGATCATCTC 2707
DB 124464 CTGCCAGGGAAGCTGCTTGTGATCAGACTCTCTAAGAGCTGGAAGTTCAGATCATCTC 124523

QY 2708 AGAGCATTTTAAAGGAGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGCTCAACTGA 2767
DB 124524 AGAGCATTTTAAAGGAGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGCTCAACTGA 124583

QY 2768 AATTA 2772
DB 124584 AATTA 124588

RESULT 11
ABA90234
ID ABA90234 standard; DNA; 548 BP.

XX ABA90234;
XX
XX 12-FEB-2002 (first entry)
DT
XX Human ORF41 coding sequence.
DE
XX Human ORF41 coding sequence.
KW ORF41: human; pharmacogenomics; cancer; hyperproliferative disorder;
KW dysproliferative disorder; neurodegenerative disorder; organ transplant;
KW cardiovascular disease; cytokine; cell proliferation; immunomodulatory;

311 370

CC sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available.

XX Sequence 2273 BP: 486 A; 670 C; 653 G; 448 T; 16 other;
 SQ Query Match 17.8%; Score 492.4; DB 20; Length 2273;
 Best Local Similarity 57.2%; Pred. No. 2.5e-119;
 Matches 1022; Conservative 2; Mismatches 665; Indels 99; Gaps 4;

169 GGCCTGCTACTGCTGGGACCCGCGGCGGACGCTGCTGGGCGGCGGCTGAGC 228
 67 GGCCTGCTGGGCGCTGGACCCCGCGGCGGACGCTGCTGGGCGGCGGCTGAGC 126
 229 GAGAGCCCGCGGCGGACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 288
 127 GCGGCGCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186
 289 ACGAGTACCGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 348
 187 GGAGCCGGGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
 349 AAGCTGCTGAGAGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
 247 AAGCTGCTGAGAGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306
 409 GCTCTTGGTCTGATTTTGTGACGCTTTTCTACATCCCTGACACACAAATTGGCC 468
 307 GTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
 469 TCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
 367 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 426
 529 ATTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
 427 GTGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
 589 TTGCTGGAAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
 487 TTGCTGGAAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
 649 GTTCTGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 547 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
 709 CTACAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 607 TTGGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 769 TCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
 667 TCGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
 829 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 888
 727 CTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786
 889 ACATATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 787 ACCTACGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
 949 AAACATCCCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
 847 AAGTACCTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 1009 TCTTTCTTTCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
 907 TCGTTCTTTCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
 1069 CAACACCCCGGAGAAAGCTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1128
 967 GAGCATCTGGGAGAAAGCTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1026
 1129 GTTGGCGTAGTACGAGCTGAT----- 1152

Db 1027 GCCTGAGATTTATGCTACTTAACCTCTCAAGCAGCAGCCGCTGCACTCCAGCTGGCAGTAC 1086
 QY 1153 ----GAGAAATCTTTTCCATTTGCAACCTGGAGCCACACTTGGAGCCCTTGCACACCTGC 1209
 Db 1087 TACGACGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
 QY 1210 AGCCCTTAC-----AATCAGAACTTAAGTTTA 1237
 Db 1147 AGACTATCTCCACTCTGCAACAGCTGAGCTGCTGAGGAATCTCAAGAGCAAAATCTGGA 1206
 QY 1238 AGAGCGAGTGCAGCTAGCTAGCCCGAGGGCGCAGATTAAGAGCCAGCAAGCTCAG 1297
 Db 1207 CTACCTTACGAGAGAGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1266
 QY 1298 TAGGTACAGAGAGTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1334
 Db 1267 AAGGAGAGAGGCTGCTCCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1326
 QY 1335 --GAGAGGAGTCCCAAGTACAGAGAGTGAAGAGCTGCAAGCAGCAGCAGCAGCAGCAG 1392
 Db 1327 CTGATGACAGAGCCGAGAGAGTGGCCCAAGAGCTGAGAGCTTTGGTGACCGCAGCCGACA 1386
 QY 1393 CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
 Db 1387 CGCAGGCTTCCGCAATCAAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
 QY 1453 CTGGCAGTATGAT 1512
 Db 1447 CTTGGGAGAGACATGCTGAGAGACAGAGCTGTAAGCTGAGCTGCTGCTGCTGCTGCTGCTG 1506
 QY 1513 CTACCCGACACTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1572
 Db 1507 CTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1566
 QY 1573 AAACGAAATTAAGAAACATTAAGTATGATTAAGATTAAGATTAAGATTAAGATTAAG 1632
 Db 1567 AAGCGAAATTAAGAAACATTAAGTATGATTAAGATTAAGATTAAGATTAAGATTAAG 1626
 QY 1633 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1692
 Db 1627 TCGGCTGAGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1686
 QY 1693 ATTCTTGAAGAGGCAATACATGATTAAGAGAGCCGAGAGAAATTAAGACAGAGA 1752
 Db 1687 ATTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1743
 QY 1753 CATGAGACACAGAGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1812
 Db 1744 ACGGAGCTGCGCGAAGAGCCCGAGCATGATGAGGAGCGCTTGGAGAGGTGAGAGAAAGAGT 1803
 QY 1813 CAGTCCATGAAATCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
 Db 1804 TTGTCATGAGAAAGAGAGCTCGAGCTTCTGCTGAGCATCTATACAGAG 1851

RESULT 13
 AAA47618
 ID AAA47618 standard; cDNA: 2335 BP.
 XX AAA47618;
 DTX 08-NOV-2000 (first entry)
 DE KCND4 Potassium channel gene.
 XX KCND4, potassium channel; cardiac arrhythmia; neonatal epilepsy;
 KW deafness; probes; treatment; therapy; transgenic animal; antibody;
 KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
 KW presbycusis; affective disorder; Alzheimer's disease; anxiety;
 KW ataxia; cognitive deficits; compulsive behavior; dementia;
 KW depression; Huntington's disease; mania; memory impairment;
 KW motor disorders; neurodegenerative disease; Parkinson's disease;
 KW Pick's disease; psychosis; schizophrenia; spinal cord damage;

KM	stroke; tremor; ds.
OS	Homo sapiens.
FH	Key
FT	CDS
FT	83..2170
FT	/tag- a
FT	/product= KCNQ4 potassium channel polypeptide
XX	MO200044786-A1.
PN	
PD	03-AUG-2000.
PF	19-JAN-2000; 2000MO-DK00024.
PR	26-JAN-1999; 99PK-0000076.
PR	19-MAY-1999; 99DK-0000693.
PA	(NEUR-) NEUROSEARCH AS.
PI	Jentsch TJ;
PS	WPI; 2000-546813/50.
DR	P-PDOB; AAB014/6.
XX	
PT	Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
PT	useful e.g. for treating tinnitus, deafness, Alzheimer's and
PT	Parkinson's diseases
PS	Claim 1; Page 43-48; 65pp; English.
XX	
CC	Mutations in 3 known genes of the KCNQ branch of the potassium
CC	channel gene family underlie inherited cardiac arrhythmia's, neonatal
CC	epilepsy and in some cases associated with deafness. KCNQ4 has been
CC	mapped to the DFN2 locus for autosomal dominant hearing loss, and
CC	a dominant negative KCNQ4 mutation that causes deafness in a DFN2
CC	pedigree has been identified. KCNQ4 is the first potassium channel
CC	gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
CC	channels with other KCNQ channel subunits, especially KCNQ3.
CC	KCNQ4 encodes the KCNQ4 protein and the protein itself may be
CC	used in the prevention, treatment and diagnosis of diseases
CC	associated with inappropriate KCNQ4 expression. The nucleotides may
CC	also be used as DNA probes in diagnostic assays (e.g. polymerase
CC	chain reactions (PCR)) to detect and quantitate the presence of
CC	similar nucleic acid sequences in samples and to identify mutations
CC	within them, and hence which patients may be in need of restorative
CC	therapy. They may also be used to study the expression and function
CC	of KCNQ4 polypeptides and their role in metabolism, for example
CC	through the production of transgenic animals. The KCNQ4 polypeptides
CC	may be used as antigens in the production of antibodies and to
CC	identify modulators (agonists and antagonists) of KCNQ4 expression
CC	and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may
CC	also be used to down regulate KCNQ4 expression and activity. They may
CC	be used in this way to treat tinnitus, loss of hearing (especially
CC	progressive hearing loss), neonatal deafness and presbycusis
CC	(deafness of the elderly) and disease or adverse conditions of the
CC	central nervous system (CNS) such as affective disorder, Alzheimer's
CC	disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC	neurodegenerative illness, cognitive deficits, compulsive behavior,
CC	dementia, depression, Huntington's disease, mania, memory impairment,
CC	memory disorders and dysfunctions, motion disorders, motor disorders,
CC	neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
CC	disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
CC	cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
CC	molecules may be administered to down regulate KCNQ4 expression by
CC	binding with the cells own KCNQ4 genes and preventing their
CC	expression.
SO	Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 other;
XX	
XX	Query Match 17.7%; Score 492; DB 21; Length 2335;
XX	Best Local Similarity 59.3%; Pred. No. 3.3e-119;
XX	Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps

[illegible]

OY	1244	GTGGCGATGGCTTACCCCGAGGGCGCAGATAT-----AAGAGCCGACAAAGCTCAGTA	1259
Db	1400	ATCCGATGGGCACTCCCTCCAGCGCGGACGGGTCTCTCCAGCAGCAGCTGGCACCTTCA	1459
OY	1300	GGTGACAGAGAGTCCCCCAAGCACCAGACATCAAGCCGAGG---GCAGTCCACCAAGTG	1356
Db	1460	ACAATGCCCCACCTCCCAAGCAGGAGCAGAGTGGGAGAGCCACCAAGCCCCACCAAGTG	1519
OY	1357	CAGAAAGCTCGAGCTTCAACGACCCGAAACCGGCTTCCGGCCCTCGCTGCGCTCAAAAGT	1416
Db	1520	CAAAAAGCTGGAGCTTCAAGACCGCACCCGCTTCCGGGCATCTCTGAGACTC-----	1573
OY	1417	TCACAGCCAAAACAGTAGTATGATGTACACAGCCCTTGGGACATGATGATATATGAT	1476
Db	1574	-----AAACCCCGCACCTCTGCTATGAGATGCC---CCTCAGAGGAATGAGCAGAG	1621
OY	1477	GAAAAAGATGCCAGTGTGATGTATCACTGGAGAAGCTCACCCACACCTTAATAACTGTC	1536
Db	1622	GAGAAAGCTACCAAGTGTGAGCTCACGGTGGACGACATCATGCTGCTGTGAAGACAGTC	1681
OY	1537	ATTGCGATCTCAGAATTATGAATTTCATGTGTGCAAAAAGGAGTTTAAGAGAACTTA	1596
Db	1682	ATCCGCTCATCAGGATCTCAAGTTCTCGTGGCCAAAAGGAAATTCAAAGGAGACACTG	1741
OY	1597	CGTCCATATGATTAATAAGATGTATGTGAACAATTTCTGCGTGCATCTGAGCATGTG	1656
Db	1742	CGACCGTACGACGCTGAAGACGTAATGAGAGTACTCAAGAGGCCACTGAGCATGTCTG	1801
OY	1657	TGTAGATTAAAAACCTTCAACACAGCTGTATCAAAATTTCTGGAAAAGGCG---AAATC	1713
Db	1802	GGCCGGATCAAGAGCGCTGCAAACTCGGGTGGACCAAAATTTGGTGGGGGGCCCCGGGAC	1861
OY	1714	ACATCAGATTAAGAAGACCCGAGAGAAATTAACGAGAAATGAGACCAACAGACGATCTC	1773
Db	1862	AGGAAGGCCCGGAGGAAGGGCGACAAAGGGGCGCTCCGACGCGAGGTGGTGATGAATC	1921
OY	1774	AGTATGCTCGGTGGGGGTCAAGGGTGAAAAACGATACATCCATTAATTCAGAGCTG	1833
Db	1922	AGCATGATGGGACGCGGTGTCAAAGGTGAGAGACAGGTGCACTTCATCAAGCAACAAGCTG	1981
OY	1834	GACTGCGCTACTAGACATCTTCAACAGAGGTCCCTTGGGAAAAGGCTGTGCTCAGAGCCCTGCT	1893
Db	1982	GACCTGCTGTGGGCTCTTATTTGCGCGCTGCTGC-----GCTCTGCGACCTGGCGACG	2035
OY	1894	TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAACCTT	1953
Db	2036	CTGGGGCGCGTGCAAGTGCGCGCTGTTCGACCCCGACATACACTCGACTACACAGCCT	2095
OY	1954	GTGATAGCAAAAGATCTTTGGGTTGCGGCNAAA	1987
Db	2096	GTGGACACGAGGACATCTCTCGTCTCGCACAGA	2129

RESULT	14
AAKX26588	
ID	AAKX26588 standard; DNA; 2169 BP.
XX	
AC	AAKX26588;
XX	
DT	16-JUN-1999 (first entry)
XX	
DE	Nucleotide sequence of murine KCNQ2 (formerly known as (KVIRL)).
KW	KCNQ protein; nervous system-specific potassium channel;
KM	neuronal excitability; neurotransmitter release; KCNQ modulator;
KW	ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KM	age-associated memory loss; learning deficiency; motor neuron disease;
KW	epilepsy; stroke; ss.
OS	Mus sp.
XX	
FH	Key
FT	Location/Qualifiers
CD	1..2169
IT	CDS

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FT      xx      /*tag= a
PN      xx      MO9907832-A1.
FD      xx      18-FEB-1999.
FE      xx      26-JUN-1998;   98WO-US13276.
PR      xx      12-AUG-1997;   97US-0055599.
PA      xx      (BRIM ) BRISTOL-MYERS SQUIBB CO.
PI      xx      Blumar MA, Dworetzky S, Gribkoff VR, Levesque PC;
PI      xx      Little MA, Neubauer MG, Yang W;
DR      xx      WPI; 1999-190047/16.
DR      xx      P-PSDB; AAY01530.
PT      xx      New potassium channels, KCNQ2 and KCNQ3 - may be involved in
FT      xx      neurotransmission and neuroprotection, used to treat, e.g. ataxia
PS      xx      Claim 7; Fig 10A-D; 64pp; English.
CC      xx      The present sequence encodes murine KCNQ2/KVIRL. KCNQ proteins are
CC      xx      nervous system-specific potassium channels. In neurons, potassium
CC      xx      channels regulate neuronal excitability, action potential shape
CC      xx      and firing pattern, and neurotransmitter release. KCNQ modulators
CC      xx      may be used to treat disorders such as ataxia, myokymia, seizures,
CC      xx      Alzheimer's disease, Parkinson's disease, age-associated memory
CC      xx      loss, learning deficiencies, motor neuron diseases, epilepsy, and
CC      xx      stroke.
SO      Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 other;

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	Query March	17.3%	Score 478.8	DB 20;	Length 2169;	
	Best Local Similarity	57.1%;	Pred. No. 9.7e-116;			
	Matches 1024;	Conservative	0;	Mismatches 662;	Indels 108;	Gaps 4
QY	169	GGCCCTGCACTCGTGCGGCCACC	CGCGCGGCACACGCTCGGTGGCGGCGGCTGGAGG	228		
Dd	67	GGCTTCGTGGGGCTGGACCCGCGGCGCCGACTCCACACGCGGACGGCGCGTATCATC	126			
QY	229	GAGAGCCGCCGGGGCACAGCAGGGGGCCCGATGAGACCTGCTGGGGAA	CGCTCTCTTAC	288		
Dd	127	GCGGCGTCCGAGGGCCCCAACGCGGGCAGCGCTTTTGACAAGCCCGGAGCGGGCGCGG	186			
QY	289	ACGAGTAGCCAGCACTGCGCGGCAACGTAAGTAGTCGGGGGTCGACAACTACCTGAC	348			
Dd	187	GGAGCCGGGAAGCCCCGGAAGCGCAACCCCTTCTACCGCAAGCTGCAAAATTTCTCTAC	246			
QY	349	AACGTGCTGAGAGACCCCGCGGCTGGGCGCTTCATCTCAACAGCTTGTTGTTTTCTCCTT	408			
Dd	247	AAGCTGCTAAGGGGGCCCCCGGCGCTGGGCGCTTACATCTACACAGCTACGTTGTTCTTTTA	306			
QY	409	GTCCTTGGTCTTGATTGTTTGTCAAGTGTTTTCTAACATCCTGAGCACAAAATTTGGCC	468			
Dd	307	GTCCTTCTCCGCTTGTGCTTCTGTGTGTTTCCACATCAAGAGATGAGAGAAGAGCTCT	366			
QY	469	TCAAGTGGCCCTTGATCTCGAGATTCGTGTAATGATGTCGCTTGTGGTGGATTCATC	528			
Dd	367	GAGGGGGCCCTTCAATCTTGGAAATGCTGACTCTGCTGATTCGGGTGGAGTACCTT	426			
QY	529	ATTTCGATCTGSGTCTGGGGTGTGCTGTGTGATAGATAAGAGATGGCAAGAACTGAGG	588			
Dd	427	GTCAGGATCTGGGGCTCGAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGCACGGCTCAAG	486			
QY	589	TTTTCTCGAAAGCCCTTCTGTGTTATAGATAACATTTCTCTTATCGCTTCAATAGACATT	648			
Dd	487	TTTGGCAGAAGCCGTTCTGTGATGATATATCATGAGTGCGTGAITGCTTCATTTGCTGTG	546			
QY	649	GTTTCTGCAAAACCTCAGGGTAATATTTTGGCCAGCTCTGACACTCAGAACTCCCGTTTC	708			
Dd	547	CTGGCTGCTGTTCCAGGCAATGCTTTTCCACATCTGGGCTTTCGAGCTTCAGCTTC	606			

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QY 709 CTACAGATCCCTCCGATGTCGCGATGAGCCGAAGGGAGGACCTTGGAAATTTACTGGGT 768
   || || || || || || || || || || || || || || || || || || || || ||
Db 607 TTGCAATATCTGGGAGATGCCGATATGACCGGAGGGGTGGCACCCTGGAAAGCTTTGGGA 666
QY 769 TCAGTGTGTTATGCTCAACAGCAAGAAATTAATCAAGCTTGGTACATAGATTTTGGTT 828
   || || || || || || || || || || || || || || || || || || || || ||
Db 667 TCGGTATGCTACGCTCAACAGCAAGAGCTGGTGAAGCTGCTGTTACATTTGGCTTCTGTC 726
QY 829 CTATATTTTTCGCTCTCTGCTATCTGCTGAGAAAAGGATGCCAATAAAGATTTTCT 888
   || || || || || || || || || || || || || || || || || || || || ||
Db 727 CTATCTCGGCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 889 ACAATATGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
   || || || || || || || || || || || || || || || || || || || || ||
Db 787 ACCTAGCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 949 AAAAGTCCCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
   || || || || || || || || || || || || || || || || || || || || ||
Db 847 AAGTACCTCCAGACCTGGAACGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
QY 1009 TCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
   || || || || || || || || || || || || || || || || || || || || ||
Db 907 TCGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 1069 CAACACCGCCGAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAACCCTATTCAGTGT 1128
   || || || || || || || || || || || || || || || || || || || || ||
Db 967 CACGATCGGAGAAAACACTTTGAGAAAAGGAGAACCCCTGCGGAGCTGCTGCTGCTGCT 1026
QY 1129 GTTTGGCGTATGATGAGCACTGATGAGAAATCTTTTCATTCGAACTGGAAGCCACAC 1188
   || || || || || || || || || || || || || || || || || || || || ||
Db 1027 GCCTGGAGATTCATGCTACTTAACCTCTACAGCACCCGACCTGACCTCCAGCGAGTAC 1086
QY 1189 T----- 1189
Db 1087 TACGAGCGAGACACTGCTGCCATGTACAGACTCATCCACCTTGAAGCCAGCTGGAG 1146
QY 1190 -----TGAAGCGCTTGCACACCTGC 1209
   || || || || || || || || || || || || || || || || || || || || ||
Db 1147 CTGCTGAGGATCTCAAGAGCAATCTGAGCTCACTTCAAGAAAGAGCCACAGCCAGAG 1206
QY 1210 AGCCCTACCAATGAGAACTAAGTTTAAAGAGCGAG--TGCAGTGGCTAGCCCGCAGG 1266
   || || || || || || || || || || || || || || || || || || || || ||
Db 1207 CCATCAACCAAGTCAAGAGTCAAGTTGAAGATGCTGCTTCCAGCCCGCAGAGCATG 1266
QY 1267 GGGCAGAGTTTAAAGCCGACCAAGCTCACTAGTGCAGAGAGTCCCGCAAGCAGCAGC 1326
   || || || || || || || || || || || || || || || || || || || || ||
Db 1267 GCTGCCAAGGAAAGGGGCTCTCCAGAGCCGACAGCGGTCCGCGGTCCCGCAGTGGGAT 1326
QY 1327 ATCAGACCGGAGGAGTCCACCAAGTGCAGAAAGAGCTGAGCTTCAAGAGCCGAAC 1386
   || || || || || || || || || || || || || || || || || || || || ||
Db 1327 CAGAGTCTTGATGACAGCCCGAGAGAGTGGCCCAAGAGCTGGAGCTTGGTACCGCAGC 1386
QY 1387 CGGTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
   || || || || || || || || || || || || || || || || || || || || ||
Db 1387 CGCAGACGCGAGGCTTCCGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 1447 ACAGCCCTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1506
   || || || || || || || || || || || || || || || || || || || || ||
Db 1447 C---TCCCTGGGAGGAGCATGTAGAGACAAAGAGCTTAACTGAGAGTTGTGACT 1503
QY 1507 GAAGACCTCAACCCAGCACTTAAACATGCTATGAGATGATGATGATGATGATGATGAT 1566
   || || || || || || || || || || || || || || || || || || || || ||
Db 1504 GAGAGTCTTACCCCTGGCCTCAAAAGTTAGCATCAGAGCTGTGTGTGTGTGTGTGTGTGT 1563
QY 1567 GTTTCAGAAACGGAAGTTTAAAGAAACATTAAGTCCATATGATGATGATGATGATGAT 1626
   || || || || || || || || || || || || || || || || || || || || ||
Db 1564 GTATCTTAAGCGAAAGTTCAAAAGAGTCTGGCGCCATATGATGATGATGATGATGAT 1623
QY 1627 CAATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
   || || || || || || || || || || || || || || || || || || || || ||
Db 1624 CAGTACTCGGCTGACACTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1683

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QY 1687 GATCAAAATCTTGGAAAAAGGCAAAATCATCATAGATAGAGAGCCGAGAGAAATATA 1746
   || || || || || || || || || || || || || || || || || || || || ||
Db 1684 GACCAAGATTTGGGGGGGGGGCCCAACAATAAGATTAAGCA---TCCGACCAAAAGCCCA 1740
QY 1747 GCAGAACATGAGACACAGACGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1806
   || || || || || || || || || || || || || || || || || || || || ||
Db 1741 GCGGAAAGGAGAGCTGCCGCAAGACCCAGCATGATGAGGAGCTTGGGAAAGTGGAGAA 1800
QY 1807 CAGGTACAGTCCATAGATCCAAAGCTGACTGCTACTAGACATCTATCAACAG 1860
   || || || || || || || || || || || || || || || || || || || || ||
Db 1801 CAGGTCTGTGATGAGAAAGAGCTGACTTCTTGGTGAACATCTATACAG 1854

RESULT 15
AA574832
ID AA574832 standard; cDNA; 7413 BP.
XX
AC AA574832;
XX
AC 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #10636.
XX
KW Human; Chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR MPI; 2001-639362/73.
XX
DR P-Psdb; ABG10645.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID No 10636; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AA594564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

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QY 1248 GCGATGGCTAGCCCGAGGCGCAGATATTAGAGCCGCAAGCCTCAGTAG-----G 1301
 Db 1450 ---CTTCTCCAGCCCCCGAGGGGTGGCTGCGCAAGGGGAAGGGTCCCCGAGGCCAGAC 1506
 QY 1302 TGACAGAGAGTCCCGACGACCATCAAGCGGAGGCGAGTCCCAACAAAGTGAGAA 1361
 Db 1507 TGTAGAGGCGTACCCAGCGCCGACGAGCTCGAGAGACAGCCCCAGAGGTGCCAA 1566
 QY 1362 GAGCTGAGCTTCAACGACCGGCTTCCGGCCCTCGCTCGCTCAAAAGTTCTCA 1421
 Db 1567 GAGCTGAGCTTCCGGGAGCCGAGCGGGGACCGCAGGCTTCCGAGTCAAGGCTGCCG 1626
 QY 1422 GCCAAAACAGTATGATGCTGACACAGCCCTTGACACTGATGATATATGATAA 1481
 Db 1627 GTCACGCGAGAACTCAGA---AGAAAGCAAGCCTCCCGGAGAGACATTTGTGATGACAA 1663
 QY 1482 AGGATGCCAGTGTATGATATCATGCTGAGAGACCTCACCCACACCTTAAACTGTCTCG 1541
 Db 1684 GAGCTGCCCTCGCGAGTTGTGACCGAGACCTGACCCCGGCTCAAAAGTCAAGCATCAG 1743
 QY 1542 AGCTATCAGAAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACATTAGCTCC 1601
 Db 1744 AGCGGTGTGTCTCATGCGGTTCCTGTCTGTCACAGCGGAAGTTTCAGGAGAGGCTGCGGCC 1803
 QY 1602 ATATGATGTAAAGATGTCTATGAAACAATATTTCTGCTGATCTGACATGTTGTGTAG 1661
 Db 1804 CTACGAGCTGATGAGACGTCATGACAGTACTGACGCGGCGCACCTGAGACATGCTGTCCG 1863
 QY 1662 AATTAAAGCCTTCAAAACAGCTGTGATCAATTTCTGGAAGAAAGGCAATATCATTACAGA 1721
 Db 1864 AATTAAAGCCTTCAAAACAGCTGTGATCAATTTCTGGAAGAAAGGCAATATCATTACAGA 1923
 QY 1722 TAAGAAAGACCGCAGAGAAATATACAGACATGATGACACAGAGATCTGATGCT 1781
 Db 1924 CAAGGA---CCGACCAAGGCGCGCGGAGCGGAGCGAGCTGCCAGAGACCCAGCATGAT 1980
 QY 1782 CGGTGGGTGTCTCAAGTTGAAAAACAGAGTACATGATAGAAATCCAGCTGAGTCTT 1841
 Db 1981 GGGAGCGGCTCGGAGAGTGGAGAGAGAGTCTTGTTCATGAGAAAGCAAGCTGATCTTCT 2040
 QY 1842 ACTAGACATCTATCAACAG 1860
 Db 2041 GGTGAATATCTACTACGAG 2059
 RESULT 17
 AAX81548
 ID AAX81548 standard; DNA; 2565 BP.
 AC AAX81548:
 XX
 DE 25-AUG-1999 (first entry)
 XX
 DE Human brain-derived potassium channel DNA structural DNA.
 XX
 KW Human: brain-derived potassium channel; neurophysiology;
 KW cognitive disorder; behavioural disorder; psychiatric disorder;
 KW neurodegenerative disorder; developmental disorder; mental retardation;
 KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
 KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09931232-A1.

XX
 PD 24-JUN-1999.
 XX
 PF 11-DEC-1998; 98MO-GB03720.
 XX
 PR 13-DEC-1997; 97GB-0026339.
 XX
 PA (ZENRE) ZENRECA LTD.
 XX
 PI Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 DR WPI: 1999-395178/33.
 XX
 PS New isolated potassium channel polypeptide
 XX
 PS Claim 2: Fig 2; 151pp; English.
 CC
 CC The present sequence represents brain-derived potassium channel DNA.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 SQ Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other;
 Query Match 16.1%; Score 447; DB 20; Length 2565;
 Best Local Similarity 56.8%; Pred. No. 2,7e-107;
 Matches 1038; Conservative 0; Mismatches 645; Indels 144; Gaps 6;
 QY 169 GGCCTGCTACTGCTGGGACCCGCGCGGCGACGCTGGTGGGCGGCGGCTGAGG 228
 Db 67 GCTTCTGCTGGGCTGGACCCCGCGCGCGGCGGCTGACACCGGAGCGGCTGATTC 126
 QY 229 GAGAGCCCGCGGCGGAGCGAGCGGCGCGGAGTGGCTGTGGGAAAGCGCTCTTAC 288
 Db 127 GCGGCTCCGAGGCGCCCAAGCGGCGGACATCTCAGCAAACTCGCGGCGGCGG 186
 QY 289 ACGAGTACCGAGAGTGGCGGCGGCAACGTCAGTACCGGCGGCTGAGAACTACTTAC 348
 Db 187 GCGCGCGGAGAGCCCGCAAGCGCAAGCGCTTCTACCGAAGCTGAGAAATTCCTTAC 246
 QY 349 AACGTGCTGAGAGAGACCCCGCGGCGGCTGATCTATACACGCTTCTTCTTCTTCT 408
 Db 247 AACGCTGCTGAGAGAGCGGCGGCGGCGGCTGATCTATACACGCTTCTTCTTCTTCT 306
 QY 409 GTCTTTGCTGCTGATTTTGTCTAGTGTCTTACCATCCCTGAGACAAATAATGGCC 468
 Db 307 GTTTTCTCTCTCTCTGCTGCTGCTGTGTTTCCACCATCAAGAGATATGAGAGCTCG 366
 QY 469 TCAGATTGCCCTTGATCTGAGAGTTCGATGATGATTTGTCTTGTGTTGGAGTTTATC 528
 Db 367 GAGGCGGCGCTTCAATCTTGAATAATCGATATCTGCTGTTTGGCGGAGTACTTC 426
 QY 529 AATGGAATCTGCTGCGGCTTGTCTGCTGATATGAGAGATGCAAGAAAGAGAGAG 588
 Db 427 GTCCGAAATCTGGGCGGAGGCTGCTGCTGCTGCTGCTGCTGAGGAGGCGGCTCAAG 486
 QY 589 TTTCCTGAAAGAGCCCTTCTGTGTATATGATATCAATGTTCTTATGCTCAATAGAGATT 648

Db	487	TTTTGCCGGAAACCGTTTCTGTGATTGACATCATGTGCTCATCGCTCCATTGCGGTG	546
QY	649	GTTTCTGCAAAAACCTCAGGGTAATATTTTGGCCAGTCTGCACTCAGAAAGTCTCCGTTTC	708
Db	547	CTGGCCGCGCGGCTCCAGGGCAACGCTTTTGGCCACATCTCGGCTCCGGAGCGTCCGTTTC	606
QY	709	CTACAGATCTCCGCAATGTCGCGATGAGACCGAAGGGGGAAGGCACTTGGAAATTCAGGGT	768
Db	607	CTCGAGATTCCTGGGATGATCCGATGTGACCGCGGGGGAAGGCACTGGAACTCTGGGC	666
QY	769	TCAGTGGTTTATGCTCACAGCAGAAAGAAATTAATCAGCTTGGTACATAGATTTTGGTT	828
Db	667	TCTGTGGTCTATGCGCCACAGAAAGAGCTGGTCACTGGCTGGTACATCGCTCTCTTGT	726
QY	829	CTTATTTTTCGTCCTTTCTGTCTATCTGCTGGAAAAAGATGGCAATTAAGAATTTTCT	888
Db	727	CTCATCTCGGCTCTGTTCTGCTGTTACTTGGCAAGAAGGGGGAAGAGCACTCTTGAC	786
QY	889	ACATATCAGATGCTCTCTGCTGGGGGCAATATACATATGACACATATGGCTATGAGAC	948
Db	787	ACCTACCGGAGATGCACATCTGCTGGGGCCGTATACACGTGACACACATTTGGCTACGGGAC	846
QY	949	AAAACTCCCTTAACCTTGGCTGGGAAGATGTCTTCTGCAAGCTTTGCACTCCTTGCAAT	1008
Db	847	AAATACCCCGACAGCTTGGAAGGGAGGCAAGCTCTTGGCGCAACCTTCACTCATCGGTGC	906
QY	1009	TCTTTCTTTGACATCTCTCGCGGCAATTTGGCTCAGGTTTGCATTTAAAGTACAAAGA	1068
Db	907	TCTCTCTTCTGCGCTGCTGCAAGGCAATCTTGGGATCTGGGTTTGCCCTGAAGSTTCAAGAG	966
QY	1069	CAACAACGCGCAGAAAACACTTTGAGAAAAGAAGAACCCAGCTGCCAACCTCATTCAGT	1128
Db	967	CAGCACAAGGCAAGAGCACTTTGAGAAGAAGGGGAACCCGGCAGCGCTGATCCAGTCG	1028
QY	1129	GTTTGGCTAGTACGACAGCTGAT-----	1185
Db	1027	GCTTGGAAATTTCTTGGCCACCACCTCTCGCGCACAGACTGACACTCCAGCTGGCAGTAC	1088
QY	1153	---GAGAATCTGTTTCCATTGCAACCTGGAAGGACCACTTGAAGGCTTGGACACCTGC	1208
Db	1087	TACGAGCGAAGGTCACCGTCCGCAATGACAGTTGGCAATCAAACTCAACCTAAGGGGGCTGC	1148
QY	1210	AGCC-----	1271
Db	1147	AGACTTATCCCCCGCTGTAACAGCTGGAGTGTGAGAGAACCTCAAGATTAATCTGGA	1208
QY	1214	-----CTAACATCAGAGCTAGTTTAAAG	1273
Db	1207	CTCGCTTTTCAGGAAGAGACCCCCCGCGGAGCCGTCTCCAGGCACAGAGTCAAGTTTGAA	1268
QY	1240	GAGCAGATGCGCATGGCTAGGCCCAAGGCGCCAGAGTATTTAAGAGCCGACACGCTCAGTA	1298
Db	1267	GATTCGTGT---CTTCTCCAGCGCCCGAGCGTGGCTGCCAAGGGAAGGGGTCCCGCGAG	1332
QY	1300	G-----GTGACAGAGAGTCCCCCAAGCACCGACATCACAGCCGAGGGGAGTCCCAACCAA	1358
Db	1324	GCCCAAGACTGTGAGCGGTGACACCCAGCGCGACAGAGCTTGAAGGACAGCCCTCACAG	1388
QY	1354	GTCGAGAAGAGCTGAGGTTCAAACGACGACACCCGCTTCCGGCCCTCGCTGCGCTCAAA	1418
Db	1384	GTGCCCCAAGAGCTGTGAGCTTCCGGGAGACCCAGCCGGGACGCCAGGCTTTTCGCAATCAG	1448
QY	1414	AGTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATTAAT	1478
Db	1444	GGTGGCGCGTCT---ACGGCAGAACTCAGAAAGCAAGCGTCCCGAGAGGCACTTGTG	1508
QY	1474	GATGAAAAAAGATGCGCAGTGTGATGATATCAGTGAAGAGACCTCCACACACTTAATAAGT	1538
Db	1501	GATGACAAAGACTGCCCTTCGAGTTTGTGACCGAGAGACTGACCCCGGGCTCCAAGTC	1568
QY	1534	GTCAATCGAGCTATCAGAAATTATGAAAATTTCAATGTTGCAAAACGAAATTAAAGAAACA	1598

Db	1561	AGCATCAGAGCCGCTGTGTCTATCCTCGTTCGTCACGAAGCGGAAGTTCAAGAGAGC	1620
Qy	1594	TTAGCTCCATATGATGTAAAGATGTCATTGAACAATATTTGCTGTCATCTGCACATG	1653
Db	1621	CTGGGGCCCTCGACAGTGTAGAGTGCATTCGAGCAGTACTAGCGCGCCACTGGACATG	1680
Qy	1654	TTGTGTAAATTAAGAGCCCTCAAAACAGCTGTGTGATCAATTTCTTGAAAAGGCAATC	1713
Db	1661	CTGTCCCAATTAAGAGCTTCGACGTCCAGATGGACAGATTCGTGGGGCGGGGCCAACG	1744
Qy	1714	ACATCAGATTAAGAGAGCCGAGAGAAAAATTAACAGCAGAACATGAGACCAAGATGTC	1773
Db	1741	ATCAGCAGCAAGGA---CCGCACCAAGAGGCCCGCGCGAGGAGCTGCCGAGGACCC	1797
Qy	1774	AGTATGCTCGTCCGGGTGTCAGTTGTAATAAAGAGATACAGTCCATGAAATCCAAAGTC	1833
Db	1798	AGCATGATGGGAGCGGCTCGGAGAGGTGGAGAGCAGGCTTGTCCATGAGAGAAAGACTG	1855
Qy	1834	GACTGCTACTATGACATCTATCAACAG	1860
Db	1858	GACTTCTGTGTGATATATCTACATGCGAG	1884
RESULT 18			
AA57059			
ID	AA57059	standard; DNA; 2914 BP.	
XX	AA57059;		
AC			
XX	22-JUL-1999	(first entry)	
DE			
XX	Human KCNQ3 cDNA.		
KW	KCNQ3: KCNQ3: human; murine; potassium channel; diagnosis; prognosis;		
KW	benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;		
KW	JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;		
KW	detection; gene therapy; drug screening; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	19..2637	
FT		/tag= a	
FT		/product= "KCNQ3"	
XX			
PN	WO921875-A1.		
XX			
PD	06-MAY-1999.		
XX			
PF	23-OCT-1998;	98WO-US22375.	
XX			
PR	24-OCT-1997;	97US-0063147.	
XX			
PA	(UTAH) UNIV UTAH RES. FOUNDD.		
PI	Charlier C, Leppert ME, Singh NA;		
XX			
DR	WPI; 1999-312938/26.		
XX	P-PSDB; AAY08344.		
XX			
PT	Nucleic acid encoding potassium channels KCNQ2 and 3		
XX			
PS	Claim 1; Page 131-136; 195pp; English.		
XX			
CC	This invention describes novel human and mouse potassium channel proteins		
CC	KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or		
CC	KCNQ3, or the loss of one copy of these genes, is used for diagnosis and		
CC	prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic		
CC	epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)		
CC	that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves		
CC	in cell-free form) are used to screen for agents that can be used to		
CC	treat or prevent these forms of epilepsy. Fragments of the encoding		
CC	nucleic acids are used as probes or primers, either for detecting		

QY	1354	GTGCACAAAGCGCTGGAGCTTTCACAGCCGAACCCGCTTCCGGGCCCTTCGCTGGCGCTTAA	1413
Db	1393	GTGCCCAAGAGCTGGAGCTTTCGGGGACCCGACGCCGACAGGCTTTCGCATCAAG	1452
QY	1414	AGTTCTCAGCCCAAAACCAGTGAATGATGCTGACACAGCCCTTGGCACTGATGATGTAT	1473
Db	1453	GGTGGCGGCTTCACGGCGGAATCTCGAAG---AAGCAAGCTCCCGGAGGAGCATTTGTG	1509
QY	1474	GATGAAAAAGATGGCCAGTGTGATGTATCAGTGTGAGAAAGCTTACCCACCATTTAAACT	1533
Db	1510	GATGACAAAGCTGCGCCCTCGAGCTTGTGACCGAGAGCTTACCCCGGGGCTTCAAGTC	1559
QY	1534	GTCAATTCGAGCTATCAGAAATTATGAAAATTTTCATGTTGCAAAAACGGAAGTTTAAAGAA	1593
Db	1570	AGCATCAGAGCCCTGTGTCTATCCGGTCTCGTGTCCAAACGGGAAGTTCAAGGAGAGC	1629
QY	1594	TTACGTCATATGATGTAAAAAGATGCTATTTAAACAATTTCTGTGTGATCTGGACATG	1653
Db	1630	CTGGGGCCCTACGACGTGATGACGCTATCAGCACTACTACGCCGCGCACCTGGACATG	1689
QY	1654	TTGTGTAGAATTAAAAACCTTCAACAACGCTGTTGATCAAAATCTTGGAAAGAGGGCAATC	1713
Db	1690	CTGTCCCGAATTAAAGAGCTCGTAGCTCCAGAGTGGACCAAGATGCTGGGGGGGCCCAAGC	1749
QY	1714	ACATCAGATAAAGAAAGCCGACAGAAATAACACAGAAATGAGAACCCACAGACGATCTC	1773
Db	1750	ATCACGGACAAAGA---CCGACCCAAAGGCCCGCGGCGGAGACTGCCCCGAGGACCC	1806
QY	1774	AGTATGCTCGTCTGGGCTGTGTCACAGGTTTGAAAAACAGTATACATATAGATCAACGTC	1833
Db	1807	AGCATGATGGAGCGGCTCGGGAAGGTGAGAAAGCAGGCTTGTCCATGGAAGAAAGCTG	1866
QY	1834	GACTGCGCTACTAGACATCTATCAACAG	1860
Db	1867	GACTTCCTGGTAATATCTTACATGAC	1893

RESULT 20
AAX57141
ID AAX57141 standard; DNA; 2814 BP.
XX AC AAX57141;
XX XX
DT 22-JUL-1999 (first entry)
XX XX
DE Mouse KCNQ3 cDNA.
XX XX
KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KM JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
XX detection; gene therapy; drug screening; ss.
OS Mus musculus.
XX XX
Key Location/Qualifiers
FH CDS 202..2814
FT /tag= a
FT /product= "KCNQ3"
XX XX
MO921875-A1.
PX PN
PD 06-MAY-1999.
XX XX
PF 23-OCT-1998; 98MO-US22375.
XX XX
PR 24-OCT-1997; 97US-0063147.
XX XX
PA (UTAH) UNIV UTAH RES FOUND.
XX XX
PI Charlier C, Leppert MF, Singh NA;
XX XX
WP1; 1999-312938/26.
DR P-PSDB; AAY08346.

Nucleic acid encoding potassium channels KCNQ2 and 3
Claim 1, Page 159-163; 195pp; English.

This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. Antibodies specific for mutant or wild-type proteins are used as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are useful in rational design of drugs and therapeutically (in replacement therapies). The forms of epilepsy associated with mutations in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available.

50 Sequence 2814 BP; 667 A; 753 C; 796 G; 590 T; 8 other;

Query Match	Score	DB	Length
Best Local Similarity	15.68	432	2814
Best Local Exact	56.79	2	6103

Matches 962; Conservative 3; Mismatches 673; Indels 58; Gaps 7,

[illegible]


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QY 123 GGGCGGGGGGAGGGGTCGTGAACCTGGCAGCCGCCA-----GGGGCGAGGGCTGCT 176
DB 142 GCGAAGCGGGGGCTATATACCCCGCCCGAGCGGGAGAGAAAGCTGAAGTGGGCTTCCT 201
QY 177 ACTGCTGGGACACCCGCGGCGCACGCTGCGTGCGGGCGGCTGGCTGAGGAGAGCCG 236
DB 202 GGGGCTGGACCCCGCGGCGCCGAGCTCCACCCGGGAGGGGGCGGCTGCTATGCGCGGCTC 261
QY 237 CCGGGGCAAGAGGGGGGCGCGAGTGAAGCTGCTGGGGAAGCCGCTCTTACACAGTACG 296
DB 262 CGAGAGCCCGCAAGGCGCGCGACATCTCCAGAAACCTCGCGGGGCGCGCGCGCGCG 321
QY 297 CCAGAGCGCGGGGCGGCGACGTCAGTACCGGGGGGCGGAGCACTACGTCAGACGTCG 356
DB 322 GAAGCCCCCAAGGCGGCAAGCCCTTACCGCAAGCTGCGAATTTCTCTACACAGCTGCT 381
QY 357 GGAGAGACCCCGCGGCTGGGGTTCATCTACACAGCTTTCGTTTCTCTGCTTTGG 416
DB 382 GGAGGGGCGCGGCGGCTGGGGTTCATCTACACAGCTTCAGTCTCTGCTGCTTCTC 441
QY 417 TTGCTGATTTTGTACAGTGTTCCTACCATCTCCCTGAGCAGACAAATTTGGCCCTAGTTG 476
DB 442 CTGCTCTGCTGCTGCTGCTTTCACCAATCAAGAGATGAGAAAGCTCGGAGGGGCG 501
QY 477 CCTCTGATCTCGAGTTCGATGATGCTGCTTTCGTTTGGAGTTCATCATTCGAAT 536
DB 502 CCTCTACATCTCGAATCTGATGATGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTG 561
QY 537 CTGCTGCTGCGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596
DB 562 CTGCGGCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
QY 597 AAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 656
DB 622 GAAACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
QY 657 AAAACCTGAGGTAATTTTTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 682 CGGCTCCGAGGCAAGCTTTCGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY 717 CCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 742 TCTGCGGATGATCCCATGACCGCGGGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 801
QY 777 TTATCTACACAGCAAGTAATTAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 836
DB 802 CTATGCCACAGCAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861
QY 837 TTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 896
DB 862 GGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
QY 897 AGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
DB 922 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
QY 957 CCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1016
DB 982 CGAGACCTGGAAGGAGGCTCTTCTGCGGAACTTCACCTCATGCTGCTGCTGCTGCTGCTT 1041
QY 1017 TGCATCTCTGCGGCAATCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076
DB 1042 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1101
QY 1077 CCAGAAACCTTGGAGAAAAGAAAGAACCCAGCTGCCAACCTCATCTGCTGCTGCTGCTGCTG 1136
DB 1102 GGAGAAAGCACTTTGAGAAAGAGCGGAAACCGCGCAGAGGCTGATCCAGTCCGCTGCTGCTG 1161
QY 1137 TAGTTACGC 1145
DB 1162 ATTCTACGC 1170

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RESULT 23
AAK57145
ID AAK57145 standard; DNA; 3237 BP.
XX
AC AAK57145;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human mutant KCNQ2 cDNA.
XX
KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KM benign familial neonatal epilepsy; BPNE; juvenile myoclonic epilepsy;
KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KM detection; gene therapy; drug screening; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 128..2920
FT /tag="a
FT /product="KCNQ2"
XX
PN W09921875-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US22375.
XX
PR 24-OCT-1997; 97US-0063147.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Charlier C, Leppert MF, Singh NA;
XX
DR WP1: 1999-312938/26.
DR P-PSDB; AAY08347.
XX
PT Nucleic acid encoding potassium channels KCNQ2 and 3
XX
PS Claim 1: Page 168-172; 195pp; English.
XX
CC This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available.
XX
SQ Sequence 3237 BP; 577 A; 1056 C; 1064 G; 533 T; 7 other;
XX
Query Match 15.5%; Score 429.4; DB 20; Length 3237;
Best Local Similarity 61.5%; Pred. No. 1.3e-102;
Matches 707; Conservative 0; Mismatches 436; Indels 6; Gaps 1;
QY 3 GCGCCGCGCACACAGCGGGAGAGAGAGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 62
DB 22 GCCATGCGGCTCCGCGCGGGGCGCTGCGGCTGCGGCGCGCGCGCGCGCGCGCTGCTGCTG 81
QY 63 GCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 122

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Db      1162 ATTCTMCGC 1170
      82 CCCCCTGAGCCTGAGCCCGACCCGCGGCGCTCCCGCCAGGACACATGCTGACAGAAATG 141
      123 GGGCCGGGGGAGGGTGGCTGCTGAACTGGAGCCGCCA-----GGGGGAGAGGCGCTGCT 176
      142 GCGCAAGGGGGGGGTATACCCCGCGGCGGAGAGAAAGCTGAAGGTGGCTGCTGCT 201
      177 ACTGCTGGGACCGCGCGGCGGACGCTGCTGGGCGGCGGCGGCTGGAGGAGAGCCG 236
      202 GGGGCTGGACCCCGCGCGCGGCGGACCTCCACCCGGGAGGCGGCGGCTGATGCGCGGCTC 261
      237 CCGGGGCAAGAGGGGGCGCGGATGAGCCTCTGGGGAAGCGCGCTCTTACAGAGTGA 296
      262 CGAGGCCCCCAAGGCGCGGACGATCTCAGCAAACTGGCGGCGGCGGCGGCGGCGG 321
      297 CGAAGCTGGCGGCGGCAAGCTCAAGTACGCGGCGGCGGAGAACTACTGTACAGCTGCT 356
      322 GAAGCCCCCAAGGCGGCAAGGCTCTACCGGAGCTGAGAAATTTCTTACAGAGTGTCT 381
      357 GGAGAGACCCCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
      382 GGAGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
      417 TTGCTTATTTTTCAGTGTGTTTCTACACCTCTGAGCACAACAAATGGCCCTCAAGTTC 476
      442 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
      477 CCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
      502 CCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
      537 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
      562 CTGGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
      597 AAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
      622 GAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
      657 AAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
      682 CGGCTCCCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
      717 CCTCGGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 776
      742 TCTGGGATGGATCCGATGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 801
      777 TTATGCTCAGACAGCAAGAAATTAATCAGACCTTGTGATAGATTTTGGTCTTATTTT 836
      802 CTATGCGCCACAGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
      837 TTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
      862 GGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
      897 AGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
      922 GATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
      957 CCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1016
      982 CGAGACCTGAGACGCGAGGCTCTTTCGCGCAACTTCACCTCATGCTGCTGCTGCTGCT 1041
      1017 TGCATTTCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
      1042 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
      1077 CCAGAAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCTTCACTGCTGCTGCTGCT 1136
      1102 GGAGAAAGCCTTTGAGAAAGAGGGAAGCCGCGAGAGAGGCTGATCCAGTCCGCGCTGGAG 1161
      1137 TAGTTAGCG 1145
      1111

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Db      1162 ATTCTMCGC 1170
      RESULT 25
      AAX26596
      ID AAX26596 standard; DNA; 2565 BP.
      XX
      AAX26596:
      XX
      DT 16-JUN-1999 (first entry)
      XX
      DE Nucleotide sequence of human KCNQ3 (formerly known as KvLR2).
      XX
      KW KCNQ protein: nervous system-specific potassium channel;
      KW neuronal excitability; neurotransmitter release; KCNQ modulator;
      KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
      KW age-associated memory loss; learning deficiency; motor neuron disease;
      KW epilepsy; stroke; ss.
      XX
      OS Homo sapiens.
      XX
      FH Key Location/Qualifiers
      FT CDS 1..2565
      FT /*tag- a
      XX
      PN WC907832-A1.
      XX
      PD 18-FEB-1999.
      XX
      PF 26-JUN-1998; 98WO-US13276.
      XX
      PR 12-AUG-1997; 97US-0055599.
      XX
      PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
      XX
      PI Bjanar MA, Dworetzky S, Gridkoff VR, Levesque PC;
      PI Little WA, Neubauer MG, Yang W;
      XX
      DR WPI: 1999-190047/16.
      XX
      DR P-PSDB: MAY01534.
      XX
      PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in
      PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
      XX
      PS Claim 6; Fig 23A-E; 64pp; English.
      XX
      CC The present sequence encodes human KCNQ3 (formerly known as KvLR2).
      CC KCNQ proteins are nervous system-specific potassium channels. In
      CC neurons, potassium channels regulate neuronal excitability, action
      CC potential shape and firing pattern, and neurotransmitter release.
      CC KCNQ modulators may be used to treat disorders such as ataxia,
      CC myokymia, seizures, Alzheimer's disease, Parkinson's disease,
      CC age-associated memory loss, learning deficiencies, motor neuron
      CC diseases, epilepsy, and stroke.
      XX
      SQ Sequence 2565 BP; 605 A; 704 C; 717 G; 539 T; 0 other:
      XX
      Query Match 15.5%; Score 428.8; DB 20; Length 2565;
      Best Local Similarity 56.8%; Pred. No. 1.7e-102;
      Matches 924; Conservative 0; Mismatches 647; Indels 57; Gaps 5;
      XX
      QY 118 GAGTCGGGCGGCGGCGGAGGCTGCTGTAACCTGCGACCGCCAGAGGCGGCGGCGGCTA 177
      DB 43 GCGGCGGCGGCGGCGGAGGAGCGGAAATGCGGCTGCGCGCCGCGGCGGAGGAGCA 102
      QY 178 CTGCTGGGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 237
      DB 103 GTCACCTTGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 162
      QY 238 GGGGCGAGCGAGGCGGCGGCGGAGTGAAGCTGCTGGGAGAACCCGCTCTTACACAGTAC 297
      DB 163 GCGCGCGAGCGAGGCGGAGGAGACCCCGAGGCGCATCGGCTCTGCGCAAGACCCCG 222

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OY	298	CAGACGTGCG-----GGCGCAAGCTAAGTACCGCGGGGTGCAGAACTACCTGTAC	348
Db	223	CTGAGCCGCCCACTCAAGAAACAAACGCCAAGTACGGCGCATCCAAACTTGGATCTAC	282
OY	349	AACGTCTGGAGAGACCCCGCGCTGGCGCTTCACTCTACCAAGCTTTCGTTTTCTCCCT	408
Db	283	GAGCGCCCTGGAGAGACCGCGGGCTGGCGCGCTTTTACCAAGCGCTTGTTCCTGATT	342
OY	409	GTCCTTGGTGGTGAATTTTGTCAGTCTTTTCTACATCCCTGAGACACAAATTTGACC	468
Db	343	GTCCTGGGTGGTGAATTTCTGGCTGTCCCTGACATTCAGAGATAGAGACTGTCTCG	402
OY	469	TCAAGTTGACCTTGATTCCTGAGTTCGTATGATGTATGTCGTTTTGGTTTTGAGTTGATC	528
Db	403	GGAGACTGGCTCTGTGTACTGGAGACATTTGTAATTTTCACTTTTGGAGCCGATTTGCT	462
OY	529	ATTGCAATCTGCTGTGCGGGTTCCTGTTGTCATATATGAGATGGCAAGAACTGAG	588
Db	463	TTGAGGATCTGGGCTGGATGTCTGCGGATACAAAGCTGGCGGGCGCATGAAG	522
OY	589	TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTTATTCGTTCAATACAGTT	648
Db	523	TTTGCGAGAAAGCCCTGTGCATGTTGGACATCTTTTGTGCTGATTTGCTTGTGCCAGTG	582
OY	649	GTTTCTGAAAAACTCAGGGTAATATTTTGGCAGCTGTGCAGTACGAAGTCTCCGTTTC	708
Db	583	GTTTCTGGAAGAACCAAGGCAATGTTCTGGCCACCT---CCCTGCGAAGCCTGGCGCTTC	639
OY	709	CTACAGATCTCTCCGATGGTGGCATAGGACCGAAGGGGAGGACCTTGAATTTACTGGT	768
Db	640	CTGAGATCCGTGGCGATGCTGCGGATGAGACCGAGAGGTGGCACTTGGAACCTTCTGGCG	699
OY	769	TCACTGGTTATGCTCACAGCAAGGAATTAATCAGACCTTGGTACATAGATTTTGTGTT	828
Db	700	TCACCACTCTGTGCCACAGCAAGCAACTCATCAGCGCTGTGTACATCGTTTTCTGACA	759
OY	829	CTTATTTTGTGTCCTTCT	873
Db	760	CTCATCTTTCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	819
OY	874	-----AATTAAGATTCTTCACTATGACAGATGCTCTCTGTGGGACACA	918
Db	820	CAAGAGAGAGATGAAGAGAGAGATTGAGACTATGACATGGCCGTGTGGGCGCTG	879
OY	919	ATTACATTTGAACATTTGGGCTATGAGACCAAACTCCCTACTTGGCTGGGAAGTGTG	978
Db	880	ATCACACTGGCCACCATTTGGCTATGAGACCAAACTCCCAAAAGTGGGAAGGCGCTGTG	939
OY	979	CTTTCTGCAAGGCTTTGCACTCCTTGGCATTTCTTTTCCACTTCTGTCCGCGCAATCTT	1033
Db	940	ATTGCGCCACCTTTCTTCTTAATTTGGCGTCTCCTTTTGGCCCTTCCAGCGGGCATCTG	999
OY	1039	GGCTCAGGTTTTGCATTTAAAGTATCAAGAACACACCGCCAGAAACCTTTGAGAAAAGA	1099
Db	1000	GGGTCCGGGGCTGGGCTTCAAGGTGAGAGAACACCGTCAAGAACCTTTGAGAAAAAG	1055
OY	1099	AGGAACCCCACTGCGCAACCTCATTCAGTGTGTTTTGGCGTAGTATACGAGCGTATGAGAAA	1155
Db	1060	AGGAAGCACTGCTGAGCTCATTTCAAGCTGCGCTGAGAGGTATTTATGCTTACCAACCCCAAC	1115
OY	1159	TCTGTTTCCATTG-----CAACTGGAAAGCACACTTGAAGGCTTGCACACCTGTC	1209
Db	1120	AGGATTTGACCTGTGGGAGACATGGAGATTTTATGAAATCAGTGTCTCTTTCTTCTTC	1179
OY	1210	AGGCTTACCAATCAGAGAGCTAATGTTTTTAAGAGCGAGTCCGATGGCTACGCCAGGGGC	1269
Db	1180	AGGAAGAACACGCTGGAGGCGCATCCAGCCAAAAGCTGGGTCCTTGGATCGGGTTTCGC	1239
OY	1270	CAGAGATATTAGAAGCCGACAAAGCTCATGATGTGACAGAGAGGTCGCCAAGCACCGCATCTC	1329
Db	1240	CTTTCTTAATCTCTGTGTAGAAATACTTAAGGAAGCTATTATACCTCTCTGAATGTATGAT	1299
OY	1330	ACAGCGGAGGCACTCCACCAAAAGTGCAGAAAGACTGGAGCTTCAAGACCGAACCCGC	1389

Db	1300	GCATATAGAAAGAAAGTCCTTTCTTAAAGAACCAAGCCCTGTGGCTTTAAACAATTAAGAGGT	1355
QY	1390	TTCCGCGCCCTGCGTCGCGCTCAAGAGTCTCAGCCAAACAGATGTAGATGCTGACACA	1445
Db	1360	TTCCGCGAGGCGCTTCCGATGAAAGCCTAAGCTTTCTGGCAGAGTTCGAAAGATGCCGGG	1415
QY	1450	GCCCTTGGCAGTATGATGTATATGATGAAAAAGAGATGCCAGTGTGATGTATCAGTGGAA	1505
Db	1420	ACAGGTGACCCCATGGC-----GGAAGACAGGGGCTATGGGAATAGACTTCCCATCGAA	1473
QY	1510	GACCTACACCCACCACTTAAAACTGTCTATTGGAGCTATCAGATTTATGAATTTTCATGTT	1565
Db	1474	GACATGATGCCACCCCTGGAAGGCGCCATCCGAGCGCGTCAAGATTTCTCAATTTCCGTCTC	1533
QY	1570	GCAAAACGGAAGTTAAGAAACATATTAGTCATATGATGTAAAAAGATGATAGAACAA	1629
Db	1534	TATTAATAAAAAATTCACAGAGACCTTTTGAGCCTTACGATGTGAAGGATGATATTGAGCAG	1593
QY	1630	TATTTCTGCTGTCATCTGAGACATGTGTGTGAATTTAAACCTTCACAAACAGTGTGAT	1689
Db	1594	TATTTCTGCGCGGACATCTGCACATGGTTTCCAGGATTAAGTACCTTCAGACAGAAATAGAT	1653
QY	1690	CAAAATCTC 1697	
Db	1654	ATGATTTT 1661	

RESULT 26
AAX26587
ID AAX26587 standard; DNA; 3287 BP

Nucleotide sequence of human KCNQ2 (formerly known as KvLR1).

KM Human; KCNQ protein; nervous system-specific potassium channel;
KM neuronal excitability; neurotransmitter release; KCNQ modulator;
KM ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KM age-associated memory loss; learning deficiency; motor neuron disease;
KM epilepsy; stroke; ss.

05 Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	61 3576

PN W09907832-A1.

PD 18-FEB-1999

PF 26-JUN-1998; 98WO-US13276

PR 12-AUG-1997; 97US-0055599

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI	Blannar MA,	Dworetzky S,	Gribkoff VK,	Levesque PC;
PI	Rittig WA	Mohrman VC	Ward J	

XX
XX
WDT, 1000-100047 /15

DK P-PSDB; AAY01529.
YY

PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in neurotransmission and neuroprotection, used to treat, e.g. ataxia

PS Claim 5; Fig 2; 64pp; English.

CC The present sequence encodes human KCNQ2/KVLRL. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium

CC channels regulate neuronal excitability, action potential shape
CC and firing pattern, and neurotransmitter release. KCNQ modulators
CC may be used to treat disorders such as ataxia, myokyma, seizures
CC Alzheimer's disease, Parkinson's disease, age-associated memory
CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
CC stroke.

SQ Sequence 3287 BP; 587 A; 1062 C; 1083 G; 555 T; 0 other;

Query Match	15.5%	Score 428.4	DB 20	Length 3287
Best Local Similarity	64.8%	Pred. No. 2.5e+102		
Matches 633	Conservative	0	Mismatches 344	Indels 0
			Gaps	0

OY	169	GGCCTGCTACTGCTGGGGACCCCGCGGACACGCTGSGTGGCGCGCGCTGTGCCTGAG	228
Db	127	GGCTTCGTGGGGGCTGGAGCCCGGGCGGCCCGGACTCCACCCGGGAGCGGCGCTGTGATC	186
OY	229	GAGAGCCCGCGGCGCAAGCAGGGGGGCCCGCATGAGCTGCTGGGGAGCCGCTCTTAC	288
Db	187	GCGGGCTCCGAGGGCCCCCAAGCGCGGCGCATCTCCAGCAAACTCGCGGGCGGCGCG	246
OY	289	ACGAGTGGCCAGACTCCCGGGCGCAAGTCACAGTACCGGGGGGGCGCAACTCTGTAC	348
Db	247	GGCGCCGGGAAGCCCCCAAGCCGAAGCCTTCTACCGCAAGCTGCGAAATTTCCTTAC	306
OY	349	AACGTGCTGAGAGACCCCGCGGCTGGGCGTCAATCACAGCGTTCGTGTTTTCTCTT	408
Db	307	AAGGTGGTGGAGCGCGCGCGCGGCGCTGGGCGGTTCATACACGCGCTACGTTTCCTCTG	366
OY	409	GCTCTTGGTGTCTGATTTTGTACAGTGTTTTCTACCATCCCTGAGCACACAAAATTGGCC	468
Db	367	GTTTTCTCTCCGCTCGCTGTCTGTGTCTTTTCCACCAAGAGTATGAGAAAGCTCG	426
OY	469	TCAAGTGCCTCTTGATCTGAGTGGAGTGGTGAATGATATCTGCTTTGGTTTGGAGTTATC	528
Db	427	GAGGGGCGCCCTCTATACCTCTGGAATAGTACATCGGGGTGTTGGCGTGGAGTACTTC	486
OY	529	ATTGCAATCTGGTCTCGCGGTTGCTGTTCGATATAGAGATGGCAAGAAAGCTAGG	588
Db	487	GTCGGGATCTGGGGCGGCAAGGCTGTGTCGCGCGGAGACGTTGGTGGAGGGGGGCTCAAG	546
OY	589	TTTGGTCAAAAGCCCTCTGTGTAATGATACAAATTGTTCTATGCGTTCAAATAGCAATT	648
Db	547	TTTGCCCGGAAACCCTTCTGTGTATTTGACATCATGATGCTCATCGCTCATTTGCGGTG	606
OY	649	GTTTCTGCAAAAACACTCAGGTAATATTTTGGCCAGCTGTCGACTGAGAGTCCCGTTTC	708
Db	607	CTGGCGCGGCGCTCCACGGGCAAGCTTTTCCACATCTCGCTCGGAGCGCTCCGCTTC	666
OY	709	CTACGATCTCCGATGATGGGATGAGACGGAAGGGGAGGCACTGGAAATTAATCTGGT	768
Db	667	CTGCGAGATTCTGGGATATATCCGCAATGGACCGCGGGGAGGACCTGGAACTCTGGGC	726
OY	769	TCAGTGGTTTATGCTACACAGCAAGGAATTAATCAAGCTTGATACATAGATTTTGGTT	828
Db	727	TCTGTGGTCAATGCCACACAGCAAGAGGCTGGTCACTGCTGTACATGCGCTCTTGT	786
OY	829	CTTATTTTTCGTCTTTCCTTCTGTCTATCTGTGGAAAAAGATGCCAATAAAGATTTC	888
Db	787	CTCATCTCGGCGCTCTGCTCTGTGTATCTTGGCAGAGAAGGGGGAAAGACCACTTTGAC	846
OY	889	ACATATGAGAGTGCCTCGTGGGGGGCAATTAATCATGACAACTAATTTGGCTATGAGAC	948
Db	847	ACCTACGGGAGTACACTGTGTGGGGCCGTGATCAAGCTTGACCAACCATTTGGCTACGGGAC	906
OY	949	AAACCTCCCTAACTTGGCTGGGAAGATGCTTTCTGCAAGGCTTTGCACCTCTTGGCAT	1008
Db	907	AAGTACCCCCAAAGCTGGAAAGCGGACGCTCTTGGCGCAACCTTACCCCTCATGCTGTC	966
OY	1009	TCTTCTTTTGACCTTCGCGGGCAATCTTGGCTCGAGTTTGGATTTAAAGTACAAAGA	1068
Db	967	TCTTCTTTGCGCTGCTGACAGCACTTGGGGTCTGGGTTTGCCCTTAAGGTTTACGAG	1026

OY 1069 CAATACGCCGCAAGAACCTTTGAGAAAAAGAAAGAACCCAGCTGCCAACCTATTCACGT 1128
 Db 1027 CAGCAGCAGCGCAGGAAGCACTTTGAGAAAGAGCGGAACCCGCGACAGCGCCTATCCACATCG 1086
 OY 1129 GTTTGGCGCTAGTACGC 1145
 Db 1087 GCCTGGAGATTTTACGC 1103

RESULT 27
AAAT85964
ID AAAT85964 standard; cDNA; 1182 BP.

DT	09-JAN-1998 (first entry)
XX	
DE	Human K+ channel gene coding sequence.
XX	
KW	Human; neuroblastoma; K+ channel; probe; diagnosis; detection;
KW	tumour; ds.
XX	

OS	Homo sapiens.	
XX		
XX		
PN	JP09191882-A.	
XX		
PD	29-JUL-1997.	
XX		
PF	16-JAN-1996;	96JP-0004726
XX		
PR	16-JAN-1996;	96JP-0004726
PA		
(NIBS)	JAPAN TOBACCO INC.	

This is a nucleotide sequence encoding a novel human K+ channel protein which is expressed on human glioma cells. The gene was isolated from a 3' directed cDNA library prepared from human neuroblastoma cell line CHP134. The screen isolated a clone designated GS008740 whose insert contained the coding sequence (presented here) and the 5' and 3' sequences of the gene (AAT8565-6 respectively). Expression of the gene was detected in neuroblastoma cell lines. Oligonucleotides derived from the sequence of the K+ channel gene can be used as probes for diagnosing human gliomas, and in the detection of new tumours.

SQ Sequence 1182 BP; 201 A; 372 C; 364 G; 245 T; 0 other;

Query Match	15.3%	Score 425;	DB 18;	Length 1182;
Similarity	64.7%	Pred No. 1.1e-101;		
Best Local				
Matches 632;	Conservative	0;	Mismatches 345;	Indels 0;
				Gaps 0;

QY	169	GGCTCTCTACTGCTGGGGCACCCGGCGGCGACGCTGGGTGGCGCGCGGTGGCTCGAAG	228
Db	67	GGCTTGTGGGGGTGTGACCCCGCGCGCCGACTCCACCGGGAGGGCGCGCTGTGTGAATC	126
QY	229	GAGAGCGCGCGGGGGCAAGCAGGGAGCGCGGATGAGCTGTGGGGAAGCGCGCTCTTTTAC	288
Db	127	GCGGCGTCCGAGGCGCCCGCAAGCGCGGACACATCTCAGCAAACTTGGCGGGCGCGGG	186
QY	289	ACGAGTAGCCAGAGCTGCGGGCGCAACGTCMAGTACCGGGGGGTGCAAGACTTACCTGTAC	348
Db	187	GCGGCGGGGAAGCCCCCAAGCGCAACGCTTCTACCGCAAGTCGAGAATTTCCCTAC	246
QY	349	AAGTGTCTGGAGAGACCCCGCGGCTGGGGGTATCTACACGCTTGTTCCTTCCTT	408
Db	247	AACGTCTGGAGGGCGCGCGGCTGGGGCTTATCTACACGCTTACGTTCTCTCTG	306

QY	409	GCCTTTGGTGGCTGATATTTTGTCAAGTGTTTCTACCATCCCTGAGCACACAAAATTGGCC	468
Db	307	GTTCCTCTCTGCTGCTGTGCTGTCTGTGTTTTCCACCATTAAAGATATAGAAAGACCTCG	366
QY	469	TCAAATTCCTCTTATGATCTGAGTTCGATGATATGTCGTCTTGTGGTGTGAGTGCAC	528
Db	367	GAGGGGGGCGCTTACATCTCGTGAATTCGACATATCTGTGTGTGGCTGTGGAGTATCTTC	426
QY	529	ATTGCAATCTGCTGTGCGGGTTGCTGTGTGCGATATAGAGATGGCAMAAGACAGAG	588
Db	427	GTCGGGATCTGGGCGGCGCAGGCTGTGCTGCGGTACCGTGGCTGGAGGGGGGGCTCAAG	486
QY	589	TTTGGCTGAAGGCCCTTCTGTGTATTAAGTACCATTTGTTCTTATGCTTCATATGACATT	648
Db	487	TTTGGCGCGGAAACCGTTCTGTGTGATTTGACAATCAATGATGCTCATGCGCTCCATTTGGGCTG	546
QY	649	GTTCCTGCAAAAACACAGAGTAAATTTTGGCACGCTGCGACCTGASAAAGTATCCGTTTC	708
Db	547	CTGGCGCGCGGCTCCAGGGCAGCTCTTTGCCATATCTGCCTCCGGAGCCTTGCGCTTC	606
QY	709	CTACAGATCTCCCGCATGTCGCGCATGGACCGAAGGGAGAGCACTTGGAAATTAATGAGGT	768
Db	607	CTGAGATTTCTGGGGATGATCCGCATGAGACCGGGGGGAGGCACTGGAACTGCTGGGC	666
QY	769	TTCAGTGGTTTATGCTGCACAGCAAGGAATTAATCAGACCTGTGTACATAGATTTTGGTT	828
Db	667	TCTGTGGCTTATGGCCACAGCAAGGAGGTGGTCACTGCTGTGTACATGCGCTTCTTGT	726
QY	829	CTTATTTTTCCTGTCCTTCCTGTCTATCTGGTGGGAAAGGATGCCAATTAAGATTTTCT	888
Db	727	CTCATCTGCGCTGTCTGTGTGTGTACTTGTGCAGAGAAAGGGGAGAAAGCACCTTTGAC	786
QY	889	ACATATGSCAGATGCTCTGTGTGGGGGCAATTAATCATTTAGACATATTTGGCTATGAGAC	948
Db	787	ACCTAGCGGAGTGCATCTGTGTGGGGCTGATACACGCTGACACCATTTGGCTACGGGAC	846
QY	949	AAAACCTCCCTTAACATTGGCTGGGAAAGATTGCTTTCTGTGAGCGCTTTGACCTCCTTGGCAT	1008
Db	847	AAATGACCCCAAGACTGGAGGCGGACGAGCTCCTTGTGGGCAACCTTACCTCATCGGTGTC	906
QY	1009	TCTTTCTTTGCACTTCGCGCGGGAATTCCTGGCTCAGGTTTGTGATTAAAGTACAGAAA	1066
Db	907	TCTCTCTTCGCGCTGCTGCAAGGATCTTTGGGGTCTGGGTTTGGCTGAAAGTCTCAGAG	966
QY	1069	CAACACCGCAGAAACATTGTGAAAAAGAAAGAACCCAGCTGCACCTCATCACTGTT	1128
Db	967	CAGACAGCGAAGAAAGCACTTTGANAAGAGGGGGAACCCGGCAGCAGGCTCATCCAGTGG	1026
QY	1129	GTTTGGCGTATGACG	1145
Db	1027	GCGTGGAGATTCTACG	1043

RESULT 28
ABN24166
ID ABN24166 standard; cDNA; 414 BP.

DT 24-JUN-2002 (first entry)
YY

DE XY	Human ORFX polynucleotide sequence SEQ ID NO:16809
	<p> 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517</p>

KW Human; open reading frame; ORF; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.

OS Homo sapiens.
XX
XX
PN WO200192523-A2.
XX
XX
PD 06-DEC-2001.
XX
XX
PF 29-MAY-2001; 2001WO-US10836.
XX
XX 30-MAY-2000; 2000US-206132P.
PR 29-AUG-2000; 2000US-228716P.
XX
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Shinketsu RA, Leach MD;
XX
XX WPI: 2002-106308/14.
DR P-PSDB; ABP08414.
XX
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -
XX
XX
PS Disclosure: SEQ ID 16809; 1037PP; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABIN5762 to ABIN27352 encode the human ORFX proteins given in AB000010 to AB011500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 414 BP; 129 A; 101 C; 96 G; 88 T; 0 other;

Query Match	14.8%	Score 410.8;	DB 24;	Length 414;
Best Local Similarity	99.5%;	Pred. No. 3.7e-98;		
Matches 412; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY 1255 GCTAGCCCCAGGGCCAGAGTATTAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTC 1314

1315 CCAAGCACCGACATTCACAGCGCGAGGGCAGTCCCAACCAAGTGCAGAAGAGCTTGCAGCTTC 1374

Db 61 CCAAGCACCGACATCACAGCCGAGGGCAGTCCCAACCAAGTCAGAAGAGCTGGAGCTTC 120

1375 AACGACCGAACCCGCTTCCGGCCCTCGCTGGCGCTCAAAAGTTCCTCAGCCAAAACCAGTG 1434

Db 121 AAGGACGACCGCTTCCGGCCCTCGCTACGCCCTCAAAAGTCTCAGCCAAACAGTG 180

1435 ATAGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAATAAGGATGCCAGTGT 1494

Db 181 ATAGATGCTGACACAGCCCTTGGCACTGATGATGCATATGATGAAAAAGGATGCCAGTGT 240

1495 GATGTATCAGTGAAGACCTCACCCCAACCACTTAAACTGTGATTCGAGCTATCAGAATT 1554

DB 241 GATGATCATGTCGAGAACCTCCACCCACCACTTAAACCTCATTCGATGATAGATTT 300
 OY 1555 ATGAATATTCATGTTGCCAAACGGAAGTTTAAAGAAACATTTACGTCATATGATGATAAA 1614
 DB 301 ATGAATATTCATGTTGCCAAACGGAAGTTTAAAGAAACATTTACGTCATATGATGATAAA 360
 OY 1615 GATGTCATGAAACATATTTCTGCTGTCATCTGACATGTTGTGTAATAATTA 1668
 DB 361 GATGTCATGAAACATATTTCTGCTGTCATCTGACATGTTGTGTAATAATTA 414

RESULT 29
 AAH99526
 ID AAH99526 standard; cDNA; 2900 BP.
 XX
 AC AAH99526;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein encoding cDNA sequence SEQ ID NO:361.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
 KW antilegic; haemostatic; vulnery; antileuk; osteopathic; eczema;
 KW dermatological; antiallergic; antisthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antidiabetic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200153455-A2.
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000MO-US35017.
 XX
 PR 23-DEC-1999; 9905-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX
 PA (HYSE-) HYSQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457603/49.
 XX
 PT P-PSDB; AAM25585.
 PT
 PT Isolated human polynucleotides encoding polypeptides, useful for the
 XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX
 PS Claim 1; Page 467; 1217P; English.
 XX
 CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: anti-inflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianemic; antilegic; antisthmatic; antidiabetic;
 CC antileuk; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for

CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 SQ Sequence 2900 BP; 676 A; 795 C; 818 G; 611 T; 0 other;

Query Match 13.4%; Score 372; DB 22; Length 2900;

Best Local Similarity 55.7%; Pred. No. 1.8e-87;

Matches 955; Conservative 0; Mismatches 695; Indels 66; Gaps 10;

OY 39 CGCGGGCTCTGAGTGAAGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 98
 DB 16 CGCAGGGCG 75
 OY 99 CAGCGCATGAAAGATGTGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 156
 DB 76 GCTAACCCAGCGGAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 135
 OY 157 GCCAGGGCG 216
 DB 136 GCG 195
 OY 217 GGTGCGCTGAGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276
 DB 196 ACCCTGCTCTGAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 255
 OY 277 CGCGCTCTTACAGAGTACAGAGTGC-----GGCGCAAGCTCACTACCG 327
 DB 256 GGGCTCTGCGCAAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 315
 OY 328 CGGGTCAGAACTACCTGTAACAAGCTGCTGAGAGACCGCGCGCGCGCGCGCGCG 387
 DB 316 CGCATCAAACTTGATCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 375
 OY 388 CAC-GCTTCGTTTCTCTCTGT-CTTGGTGGCTGATTTGTCAGT-GTTTCTTACC 444
 DB 376 CACAGGCTGTGCTTCTCTGATGTCTGAGGAGTGTGATCTGTGCTGTCTGACACCA 435
 OY 445 ATCCCTGAGCACAAATTTGGCTCAAGTGTGCTTGTGATCTGAGATTCGATGAT 504
 DB 436 TTCAGAGATGATGAGCTGTCTCGGAGACTGGCTTCTGTACGAGACATTTGCTATT 495
 OY 505 GTGCTTTGGTTGGAGTTCAATTCGATTCGATCTGTCGGGTTGCTGTTCGATAT 564
 DB 496 TTCATCTTTGAGCCGAGTTTGTCTTGAAGTCTGCGCTGCTGATGTGCTGCGATAC 555
 OY 565 AGAGATGCGAAGAGAGAGTGTGCTGCGAAGCGCTTGTGATGATGATACAT 624
 DB 556 AAAGGCTGGGCG 615
 OY 625 GTTCTATCCCTCAATAGAGTTGTTCTGCAAAACTCAGAGGATATATTTTCCACG 684
 DB 616 GTGCTATGCTCTGTCGCGAGTGTGTTGGGAAACAGGCAATGTTCTGCGCAC 675
 OY 685 TTGCACTCAGAACTCTCGTTCTCTACAGATCTCGGAGAGTGGCATGGACGGAAG 744
 DB 676 T---CCCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 732
 OY 745 GGAGG-----CACTGGAATTAATCTGAGTGTGATGATCTGCAAGCAAGATTAAT 800
 DB 733 GAAAGTGGACCTGGAAGCTTCTGAGGCTGACGACATCTGTGCCACAGCAAGACTCAT 792
 OY 801 CACAGCTTGTATAGATTTTGTCTTATTTTGTCTTCTTCTTCTTCTTCTTCTTCT 860
 DB 793 CAGGCGCTGTATAGTGGTTTCTGACACTCATCTTCTTCTTCTTCTTCTTCTTCT 852


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OY 328 CCGGTGACAGACTACCTGTACAGCTGCTGGAGAGACCCCGGGCTGGGCTTCATCTAC 387
Db 316 CGCATCAAACTTGTATCTACGACGCCCTGGAGAGACCGGGGCTGGGCTGCTTTAC 375
OY 368 CAC-GCTTCTGTTTTCTCCCTGTG-TTGGTGTGCTGATTTGTGAGT-GTTTCTACC 444
Db 376 CACAGCGTGGTGTCTTCTATGCTCTAGGGGTCTTGATTTGCTGCTCTGGACACA 435
OY 445 ATCCCTGACACACAAATTTGGCTCAAGTTGCTTGTGATCTGAGTTCGTGATGAT 504
Db 436 TTCAAGGATATGAGACTGCTCGGGAGACTGGCTTCTGTACGAGACATTTGATTT 495
OY 505 GTGCTCTTTGTTGGAGTTTCATATTCGATCTGCTGCGGGTTCGTGCTGATAT 564
Db 496 TTCACTTTTGGAGCCGAGTTTGTGAGGATCTGGGCTGTGATGTTGCTGCGCATAC 555
OY 565 AGAGATGGCAAGAGAGACTGAGTGTGCTGCAAAAGCCCTTGTGTTATGATACAT 624
Db 556 AAAGCTGGCGGGCGGCGACTGAAGTTGCCAGAGAGCCCTGTGATGTTGACATCTTT 615
OY 625 GTTCTTATGCTTCAATAGCAGTTGTTTTCGAAAACTAGGGTATATTTTGGCCAG 684
Db 616 GTGCTGATTTGCTCTGTGCGAGTGTGCTGTGGGAAACCAAGCAATGTTCTGCGCAC 675
OY 685 TCTGCACTGAGAGTCCGTTTCTCTACAGATCCTCGCATGCTGGCATGACCGAAG 744
Db 676 T---CCCTGCGAAGCTCGCGCTTCTCTACAGTCTCGCATGCTGCGGATGACCGGGA 732
OY 745 GGAG-----CACTTGGAAATTAAGTGGTTCAGTGTATGCTCAGACAGAAATTAAT 800
Db 733 GAAGGTGGCACTGGAAAGCTTCTGGGGCTCAGCCATCTGTCCACAGCAAAAGCTCAT 792
OY 801 CACAGCTGTGATAGATTTTGTGTTCTTATTTTTCGTTCTTCTGCTATCTGCT 860
Db 793 CAGGCTGTGATATCGTTTCTCTGACATCATCTTCTTCTTCTTCTGCTTACTGCT 852
OY 861 GGAAGAGATGCC-----AATAAGAGTTTCTTAC 890
Db 853 TGAGAAAGAGCTCCAGAGGTGATGACAGAGAGAGAGATGAAGAGAGATTTGAGAC 912
OY 891 ATATGAGATGCTCTCTGTGGGGCAGCAATTAATGCAACTATTTGCTATGAGACAA 950
Db 913 CTATGAGATGCTCTGTGGGGCAGCAATTAATGCAACTATTTGCTATGAGACAA 972
OY 951 AACTCCCTTAAGTGTGGTGGAGAAATGCTTCTGACAGCTTGTGACCTCTGCAATTC 1010
Db 973 GACACCCAAAACGTGGAGAGCGCTGATGCGCCACCTTTTCTTAATTTGGCGCTCTC 1032
OY 1011 TTTCTTGGACCTTCTGCGGGCATCTTCTGCTCAGGTTTGTGATTAAGATCAAGACA 1070
Db 1033 CTTTGTGCTTCTGACGGGCTATCTGCGGTGCGGCTGCGCCCTCAAGGTGACAGAGA 1092
OY 1071 ACACCGCAGAAACATTTGAGAAAAGAGAACCCAGCTGCAACTTCATCTAGTGT 1130
Db 1093 ACACCGCAGAAACATTTGAGAAAAGAGAACCCAGCTGCTGAGCTATCTAGTGT 1152
OY 1131 TTGGCGTAGTACCAAGCTGATGAGAAATCTGTTCCATTTG-----CAACCTGGA 1181
Db 1153 CTGGAGTATTAATCTACCAACCCCAACAGATTAACCTGGGGGACATGAGATTTTA 1212
OY 1182 GCCACACTTGAAGCCCTGACACACTGACCAATCAAGAGCTTAAGTTTAAGA 1241
Db 1213 TGAATCACTGCTCTCTTTCTTTCTTTCAGGAAAAGACGTGGAGGAGCATCCAGCA 1272
OY 1242 GCGAGTGGCATGCTGAGCCCGGAGGCGCAGATTAAGAGCCCAAGCCCTCACTAG 1301
Db 1273 AAAGCTGGCTCTCTGATCGGGTTCGCTTCTATCTCTGTGAGCAATTAAGG 1332
OY 1302 TGACAGGAGTCCCAAGCAGCAGATCAACCCGAGGGGAGGCCCAAGCAAGTGGAGA 1361
Db 1333 AAAGCTATTAATCCCTCTGATATGATGACATAGAGAAAGTCTTTTAAGAACCAAA 1392

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OY 1362 GAGCTGAGCTTCAACAGACCCAGCCGCTTCGCGCCCTGCTGCGCTCAAAAGTTCTCA 1421
Db 1393 GCGTGTGGCTTAACCAATTAAGAGGCTTCCGACAGGGCTTCGCGATGAAGCCCTACGC 1452
OY 1422 GCCAAACCAAGTATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATAA 1481
Db 1453 TTTCTGCGAGAGTCTGAAGATGCGGGAGAGTGCACCCATGCGGGA-----GACAG 1506
OY 1482 AGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1541
Db 1507 GGGCTATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
OY 1542 AGCTATGCAATTAAGAAATTTCAATGTTGCAAAACGAAATTAAGAAACATTAAGTCC 1601
Db 1567 AGCCGTCAAGATTTCAATGTTGCAATGTTGCAATGTTGCAATGTTGCAATGTTGCA 1626
OY 1602 ATATGATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1661
Db 1627 TTACGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1686
OY 1662 AATTAAGCTTCAACAGAGTGTGATCAATTTCT 1697
Db 1687 GATTAAGTACCTTCAACAGAGATGATGATTTT 1722

RESULT 31
AAS83921
ID AAS83921 standard; cDNA; 4154 BP.
XX
XX AAS83921;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #19725.
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX Food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dermanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX P-PsDB; ABG19734.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX
XX Claim 1; SEQ ID No 19725; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical

```


KM neuronal excitability; neurotransmitter release; KCNQ modulator;
 KM ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KM age-associated memory loss; learning deficiency; motor neuron disease;
 KM epilepsy; stroke; ss.
 OS Rattus sp.
 PN M09907832-A1.
 XX
 XX 18-FEB-1999.
 PD 26-JUN-1998; 98MO-US13276.
 PF 12-AUG-1997; 97US-0055599.
 PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Blannar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 PI Little WA, Neubauer MG, Yang W;
 XX WPI: 1999-190047/16.
 DR P-PSDB; AAY01531.
 XX
 XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 PT neurotransmission and neuroprotection, used to treat, e.g. ataxia
 XX
 XX Disclosure; Fig 16; 64pp; English.
 PS
 XX The present sequence encodes rat KCNQ2/KVLRI. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.
 XX
 XX Sequence 735 BP; 143 A; 191 C; 214 G; 187 T; 0 other:
 SQ
 Query Match 11.9%; Score 331; DB 20; Length 735;
 Best Local Similarity 68.1%; Pred. No. 6e-77;
 Matches 460; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

DB 450 GGATGCACTCTGTGGGGTCTGATACCCCTGACACACCATTTGGCTACGGGAGCAATACC 509
 QY CCTAATTGGCTGGGAGGATTTGCTTCTGACAGGCTTTGACCTCTTGGCATTTCTTCTT 1016
 DB 510 TCAGACCTGGAAACGGAGGCTGTTAGCAGCAGCATTTACCTTATTTGTTCTTCTT 569
 QY 1017 TGCACCTTCCGCGGCAATCTTGGCTCAGCTTTGCAATTAAGATCAAGAACACCG 1076
 DB 570 CGCTCTCTGCTGGCATTTTGGATCCGAGCTTTGCCCTGAAGTCCAGAGCAGCATCG 629
 QY 1077 CCAGAAACACTTTGAGAAAAAGAGAACCCAGCTGCCAACCCTATTTAGTGTCTTGGCG 1136
 DB 630 GCAAAAACACTTTGAGAAACGGGGAATCTCGGCGAGGTCTCATCCAGCTCTGGAG 689
 QY 1137 TAGTTACGCGAGCTGA 1151
 DB 690 ATTCTATGCTACTTA 704

RESULT 33

AA573266

ID AA573266 standard; cDNA; 1320 BP.

AA573266;

13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #9070.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dmanac RT, Liu C, Yang YT;

WPI: 2001-639362/73.
 P-PSDB; ABG09079.

New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

Claim 1; SEQ ID No 9070; 103pp; English.

The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

OY 640 ATAGCAGTGTCTTCTGCAAAAACACAGGTAATTTTGGCAGCTGCACTGAGAGT 699
 DB 253 GTGGCAGTGTCTTCTGCAAAAACACAGGTAATTTTGGCAGCTGCACTGAGAGT 309
 OY 700 CTCCTGCTTCTGCAAGATCTCTCCGATGTCGATGACCAAGAGGAGGACACTTGGAAA 759
 DB 310 CTCCTGCTTCTGCAAGATCTCTCCGATGTCGATGACCAAGAGGAGGACACTTGGAAA 369
 OY 760 TTAAGTGGTTCAGTGTGTTTATGCTCAGACAGAAAGTAATTCACAGCTTGTGATAGGA 819
 DB 370 CTCCTGCTTCTGCAAGATCTCTCCGATGTCGATGACCAAGAGGAGGACACTTGGAAA 429
 OY 820 TTTTGGTCTTATTTTGTGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 873
 DB 430 TTTTGGTCTTATTTTGTGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 489
 OY 874 -----ATAAAGAGTTTCTTACATATGAGATGCTTCTG 909
 DB 490 GTGAGTGCACAAAGAGAGAGATGAAAGAGAGTTTGAGACTATGAGATGCTTCTG 549
 OY 910 TGGGGCAAAATACATTAATGACACTATTTGGCTATGAGACAAAACTCCCTTAATTTGCTG 969
 DB 550 TGGGGCTGATACACTGACCTGACCACTGCTATGAGACAAAGAGAGAGAGAGAGAGAGAG 609
 OY 970 GGAAGATGCTTCTGAGGCTTTCAGCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1029
 DB 610 GGGCGTCTGATGCTGCTGCTGCTTCTTAAATGCTGCTTCTTCTGCTTCTGCTTCTGCTG 669
 OY 1030 GGCATCTGCTGCTGCTGCTTTCATTAAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1089
 DB 670 GGCATCTGCTGCTGCTGCTTTCATTAAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 OY 1090 GAGAAAG 1145
 DB 730 GAGAAAG 785

RESULT 35
 AAS67245
 ID AAS67245 standard; cDNA; 1566 BP.
 AC AAS67245;
 AC 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #3049.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PE 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Dmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG03058.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX
 PS Claim 1: SEQ ID NO 3049; 103bp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SO Sequence 1566 BP; 348 A; 473 C; 397 G; 348 T; 0 other;

Query Match	11.1%	Score 307.6	DB 23	Length 1566
Best Local Similarity	64.4%	Pred. No. 1.3e-70		
Matches 510	Conservative 0	Mismatches 249	Indels 33	Gaps 2
OY 364	CCCCGGCGCTGGGCGTTCATCTACACGCTTCTTCTTCTCTGCTTCTGCTTCTGCTTCTGCT	423		
DB 778	CCCCCTAGACGGGGCCCCCGCCCGCTACGCGCTGATGATGCTCTGCTGCGGCTGCTG	837		
OY 424	ATTTTGTGCTGTTTCTTACCATCTGAGACACAAATTTGGCTCAAGTGGCTCTG	483		
DB 838	ATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	897		
OY 484	ATCCTGAGTTCGATGATGATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT	543		
DB 898	TTACTGAGACATTTTCTATTTTCTTCTGAGGCGAGTTTCTGAGGATCTGGCT	957		
OY 544	GCGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	603		
DB 958	GCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1017		
OY 604	TTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	663		
DB 1018	CTGTCATGTTGACATCTTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1077		
OY 664	CAGGTAATATTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	723		
DB 1078	CAGGCAATGTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1134		
OY 724	ATGTCGCGCATGACCGGAG	783		
DB 1135	ATGTCGCGCATGACCGGAG	1194		
OY 784	CACAGCAAGAAATTAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	843		
DB 1195	CACAGCAAGAAATTAATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1254		
OY 844	TTCTTGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	873		
DB 1255	TTCTTGTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1314		
OY 874	ATAAAGAGTTTCTTACATGACAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	933		
DB 1315	AAAGAGAGTTTGGAG	1374		
OY 934	ATTGGCTATGAGACAAATCTCCCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	993		

Db 1375 ATGGCTATGAGACAGACACCCAAACGCTGGAGGCGCTGTGATTGCCGCCACCTTT 1434
 QY 994 GCACCTCCTGGCATTTCTTTCTTGGCATTCCTGCGGACATTTCTGGCTCAGGTTTGGCA 1053
 Db 1435 TCCCTTAATGTGGCTCCTTTTTCCTTCCAGCGGGCATCTCGGGGTCCGGGCTG6CC 1494
 QY 1054 TTTAAAGTACAGAACACACCGCCAGAAACTTTGAGAAAAGAGAACCCAGCTGCC 1113
 Db 1495 CTCAGAGTGCAGAGACACACCGTCAAGACACTTTGAGAAAAGAGAACCCAGCTGCT 1554
 QY 1114 AACCTCATTCAG 1125
 Db 1555 GAGCTCATTCAG 1566
 RESULT 36
 AAS84027
 ID AAS84027 standard; cDNA; 1566 BP.
 XX AAS84027;
 DE 13-FEB-2002 (first entry)
 XX DNA encoding novel human diagnostic protein #19831.
 DE Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX MO200175067-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 DR P-PSDB; ABLG19840.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 1; SEQ ID No 19831; 103bp; English.
 PS The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 1566 BP; 348 A; 473 C; 397 G; 348 T; 0 other;
 Query Match 11.1%; Score 307.6; DB 23; Length 1566;
 Best Local Similarity 64.4%; Pred. No. 1.3e-70;
 Matches 510; Conservative 0; Mismatches 249; Indels 33; Gaps 2;
 QY 364 CCCCCGGGCTGGGCGCTTCATCTACACACCTTTCCTTTCCTCTGCTGCTGCTGCTG 423
 Db 778 CCCCCAGACCGGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 837
 QY 424 ATTTGTCAGTGTGTTTCTTACATCCCTGAGACACAAATGGGCTCAGTCCCTCTTG 483
 Db 838 ATTTGTCAGTGTGTTTCTTACATCCCTGAGACACAAATGGGCTCAGTCCCTCTTG 897
 QY 484 ATCTGGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
 Db 898 TTACTGAGACATTTCTCTATTTTCATCTTTGAGCCGAGTTTGCTTGGAGATCTGGCT 957
 QY 544 GCGGCTGCTGTGTTGATATAGAGATGCGAAGAAAGACTGAGGTTGCTGCAAGGCC 603
 Db 958 GCTGATGTTGCTGCGCATACAAAGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGG 1017
 QY 604 TTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 663
 Db 1018 CTGTGATGTTGATGATATGATATGATATGATATGATATGATATGATATGATATGAT 1077
 QY 664 CAGGCTAATATTTTGGCCAGTCTGACAGAGTCTGCGTTTCTACAGATCTCCGC 723
 Db 1078 CAGGCAATATTTTGGCCAGTCTGACAGAGTCTGCGTTTCTACAGATCTCCGC 1134
 QY 724 ATGTCGCGATGAGACCGAAGGGGAGGAGGACACTTGGAAATTTAGTGGTTATGCT 783
 Db 1135 ATGTCGCGATGAGACCGAAGGGGAGGAGGACACTTGGAAATTTAGTGGTTATGCT 1194
 QY 784 CACACCAAGGAATTAATACACAGCTTGTATCATATGATATGATATGATATGATATGAT 843
 Db 1195 CACACCAAGGAATTAATACACAGCTTGTATCATATGATATGATATGATATGATATGAT 1254
 QY 844 TTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 873
 Db 1255 TTCTGTTATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 1314
 QY 874 AATAAGAGTTTTCATCATATGATATGATATGATATGATATGATATGATATGATATGAT 933
 Db 1315 AATAAGAGTTTTCATCATATGATATGATATGATATGATATGATATGATATGATATGAT 1374
 QY 934 ATGGCTATGAGACAAACCTCCCTAATCTGCTGGAAGATGCTTCTGAGAGCTTT 993
 Db 1375 ATGGCTATGAGACAAACCTCCCTAATCTGCTGGAAGATGCTTCTGAGAGCTTT 1434
 QY 994 GCACCTCCTGGCATTTCTTTCTTGGCATTCCTGCGGACATTTCTGGCTCAGGTTTGGCA 1053
 Db 1435 TCCCTTAATGTGGCTCCTTTTTCCTTCCAGCGGGCATCTCGGGGTCCGGGCTG6CC 1494
 QY 1054 TTTAAAGTACAGAACACACCGCCAGAAACTTTGAGAAAAGAGAACCCAGCTGCC 1113
 Db 1495 CTCAGAGTGCAGAGACACACCGTCAAGACACTTTGAGAAAAGAGAACCCAGCTGCT 1554
 QY 1114 AACCTCATTCAG 1125
 Db 1555 GAGCTCATTCAG 1566
 RESULT 37
 ABL28585
 ID ABL28585 standard; DNA; 1280 BP.
 XX ABL28585;
 XX 26-MAR-2002 (first entry)

FT	mutation	replace(928,A)
FT	mutation	/*tag- j
FT	mutation	replace(1046,G)
FT	mutation	/*tag- k
FT	mutation	replace(1066,T)
FT	mutation	/*tag- l
FT	mutation	replace(1097,A)
FT	mutation	/*tag- m
FT	mutation	replace(1172,T)
FT	mutation	/*tag- n
FT	mutation	replace(1343,G)
FT	mutation	/*tag- o
FT	mutation	replace(1588,T)
FT	mutation	/*tag- p
FT	mutation	replace(1697,T)
FT	mutation	/*tag- q
FT	mutation	replace(1747,T)
FT	mutation	/*tag- r
FT	mutation	replace(1781,A)
FT	mutation	/*tag- s
XX		
PN	WO200124681-A2.	
PD		
PD	12-APR-2001.	
XX		
PE	09-AUG-2000; 2000WO-US21660.	
XX		
PR	09-AUG-1999; 99US-0147488.	
PR	17-MAR-2000; 2000US-0190057.	
XX		
PA	(UTAH) UNIV UTAH RES FOUND.	
XX		
PL	Keating MT, Splawski I;	
DR	WPI: 2001-290564/30.	
XX	P-PSDB; AAB82220.	
PT		
PT	New KVLQ1 and SCN5A genes, which contains alterations or mutations,	
PT	useful in diagnostic/prognostic or drug screening methods, particularly	
PT	long QT syndrome analyses for screening individuals with or at risk for	
PT	long QT syndrome	
XX		
PS	Claim 1; Page 56-59; 76pp; English.	
XX		
XX	The present sequence is that of the human KVLQ1 gene. This gene	
CC	is implicated in Romano-Ward syndrome, the autosomal dominant form	
CC	of long QT syndrome (LQTS), and in Jervell and Lange-Nielsen	
CC	syndrome, a form of LQTS associated with deafness, a phenotype	
CC	abnormally inherited in an autosomal recessive fashion. Novel	
CC	mutations have been identified in the gene using single strand	
CC	conformation polymorphism analysis. These are: A332G (altering	
CC	codon TAC to TGC, resulting in a Y11C mutation in the encoded	
CC	protein); G478A (GAG/AAG, E160K); G521A (CGC/CAC, R174H); G535A	
CC	(GGC/AGC, T391I); G580C (GGC/CCG, A194P); C727T (CGC/TCG, R243C);	
CC	T742C (TGG/CGG, W248R); T797C (CTG/CCG, L266P); G921-11T (GTG/GTGT,	
CC	alters reading frame leading to protein truncation); A922-2C;	
CC	G928A (GTC/ATC, V310I); C1045G (TGC/TGG, S349W); C1066T (CAG/TAG,	
CC	truncation after amino acid 355); G1097A (CGG/CAG, R366Q); C1172T	
CC	(ACC/ATC, T391I); C1343G (CGA/CGA, P488R); C1588T (CAG/TAG,	
CC	truncation after amino acid 529); C1697T (TGC/TTG, S566F); C1747T	
CC	(CGC/TCG, R583C); and G1781A (CGA/CAA, R594Q). Isolated DNA	
CC	sequences comprising 1 or more of these mutations are claimed.	
CC	Also claimed are nucleic acid probes that specifically hybridise	
CC	to a mutated KVLQ1 gene but not to the wild-type gene. These are	
CC	used in claimed methods: for detecting a mutation in the KVLQ1	
CC	gene; assessing risk of an individual for LQTS; and diagnosing a	
CC	mutation which causes LQTS. Assays may be performed using nucleic	
CC	acid microchip technology. Mutated KVLQ1 proteins (see	
CC	AAB82221-38) are also used in a claimed diagnostic method, and in	
CC	a claimed method of screening for drugs useful in treating a	
CC	person having a mutation in the KVLQ1 gene.	
XX		
XX	Sequence 2028 BP; 367 A; 691 C; 612 G; 358 T; 0 other;	

Query Match	9.78;	Score 267.8;	DB 22;	Length 2028;
Best Local Similarity	59.58;	Pred. No. 5e-60;		
Matches 499;	Conservative 0;	Mismatches 322;	Indels 18;	Gaps 2

OY	331	GTGCGAAGACTTACCTGATCAAGCTGTGGGAGAACCCCGGGGTGG---GCGTATATAC	387
Db	316	GTCCAGGGGCGGGTCTACAACTCTCTCGAGCGTCCACCGGCTGGAAATGCTTCCCTTAC	375
OY	388	CACGCTTTGTTTTTCTCCCTGTGCTTTGGTGTGCTGATTTTGTGCAGTGTTTTCTACATC	447
Db	376	CACCTTCGCGGCTTCTCTCATGCTGTGCTGTGCTTCCATCTTCAGAGTCTGTGTCACATC	435
OY	448	CCTGAGCACACAAAATTTGGCCCTCCAGTTGGCCCTTGATCTCGAGAGTTGGTATATGTTTC	507
Db	436	GAGCAGTATGCCGCCCTGGCCACGGGGAGCTCTTCTTGAAGAGATGTGCTGTGGTGTG	495
OY	508	GTCCTTTGGTTTTGAGTTATCATATTCGAATTCGATGTGGGGTGGTGTGTTGTCGATATAGA	567
Db	496	TTCTTCGGGAGGAGTACGTAGTGGTCCGCTCTGAGTCCGCGGGGTGCGGACGAGATACGTG	555
OY	558	GGATGGCAGAGAAAGCTAGGTTTGTCTGGAAAGCCCTCTGTGTTATAGATACATTTGT	627
Db	556	GGCCTCTGGGGGCGGCTCGGCTGGTCCCGGAAGGCCATTTCCATCATGAGCCTCACTGTG	615
OY	628	CTTATCGCTTAATAGCAGTTGTTTCTCAAAAATCTCAGGGTAAATATTTTGGCCAGCT	687
Db	616	GTGCGTGGCTCCATGAGTGTGTCTGTGGCTGTGGGCTCCAGGGGAGAGTTTGGCACGTGC	675
OY	688	GCATCAGAAAGTCTCCGTTTCCCTACAGATCTCTCCGATGATGGCGCATGAGCCGAAAGGGA	747
Db	676	GCCATCAGAGGAGCATCCGCTCTCTCGAGATCCGAGAGATCCAGACAGTCCAGCCGACGGGA	735
OY	748	GGCACTTGGAAATTACTGGGTTTCAAGTGGTTTATGCTCAGACAGAGATTTAATCAAGCT	807
Db	736	GGCACTGAGAGGCTCTCTGGGCTCCGCTGTCTTATCCACCGCCAGAGACTATATACCAAC	795
OY	808	TGTTACATAGCATTTTGGTTCTATATTTTTCGTTCTTGTCTATCTGTGGTGAAG	867
Db	796	CTGATACATCGGCTTCTCTGGGCTCATCTTCTCTCTGATCTTGTGATCTGGCTGAGAG	855
OY	868	GATGCGAATTAAT-----GAGTTTCTACATATGAGAGATGCTCTGGTGG	912
Db	856	GAGCGGATGGAACGAGTCAAGGCGGGGTGAGTTCCGCAAGTACGAGATGCGCTGTGTGG	915
OY	913	GGCAATATTACATTGACAACTATTGGCTATGAGAGACAAAACTCCCTTAATCTTGGCTGGGA	972
Db	916	GGGGTGTGTACAGTACACCAATCGGCTATGGGAGACAAAGTCCCGACAGACTGGGTGGG	975
OY	973	AGATTGCTTTTGGAGGCTTTTGACACTCTCTGGCAATTTCTTCTTGACATCTCCGCGGG	1032
Db	976	AAGACATAGCCTCTCTGCTCTCTGTGTCTTTTGGCATTTCTCTTCTTTTGGCTCCAGCGGGG	1035
OY	1033	ATTCCTGGCTCAGGTTTTGGCATTTAAAGTACAGAACACACCGCAGAAACACTTTGAG	1092
Db	1036	ATTTTCTTGGCTTCGGGGTTTCCCTGAAGGTGACAGAAAGGAGGACGACATTCATAC	1095
OY	1093	AAAGAAGAGAAACCCAGCTGCCAACCCTCATTCAGTGTGTTTGGCTAGTACGACAGCTGA	1151
Db	1096	CGGCAGATCCCGGGGCGAGCCTCACTCATTTACAGCCGATGAGAGTGTCTATGTGCGGA	1154
RESULT 39			
AAZ90669			
ID	AAZ90669 standard; cDNA, 3181 BP.		
XX	AAZ90669;		
AC			
XX			
DT	19-JUN-2000 (first entry)		
XX			
DE	Human KVLQTL protein encoding cDNA.		
XX			
XX	KVLQTL; KONE1; long QT syndrome; LQT syndrome; mink protein;		

OY 1151 A 1151
 Db 869 A 869

RESULT 43
 AAT94004
 AAT94004 standard; DNA: 2821 BP.

AC AAT94004;
 AC 28-FEB-1998 (first entry)
 AC DNA encoding human KVLQT1.
 AC KVLQT1, long QT syndrome; arrhythmia; mink; potassium channel;
 AC diagnosis; therapy; human; ds.
 AC Homo sapiens.

FT Key Location/Qualifiers
 FT CDS 88..1833
 FT /*tag= a

XX MO9723632-A1.
 XX 03-JUL-1997.
 XX 20-DEC-1996; 96MO-US19917.
 XX 29-OCT-1996; 96US-0739383.
 XX 22-DEC-1995; 95US-0019014.
 XX (GENZ) GENZYME GENETICS.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX Connors TD, Curran ME, Keating MF, Landes GM;
 DR WP1: 1997-402191/37.
 DR P-PSDB; AAW33355.
 XX

New isolated human potassium channel gene, KVLQT1, - used to develop products for diagnosis, prevention and therapy of long QT syndrome

PS Claim 2; Page 76-79; 117pp; English.

CC This cDNA sequence includes a full-length coding sequence for human KVLQT1 (see AAW33355), a novel cardiac potassium channel protein. The sequence was assembled from partial clones isolated from human pancreatic and cardiac cDNA libraries. KVLQT1 was mapped to chromosome 1p15.5 making it a candidate for the long QT syndrome (LQT) gene. LQT is an inherited cardiac arrhythmia. 16 families with mutations in KVLQT1 have been identified and it was shown that in all 16 families there was complete linkage between LQT1 and KVLQT1. The KVLQT1 gene product coassembles with human mink to form a cardiac arrhythmia. Its dysfunction is a cause of cardiac arrhythmia. Coexpression of KVLQT1 and mink in a host cell provides a means for screening for drugs useful in treating or preventing LQT. Analysis of the KVLQT1 gene will provide an early diagnosis of subjects with LQT. A claimed method of assessing the risk in a human for LQT syndrome comprises screening for a mutation in the KVLQT1 gene. Transgenic animals expressing human mink and KVLQT1 can be used to test therapeutic agents against LQT.

XX Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 9.6%; Score 266.6; DB 18; Length 2821;
 Best local similarity 59.3%; Pred. No. 1.2e-59;
 Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

OY 329 GGGTGCAAGAACTACCTGTACAAAGCTGAGAGAGACCCGCGGCTGG--GCGTTCATCT 385
 116 GCGGCGAGGCGCGGCTGTACAAATTCCTGAGCGCTCCACCGCGGTGAAATGCTTCTGTT 175

OY 386 ACCAGCCTTTCGTTTTCCTCCTTGTGCTTGTGCTGATTTTTCAGTGTTCACCA 445
 176 ACCACTTCGCGCTTCCTTCATCGTGTGCTGCTCCTCATCTTCAGCGCTGCTCCACCA 235
 OY 446 TCCCTGAGACACAAAATTGGCTCAAGTGGCTCTTGTGCTGAGTGGATGATG 505
 236 TCGAGCAGTATGCGCCCTGGCCACAGGGAGCTCTTCTGATGATGATGATGCTGCTG 295
 OY 506 TCGTCTTGTGTTGGAGTTTCATTCGATTCGATTCGAGGTTGCTGCTGATATA 565
 296 TGTTCCTTGGGAGCAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
 OY 566 GAGATGCAAGAAAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
 356 TGGGCTCTTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
 OY 626 TTTCTATCGCTTCATATGACAGTTGTTTCTGCAAAACTCAGGGTATATATTTTGGCCAGT 685
 416 TGTGCTGCTGCTTCATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
 OY 686 CTGCACCTCAGAACTCTCCGTTTCTTACAGATCTCCGATGCTGCTGCTGCTGCTGCTG 745
 476 CGGCATCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
 OY 746 GAGCACTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 805
 536 GAGGCACTGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 595
 OY 806 CTGTGATACATAGATTTTGTGTTCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 865
 596 CCTGTACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
 OY 866 AGGATGCCAATAA-----GAGTTTCTACATATGCAATGCTCTGCTG 910
 656 AGGACGCGGTGAACGAGTCAAGCCGCGGTGAGTTGCGCAGCTACGACATGCGCTGCTG 715
 OY 911 GGGGCAAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 970
 716 GGGGGGTGTGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 775
 OY 971 GAAAGATGCTTCTGCAAGCTTGTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1030
 776 GGAAGACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
 OY 1031 GCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
 836 GATTCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
 OY 1091 AGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1150
 896 ACCGGAGATCCCGGGGAGAGCTCACTCATTCAGACCGCATGAGAGGTGCTATGCTGCCG 955

OY 1151 A 1151
 Db 956 A 956

RESULT 44
 AAT90730
 AAT90730 standard; cDNA: 2821 BP.

AC AAT90730;
 AC 12-FEB-1998 (first entry)
 AC Human KVLQT1 full-length cDNA.
 AC KVLQT1, long QT syndrome; arrhythmia; mink; potassium channel;
 AC diagnosis; therapy; human; ds.
 AC Homo sapiens.

Key Location/Qualifiers
 CDS 88..1833
 /tag= a

MO9723598-A2.

03-JUL-1997.

20-DEC-1996: 96MO-US19756.

29-OCT-1996: 96US-0739383.

22-DEC-1995: 95US-0019014.

(UTAH) UNIV UTAH RES FOUND.

Curran ME, Keating MT, Sanguinetti MC;
 WPI: 1997-402190/37.
 P-PSDB: AAW30038.

Human mink and xenopus KVLQT1 coding sequences - used for assays for
 identifying drugs which can be used for preventing or treating long
 QT syndrome

Example 9; Page 76-79; 105pp; English.

This CDNA sequence includes a full-length coding sequence for human
 KVLQT1 (see AAW30038), a novel cardiac potassium channel protein.
 The sequence was assembled from partial clones isolated from human
 pancreatic and cardiac cDNA libraries. KVLQT1 was mapped to
 chromosome 11p15.5 making it a candidate for the long QT syndrome
 (LQT) gene. LQT is an inherited cardiac arrhythmia. One intragenic
 deletion and 10 different missense mutations which cause LQT have
 been identified in KVLQT1. The KVLQT1 gene product coassembles
 with human mink to form a cardiac IKs potassium channel.
 Coexpression of these 2 proteins in a host cell provides a means
 for screening for drugs useful in treating or preventing LQT. The
 products can also be used for studying mechanisms underlying common
 arrhythmias and for presymptomatic diagnosis of LQT. Transgenic
 animals expressing human mink and KVLQT1 can be used to test
 therapeutic agents against LQT.

Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 9 68: Score 266.6; DB 18; Length 2821;
 Best Local Similarity 59.38; Pred. No. 1.2e-59;
 Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

329 GGGTGCAGAACTACCTGTACACAGCTGTGAGAGAGACCCCGCGGTG---GCGTTCATCT 385
 116 GCGGCGACAGGCGCGCTACAACTTCCTGAGCGTCCACCGCTGGAATGCTTGGTT 175
 386 ACCACGCTTTGCTTTTCTCCTTGTCTTGTGCTGATTTTGTACAGTTCATACCA 445
 176 ACCACTTCGCGCTTCCTCATGCTGCTGCTCATCTTCACAGCTGCTTCACCA 235
 446 TCCCGACACACAAATTTGGCTCAAGTTCCTTGAATTCAGATTGATGATG 505
 236 TCGACAGATATGCGCCCTGCGCAGGAGACTCTCTTGTGATGAGATGCTGCTG 295
 506 TCGCTTTGGTTGGAGTTCATCATTCGAATCTGTGTGCGGGTGTCTGTTCGATATA 565
 296 TGTTCCTGGGAGCGAGTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
 566 GAGGATGCGCAAGAGCTGAGTTCGTGCGAAGCCCTCTCTGTATATGATACCAT 625
 356 TGGGCTCTGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
 626 TTTCTATCGCTTCATATGAGTGTCTTGTGCAAAATCTCAGGTAATATTTTGCAC 685
 416 TGTGCTGCGCTTCATATGAGTGTCTTGTGCAAAATCTCAGGTAATATTTTGCAC 475
 686 CTGCACTCAAGAGTCTGCTTCTTCAAGATCTCTCCGATGTGCGCATGAGCAGG 745

476 CGGCCATCAGGGGACATCCGCTTCTCAGATCCTGAGAGATGTACACGTGACCGCAGG 535
 746 GAGGACCTTGGAATTAATCTAGTGTGTTATGCTACAGCAAGAAATTAATACAG 805
 536 GAGGACCTTGGAATTAATCTAGTGTGTTATGCTACAGCAAGAAATTAATACAG 595
 806 CTGTCATATGAGTATTTTGTGCTTATTTTGTGCTTATTTTGTGCTTATGCTG 865
 596 CCTGTATATCGCTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTG 655
 866 AGGATGCCAATAA-----GAGTTTCTACATATGAGATGCTCTGCT 910
 656 AGGACCGGAGTACAGATCAGCGCGCTGAGATTCGCGAGATGAGATGCTGCTG 715
 911 GGGGACAAATTAATTAATGACATATGAGTATGAGCAAAATCCCTTACTTGGCTG 970
 716 GGGGGGTGTACAGTACACCAATGCGCTATGAGGACAGAGTCCCAAGCTGAGT 775
 971 GAAGATTGCTTTTGTGAGCTTTGACCTCTTGCATTTCTTTTGTGCACTTCTGCG 1030
 776 GGAAGACATCGCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTG 835
 1031 GCATTTGCTGCTCAGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTG 1090
 836 GGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
 1091 AGAAAG 1150
 896 ACCGCGAGATCCGCGCGGACAGCTTCACTTCACTTCACTTCACTTCACTTCACT 955
 1151 A 1151
 956 A 956

RESULT 45
 ABN96861
 ID ABN96861 standard; DNA: 2821 BP.
 AC ABN96861;
 XX 13-AUG-2002 (first entry)
 DE Gene #3359 used to diagnose liver cancer.
 KW Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX Homo sapiens.
 XX MO200229103-A2.
 XX 11-APR-2002.
 XX 02-OCT-2001; 2001WO-US30589.
 XX 02-OCT-2000; 2000US-237054P.
 XX (GENE-) GENE LOGIC INC.
 XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI: 2002-426119/45.
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample
 PS Claim 1; SEQ ID NO 3359; 298bp; English.

CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in AB93503-AB97455 in a
 CC tissue sample. The method of the invention has hepatotrophic, and
 CC cytoskeletal activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 9.6%; Score 266.6; DB 24; Length 2821;
 Best Local Similarity 59.3%; Pred. No. 1.2e-59;

Matches 499; Conservative 0; Mismatches 324; Indels 18; Gaps 2;

QY 329 GGGTCAGAACATCTGATGCTGAGAGAACCCCGGGCTGG---GGCTCATCT 385
 Db 116 GCGGCGCAGGCGCCCTACAACTTCTCGAGCCCTCCACCGGCGGAATGCTGTTT 175
 QY 386 ACCACGCTTCTGTTTCTCTGTTGTTGCTGATTTGTCAGTGTTCACCA 445
 Db 176 ACCACTTCGCGCTCTCTCATGCTGCTGCTCATCTTCAGCGCTGCTCCACCA 235
 QY 446 TCCCTGAGCACAAATAATGGCCCTCAAGTTCCTTATCTGAGATTCGTGATGTTG 505
 Db 236 TCGAGCATATGCGCCCTGCGCACGCGGAGCTCTTGTGATGAGATCGTGTGTTG 295
 QY 506 TCGCTTGTGTTGATTCATTCATTCGATGCTGCGGGGCTGCTGTTGTCATATA 565
 Db 296 TGTCTTCGGAGCAGAGTACGTGTCGCCCTCTGCTCCGCGGCTGCCACCAAGTACG 355
 QY 566 GAGATGCGCAGGAAGATGAGTGTGCTCGAAGCCCTTCTGTTATATGATACATTG 625
 Db 356 TGGGCTCTGTGGGGCGGCTGCTGCTGCGGAGCCATTCATCATCGACGTATG 415
 QY 626 TTTCTATCGCTTCATATAGCAGTGTGTTCTGCAAAAACATCAGAGTATATTTTGCACGT 685
 Db 416 TGTGCTGCGCTCATCTGCTGCTGCTGCGGCTCCAAAGGGGAGGTGTTGTCACGT 475
 QY 686 CTGCACTCAAGATGCTCGTTTCTTACAGATCTCCGATGATGCGCATGACCGCCAGG 745
 Db 476 GCGCCATCAAGGGGATCCGCTTCTGAGATCTGAGGATGCTTACACCTCCAGCCGACG 535
 QY 746 GAGGCACTGGAATTAATGAGTGTGTTTATGCTCAGACAGCAAGGAATTAATACAG 805
 Db 536 GAGGCACTGGAAGTCTCTGCGGCTCGGTCTTATCACCAGGAGAGTGAATACCA 595
 QY 806 CTGTGATACATAGATTTTGTCTTATTTTGTCTTCTTCTGATGATGAGGAAA 865
 Db 596 CCTGTACATCGGCTTCTGCGGCTCATCTTCTGCTGATCTTGTGATCTGCTGAGA 655
 QY 866 AGGATGCCAATAA-----GAGTTTCTACATATGAGATGCTCTGTTG 910
 Db 656 AGGACCGGTGAGAGTACGAGCGCGGTGAGTTCGCGAGCTACGAGATCGGTGAGT 715
 QY 911 GGGGCAATTAATGATGAGCAATATGCTATGAGAGCAAAACCTCCCTAATGCTGCTG 970
 Db 716 GGGGGGTGTACAGTACACCATCGATGAGGGGAGGTCACCGACGCGGGTGG 775
 QY 971 GAAGATTTGCTTCTGAGGCTTGTGACCTCTTGTGATTTCTTCTTGTGACTTCTGCGG 1030
 Db 776 GGAAGACATAGCGCTCTCTCTCTGCTTGTGCAATCTCTTCTTGTGCGTCCACGCG 835
 QY 1031 GATTTCTTGGCTCAGTGTTCATTAAGATCAAGAAACACCGCCGCAAAACCTTTG 1090
 Db 836 GGAATCTTGGCTCAGTGTTCATTAAGATCAAGAAACACCGCCGCAAAACCTTTCA 895

QY 1091 AGAAAGAGCAACCCAGCTGCAACCTTCATGCTGTTGGGTAGTACGACAGT 1150
 Db 896 ACCGGCAGATCCCGCGGAGCTCATATTCAGACCGCATGAGAGTGTCTGTCGG 955
 QY 1151 A 1151
 Db 956 A 956

RESULT 46

AAC89914
 ID AAC89914 standard; cDNA: 3182 BP.
 XX

AC AAC89914;

DT 08-MAR-2001 (first entry)

DE Mutant human KVLQT1 coding sequence #2.

KW Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;

KW cardiac potassium channel; Jervell and Lange-Nielsen syndrome; JLN;

OS chromosome 11p15.5; Long QT syndrome; ss.

XX Homo sapiens.

PN US6150104-A.

PD 21-NOV-2000.

XX 17-AUG-1998; 98US-0135021.

PR 29-JUL-1998; 98US-0094477.

PR 13-JUN-1997; 97US-0874655.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX WPI: 2001-060013/07.

XX P-PSDB; AAB49495.

XX DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen

XX syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,

XX or diagnosing or prognosing JLN -

XX Example 4; Columns 63-68; 58pp; English.

XX KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene

XX cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to

XX chromosome 11p15.5. The present sequence is a mutant KVLQT1 coding

XX sequence. The mutant KVLQT1 coding sequence is useful in the diagnosis of

XX long QT syndrome and in screening humans for the presence of KVLQT1 gene

XX variants which cause JLN syndrome.

XX

SQ Sequence 3182 BP; 581 A; 1073 C; 969 G; 559 T; 0 other;

Query Match 9.3%; Score 258.4; DB 22; Length 3182;
 Best Local Similarity 59.5%; Pred. No. 1.9e-57;

Matches 500; Conservative 0; Mismatches 321; Indels 19; Gaps 3;

QY 331 GTGCAAACTACCTGACAAAGTGTGAGAGACCCCGGGCTGG---GGCTCATCTAC 387
 Db 478 GTCCAGGGCGCGGTGTACAACTTCTCGAGCGTCCACCGGCTGGAATGCTTCTGTTAC 537
 QY 388 CACGCTTTCGTTTCTCTCTTCTTGTGTTGCTGATTTTGTACAGTGTTCACATC 447
 Db 538 CACTTCGCGCTTCTCTCTCTCTCTGCTGCTCATCTTCAAGCTGTGTCACATC 597
 QY 448 CCGTGCACACAAATAATGAGTTCGCTTGTGATCTGAGTTCGATGATGATTC 507
 Db 598 GAGCAGTATGCGCGCCCTGCGCACGGGAGACTCTTCTGTGATGAGATGCTGTGTTG 657


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Db      686 TGGCAGCTCCACCAATGCCCACCTCCCAAGCAGCGAGGTGGGTGAGGCGCACACC 745
QY      1346 CCACCAAGTGGAGAGAGCTGGAGCTTCAACACCAACCCGCTTCCGCGCTGCTGC 1405
Db      746 CCACCAAGTGGAGAGAGCTGGAGCTTCAATAGCCACCCGCTTCCGCGCATCTCTGA 805
QY      1406 GCGTCCAAAAGTCTCAGCCAAAACAGATGATGCTGACACAGCCGCTTGGCAGCTGATG 1465
Db      806 GACTC-----AAACCCCGCAGCTCTGCTGAGATGCCC---CTCAGAGG 847
QY      1466 ATGTATATGATGAAAAAGATGCCAGTGTGATGATATCATGAGAGACCTCACCACAC 1525
Db      848 AAGTAGCAGAGAGAGAGAGACTACAGTGTGAGCTCAGCGTGGAGACATCATGCTGCTG 907
QY      1526 TTTAAACGTCTATGAGCTATCAGATATGAAATTTCTATGTTGCAAAAGCAAGTTTA 1585
Db      908 TGAAGACAGTCACTCCGCTCCTCAGATGAGATTCTCAAGTTCTGTCGCGCAAAAGCAATTC 967
QY      1586 AGGAACATTAAGTCCATATGATGTTAAAGATGTCAATGTAACAATTTCTGCTGATC 1645
Db      968 AGGAGACACTGGGACCGTAGACAGCTGAAGAGCTCATTTGAGCACTCAGCAGGCCACC 1027
QY      1646 TGGACATTTTGTGTGAATTAAGCCTTCAACACAGCTGTGATCAAAATTTCTTGAAGA 1705
Db      1028 TGGACATGCTGGCGCGGATCAAGAGAGCTCAAACTGGGTGGACCAAAATTTGTGGTGG 1087
QY      1706 GGC---AAATCATCATCATAGATAGAGAGCGGAGAGAAATTAACAGCAGACATGAGACA 1762
Db      1088 GGCCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
QY      1763 CAGACGATCTAGATGCTGCTGGGTGGGTGTCAGAGTTGAAAAACAGAGTACAGTCAATG 1822
Db      1148 TGTATGAATCATGATGATGAGGAGCGGTGTCAAGGTGAGAGAGAGTCAAGTCAATG 1267
QY      1823 AATCAAGCTGAGCTGCTAGTACAGATCATCAACAGTCTCTTGGAAAGGCTCTGCT 1882
Db      1208 AGCAGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
QY      1883 CAGCCCTGCTTGGCTTGCATTCAGATCCAGATCCAGCTTTGAATGTGAACAGATCTGACT 1942
Db      1262 CCTCGGCGAGCTGAGGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
QY      1943 ATCAAGAGCTGAGTATGAGCAAGATCTTTGGGTTCCGACAA 1987
Db      1322 ACCACAGCTGCTGAGAGAGAGAGAGATCTCGCTCCGACAGA 1366

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RESULT 48

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ID      AAK92009 standard; cDNA: 798 BP.
XX      AAK92009;
XX      AC
XX      DT      06-NOV-2001 (first entry)
XX      XX
XX      DE      Human cDNA 5'-end sequence, SEQ ID NO: 469.
XX      XX      Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
XX      XX      Homo sapiens.
XX      PN      EP1130094-A2.
XX      PD      05-SEP-2001.
XX      PF      07-JUL-2000; 2000EP-01114089.
XX      PR      08-JUL-1999; 99JP-0194486.
XX      PR      11-JAN-2000; 2000JP-0118774.
XX      PR      02-MAY-2000; 2000JP-0183765.
XX      PA      (HELI-) HELIX RES INST.

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XX      Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX      WPI; 2001-524255/58.
XX      DR
XX      PT      830 Primers useful for synthesizing full length cDNA clones and their
PT      use in genetic manipulation -
XX      PS      Claim 2: SEQ ID NO 469; 1380bp + sequence listing; English.
XX      CC      The invention relates to primers for synthesizing full length cDNA
XX      CC      clones. 830 cDNA molecules encoding a human protein have been
XX      CC      isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX      CC      molecules have been determined. Primers for synthesizing the full length
XX      CC      cDNA are useful for clarifying the function of the protein encoded by
XX      CC      the cDNA. The full length clones were obtained by construction of full
XX      CC      length enriched cDNA libraries that were synthesised by the oligo-capping
XX      CC      method. The primers enable the production of the full length cDNA easily
XX      CC      without any special methods. The present sequence is the nucleotide
XX      CC      sequence of the 5'-end of a cDNA provided in the invention.
XX      CC      Note: The sequence data for this patent did not form part of the printed
XX      CC      specification, but was obtained in CD-ROM format directly from EPO.
XX      SQ      Sequence 798 BP; 153 A; 274 C; 222 G; 146 T; 3 other:

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Query Match      7.58; Score 208.4; DB 22; Length 798;
Best Local Similarity 71.2%; Pred. No. 1.5e-44;
Matches 275; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

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QY      791 AGCAATTAATCAGAGCTTGTGATAGATTTTGTCTTATTTTGTCTTCTGCTGCTG 850
Db      26 AGAGCTGATACACCGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 85
QY      851 TCTATCTGCTGAGAAAGATGCCAATPAAGATTTTCTACATATGAGATGCTCTGCT 910
Db      86 TCTACTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 145
QY      911 GGGGACAAATTAATGACAACTATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 970
Db      146 GGGGAGCAATTAATGACAACTATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 205
QY      971 GAAGATTTGCTTGTGAGAGCTTGTGACCTCTTGGCACTTTCTTTTGTGACTTCTGCGG 1030
Db      206 GCAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
QY      1031 GCATCTTGGCTCAGGTTTGCATTAAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1090
Db      266 GCATCTGAGCTCCGCTTGGCTTGAAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY      1091 AGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150
Db      326 AGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385
QY      1151 ATGAGAAATCTGTTTCAATGCAAC 1176
Db      386 ATATGAGCGGCGCTACCTGACAGCC 411

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RESULT 49

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ID      AAK93662 standard; cDNA: 798 BP.
XX      AAK93662;
XX      AC
XX      DT      06-NOV-2001 (first entry)
XX      XX
XX      DE      Human cDNA clone representative sequence, SEQ ID NO: 2122.
XX      XX      Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
XX      XX      Homo sapiens.

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PN EP1130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI: 2001-524255/58.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 PS Example 11; SEQ ID NO 2122; 1380bp + sequence listing; English.
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence was used as the
 CC representative sequence from a human clone which was used in
 CC homology searches to identify the clone.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 XX
 SQ Sequence 798 BP; 153 A; 274 C; 222 G; 146 T; 3 other;
 Query Match 7.5%; Score 208.4; DB 22; Length 798;
 Best Local Similarity 71.2%; Pred. No. 1.5e-44;
 Matches 275; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
 OY 791 AGCAATTATCAGACGCTGTATAGAGATTGTTGCTTATTTTCTGCTTCTG 850
 DB 26 AGAGCTGATACCGCTGCTGATCGGTTCTGCTGCTATCTTCTGCTTCTG 85
 OY 851 TCTATCTGGGAAAAGGATGCCAATAAGAGTTTTCACATATGCAATGCTCTG 910
 DB 86 TCTACTGGCCGGAAGAGACGCACTTCTCTCTACGCCGACCTGCTTGGT 145
 OY 911 GGGGCAATTTACATGACACTATGCTATGAGACAAAACCTCCCTAATCTGAGCTG 970
 DB 146 GGGGAGCATTTATCATGACCAACATCGGTATGTAACAGACACCGACACATGCTG 205
 OY 971 GAAGATTGCTTTGCAAGCTTTGCACTCTTCTGCAATTTCTTTTGCACCTTCTGCG 1030
 DB 206 GGAGGCTCTGCTGCTGCTGCTTCTTCTTCTGCTGCTTCTTCTGCTGCTGCG 265
 OY 1031 GCATTCTGGCTAGGTTTTCATTAAGATCAAGAAACACCGCCAGAAACCTTTG 1090
 DB 266 GCATCTTAGGCTTCGGCTTGGCTTGAAGGTCAGAGACACCGGAGAGCACTTG 325
 OY 1091 AGAAAAAGAGAACCCAGCTGCAACCTCATTTAGTGTGTTGGCTAGTTAGAGAGCTG 1150
 DB 326 AGAAGGAGGAGGAGGAGCGGAGCAACCTCATTCAGGCTGCTGCTGCTGCTGCTG 385
 OY 1151 ATGAGAAATCTGTTTCCATTGCAAC 1176
 DB 386 ATATGAGCGGCGCTACTGACAGCC 411

ID AAS74833 standard; cDNA; 2121 BP.
 XX
 AC AAS74833;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #10637.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HXSE-) HXSEQ INC.
 XX
 PI Drmanac R, Liu C, Tang YF;
 PI WPI: 2001-639362/73.
 DR P-PSDB; ABG10646.
 DR
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 1; SEQ ID NO 10637; 103pp; English.
 CC
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
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 SQ Sequence 2121 BP; 406 A; 675 C; 696 G; 344 T; 0 other;
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 Best Local Similarity 60.3%; Pred. No. 2.1e-22;
 Matches 226; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
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 OY 1362 GAGCTGAGCTTCAAGACCGAACCCTTCCGGCCCTGCGTCCGCTCAAAAGTTCTCA 1421
 DB 798 GAGCTGAGCTTCCGGGAGCCGACCGGAGCCGACGCTTTCGATCAAGAGGTGGC 857
 OY 1422 GCCAAAACAGTGAATGATGCTGACACAGCCCTTGGCACTGATGATATGATGAAAA 1481

Db 858 GTACAGGC---AGAACTCAGAAAGCAAGCCTCCCCGGAGAGACATTGTGATGACAA 914
QY 1482 AGGATGCCAGTGTGATGATCATGAGAAAGCCTCACCCACCACTTAAACTGTCATTGC 1541
Db 915 GAGCTGCCCTCGCGAGTTGTGACCGAGACCTGACCCCGGCTTCAAAGTCAGACATCAG 974
QY 1542 AGCTATCAGAAATTAATTTGATGTTGCCAAAGCGAAGTTTAAAGAAACATTACSTCC 1601
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QY 1602 ATATGATGTAAAGATGTGATGAAACAATATTTCTGCTGTCATCTGAGACATGTTGTAG 1661
Db 1035 CTACGACGTGATGAGATCATGACAGCACTACGCGCCACCTGAGACATGCTGCCCG 1094
QY 1662 AATTAAAGCCTTCA 1676
Db 1095 AATTAAAGCCTTCA 1109

Search completed: June 19, 2003, 08:13:53
Job time : 641 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 04:49:01 ; Search time 6932 Seconds

(without alignments)
11637.764 Million cell updates/sec

Title: us-09-825-147-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

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25: em_pl: *
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27: em_sts: *
28: em_un: *
29: em_vt: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rod: *
36: em_hcg_mam: *
37: em_hcg_vrt: *
38: em_sy: *
39: em_hcgo_hum: *
40: em_hcgo_mus: *
41: em_hcgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2772	100.0	3111	6	AX268476	AX268476 Sequence
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4	2723.8	98.3	3074	6	AX456864	AX456864 Sequence
5	2723.8	98.3	3074	6	AF249278	AF249278 Homo sapi
6	2630	94.9	3137	6	AX056817	AX056817 Sequence
7	2630	94.9	3137	6	AF202977	AF202977 Homo sapi
8	2625.2	94.7	2694	6	AX322509	AX322509 Sequence
9	2510.8	90.6	2832	9	AF263835	AF263835 Homo sapi
10	2159.8	77.9	3108	10	AF263836	AF263836 Homo sapi
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12	965	34.8	120846	9	AL365232	AL365232 Human DNA
13	769.2	27.7	162123	2	AC115920	AC115920 Mus muscu
14	755	27.2	179192	2	AC095904	AC095904 Rattus no
15	498.6	18.0	548	6	AX318576	AX318576 Sequence
16	498.6	18.0	548	6	AX318764	AX318764 Sequence
17	492	17.7	2335	6	AX032994	AX032994 Sequence
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37	429	15.5	3232	9	AF033348	AF033348 Homo sapi
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52	339	12.2	215256	2	AC124139	AC124139 Mus muscu
53	339	12.2	267605	2	AC125483	AC125483 Mus muscu
54	339	12.2	331447	2	AC127359	AC127359 Mus muscu
55	295.6	10.7	1372	5	XL071076	U71076 Xenopus lae
56	293	10.6	293	5	HSAT272506	AJ272506 Homo sapi
57	273.6	9.9	3183	5	SAC232714	AJ232714 Squalus a
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VERSION	AX268476.1	GI:16541653	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hu X., Kiehn J.A., Turner A.C., Nehls M.C., Friedrich G.B., Zambrowicz B. and Sands A.T.		
TITLE	Human ion channel protein and polynucleotides encoding the same		
JOURNAL	Patent: WO 0175108-A 3 11-Oct-2001; Lexicon Genetics Incorporated (US) location/Qualifiers		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 3074)		
TITLE	Lecher,C., Scherer,C., Seeborn,G., Busch,A. and Steinmeyer,K. Potassium channel protein knom5, a target for diseases of central nervous system and cardiovascular system		
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REFERENCE
 1 Argenti, T.M. and Sheldon, J.H.
 Methods of selecting compounds for modulation of bladder function
 Patent: WO 0232960-A 5 25-APR-2002;
 Wyeth (US)

FEATURES
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 AUTHORS Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and Jentsch, F.J.
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 JOURNAL Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse 85, Hamburg 20246, Germany
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LOCUS Sequence 1 from Patent WO0192526.
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ACCESSION AX322509
VERSION AX322509.1 GI:18093555
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Dworetzky, S.I., Ramanathan, C.S., Trojnecki, J.T., Boissard, C.G. and
Gridboff, V.K.
TITLE Human kcnq5 potassium channel, methods and compositions thereof
JOURNML Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
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Best Local Similarity 98.9%; Pred. No. 0;
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 AF263835.1 GI:8132996
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 SOURCE
 ORGANISM
 Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2832)
 Kniazeva,M. and Han,M.
 A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders
 Unpublished
 2 (bases 1 to 2832)
 Kniazeva,M. and Han,M.
 Direct Submission
 Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA
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1 (bases 1 to 3108)
kniazeva,M. and Han,M.
A new gene of the voltage-gated potassium channel KCNQ family,
KCNQ5, is a candidate gene for retinal disorders
Unpublished
2 (bases 1 to 3108)
kniazeva,M. and Han,M.
Direct Submission
Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
Porter Biosciences Bldg., Boulder, CO 80309, USA
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BASE COUNT 830 a 779 c 748 g 743 t 8 others
ORIGIN

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Query Match 77.9%; Score 2159, 8; DB 10; Length 3108;
 Best Local Similarity 89.18; Pred No. 0;
 Matches 2351; Conservative 0; Mismatches 260; Indels 27; Gaps 1;

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 222 CTTGAGGAGAGAGCCCGGGGCAACGAGGGGCCCGGATGAGCTGCTGGGAGAGCCGT 281
 61 CTTGAGGAGAGAGCCCGGGGCAACGAGGGGCCCGGATGAGCTGCTGGGAGAGCCGT 120
 282 CTTTACAGAGAGAGCCCGGAGAGCTGGCGGCAACGATGAGCTGGGGGCTGAGAGCTA 341
 121 CTTCTACAGAGAGAGCCCGGAGAGCTGGCGGCAACGATGAGCTGGGGGCTGAGAGCTA 180
 342 CTTGAGAGAGAGAGCCCGGGGCAACGAGGGGCCCGGATGAGCTGGGGGCTGAGAGCTA 401
 181 TCTGTACAGAGAGAGCCCGGGGCAACGAGGGGCCCGGATGAGCTGGGGGCTGAGAGCTA 240
 402 TCTGCTGCTGCTGGGCTGCTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGAT 461
 241 TCTGCTGCTGCTGGGCTGCTGATGCTTGTGATGCTTGTGATGCTTGTGATGCTTGTGAT 300
 462 ATTGAGAGAGAGAGCCCGGGGCAACGAGGGGCCCGGATGAGCTGGGGGCTGAGAGCTA 521
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 642 AGCAGTGTGCTGCAAAACCTGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
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Dp	2101	CTGGGCATCAAGACACTGTCCAGGCGAAGAACTCTGCTCTCAAAACCCACGGCTTACA	2166
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Qy	2475	CCGTATCAGGTCGACCGAGAACCTAATACAACTTTAGGAGTGTAGTCAAGTGCCTC	2534
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Qy	2595	AGAGGTGGGTCGCGAAGAGACAGACACTTTTGATGCGCACCGCAGCCTGCGAC	2654
Db	2461	GGAGGTGGGTCGCGAAGAGACAGAAACAGATACCTTTTGAGCGGACCCACCGCTGGGG	2520
Qy	2655	GGAAGCTGCTTTGCAATCAGACTCTTAAAGCACTGGAGGTCAAGATCATCTAGACAT	2714
Db	2521	GGAGGTGCTTTTCTCATCAGACTCTTAAAGCACTGGAGGTCAAGTCAATCTAGAACAT	2580
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ACCESSION	AJ272519		
VERSION	AJ272519.1	GI:18873690	
KEYWORDS	KCNQ5 gene; KCNQ5 protein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and Steinlein,O.K.		
TITLE	The new voltage gated potassium channel KCNQ5 and earlyinfantile convulsions		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1691)		
AUTHORS	Steinlein,O.K.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-FEB-2000) Steinlein O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY		
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ORIGIN			

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Db	344	GGAAGGCTTGCCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTG	403	
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Db	404	AACAGACATCTGACTATCAAAAGCCCTGGGATAGCAAAAGATCTTTGGGTTCCGCACAAA	463	
QY	1988	ACAGTGGCTCTTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTCGTAGTTCAATTC	2047	
Db	464	ACAGTGGCTCTTATCCAGATCAACTAGTGGCAACATCTGAGAGGCTCGTAGTTCAATTC	523	
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Db	524	TGACGCCAATAGATTCAGTGGCCAGACTTTTACGGCTTAGCCCTACTATGACAGTC	583	
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QY	2528	GTGGGTCACAGAGCAGCCAGATTTTTTAAACCCAAATGGAGGAATCCAAATGTTTTATA	2587	
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QY	2648	CTGCCAGGGAGGTGGCTTGGATCAACACTCTTAAGAGCTGGAAGGTACAGATCAATCTC	2707	
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RESULT 12
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DEFINITION
AL365232
ACCESSION
AL365232
VERSION
AL365232.24
KEYWORDS
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GI:13234949
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 120846)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Mar 5, 2001 this sequence version replaced g1:13160293.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/chr6
Rpl1-257K9 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
Rpl1-257K9 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone Rpl1-257K9 is at 1 in this sequence. The
true left end of clone Rpl-319022 is at 120747 in this sequence.
The true right end of clone Rpl1-380K3 is at 18652 in this
sequence.

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/note="TRHC repeat: matches 1..371 of consensus"
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repeat_region 13931..14179
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repeat_region 14522..14579
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repeat_region 16405..16696
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repeat_region 16697..16722
/note="L3 copies 2 mer ga 92% conserved"
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repeat_region 18473..18730
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repeat_region 18829..19080
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repeat_region 19213..19412
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repeat_region 19507..19632
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repeat_region 21835..21924
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repeat_region 27647..27824
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QY 2468 TGCAAACCTGATCAGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2527
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DEFINITION pieces.
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VERSION AC115920.3 GI:21536151
KEYWORDS HTG, HTGS_PHASE2, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 162123)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-496H1
JOURNAL Unpublished

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Db      136143 AACAGCGGCTGTTTAAAGAGGTGACGACGACGACATCTCAAGAGAGCCGACATTCATC 136084
QY      2047 CTGACGCCAAATGAGTCTAGTCCGACGACTTCTTACGCGCTTACGCCCTACTATGACACAGT 2106
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QY      2587 ACTGATGAGAGAGTGGTCCGCAAGAGACAGACAGACATTTTATGCGCGGACCGCAG 2646
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QY      2647 CTTGCCAGGAGAGTCTCTTTCATGACATCTCTTAAGAGTGAAGTGCATGATCATCT 2706
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QY      2707 CAGAGCATTTGTAAGGAGGAGAAAGTACAGATGGCTCAGCTTGGCTCATGCAAACTG 2766
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QY      2767 AAATAA 2772
Db      135363 AACTAA 135358

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RESULT 14
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LOCUS Rattus norvegicus clone CH230-10L20, *** SEQUENCING IN PROGRESS
DEFINITION *** 57 unordered pieces.
AC095904 AC095904.4 GI:21722989
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 179192)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
          Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
          Barberia,J., Benton,J., Bimarge,K., Blankenburg,K., Bonnin,D.,

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Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
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Peters,L., Pickens,R., Primus,E., Pu,L.L., Qulles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojoubkan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,P., Telford,B., Thomas,N., Thomas,S.,
Umanli,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
2 (bases 1 to 179192)
Worley,K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 179192)
Worley,K.C.
Direct Submission
Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17943539.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVD
Center clone name: CH230-10L20
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 128957 bases at least Q40
Consensus quality: 135269 bases at least Q30
Consensus quality: 140867 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Best Local Similarity 87.0%  Pred. No. 2,1e-152;
Matches 841; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

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VERSION	AX318576.2	GI:21713342			
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1				
TITLE	Fernandes,E., Vernet,C.A., Mishnu,V.S., Leach,M.D., Shinkets,R.A.,				
JOURNAL	Orf's polynucleotides and polypeptides				
COMMENT	Patent: WO 0177155-A 81 18-OCT-2001;				
FEATURES	Curagen Corporation (US)				
SOURCE	On Jul 8, 2002, this sequence version replaced gi:17900990.				
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REFERENCE	1
AUTHORS	Fernandes,E., Vernet,C.A., Mishnu,V.S., leach,M.D., Shinkets,R.A., zerhusen,B.D. and Kekua,R.
TITLE	Orex polynucleotides and polypeptides
JOURNAL	Patent: WO 0177155-A 269 18-OCT-2001;
FEATURES	Cutagen Corporation (US)
source	Location/Qualifiers 1..548

BASE COUNT	ORIGIN
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194 g	119 t

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OY	554	GTTTGCAATATGAGATGAGCAAGAAAGCATGAGTTTGTCTGAAGCCCTTC	606
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ACCESSION	AX032994
VERSION	AX032994.1 GI:10279897
	PAT 21-SEP-2000
	linear

SOURCE ORGANISM	human.	Homo sapiens

REFERENCE 1 (bases 1 to 2335)

TITLE Novel potassium channels and genes encoding these potassium channels
DATA PNAS 95:10347-52, 1998
DATE 1998-03-01

FEATURES	Location/Qualifiers
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CDS 83. .2170

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BASE COORD	DATE	TIME	LOCATION
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Db	320	TACCGCGGGCTGAGAAACTGGGCTCTACAAAGTGCCTGGAGGGGCGCGGGCTGGCGCTTC	379	
QY	382	ATCTACCAACGCTTTCGTTTCTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	441	
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QY	442	ACCATCCCTGCAGACACAAATAATGGGCTCAAGTTCGCTGTATTCGTATTCGTATTCGTATTCGTATTC	501	
Db	440	ACATATCCAGAGAACACAGAACTTGGCCAAACGAGTGTCTCTCATCTTGGAAATTCGTATTCGTATTCGTATTC	499	
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QY	562	TATAGAGGATGSCAAGAAAGACTGAGGTTTGCCTGAAAGCCCTTCCTGTATATAGATAC	621	
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QY	622	ATATGCTGTCTTATGCTCTCAATAGACATGTTTTCGCAAAACCTCAGGGTATATTTTGGC	681	
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QY	682	ACGCTGTCACTGCAGAACTCCCTTCCTTCAGATTCCTCCGATGCTGCATGAGACGA	741	
Db	680	ACGCTGTCACTGCAGAACTCCCTTCCTTCAGATTCCTCCGATGCTGCATGAGACGA	739	
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Db	740	CGGGGGGGACCTGGAAAGCTGTGGGGCTCATGGCTTACCGGATAGCAAGAGAGCTATTC	799	
QY	802	ACAGCTTGGACATATAGATTTTGGTTCTTATTTTTCGCTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	861	
Db	800	ACAGCTTGGACATATAGATTTTGGTTCTTATTTTTCGCTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	859	
QY	862	GAAAAGGATGCCAATAAAGATTTTCTTACATATGACAGATGCTCTGTGGGGCACATTT	921	
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QY	922	ACATTTGACAACTATTTGGCTATGAGACAAAACCTCCCTAATTGGCTGGGGAAGTTTGGCTT	981	
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QY	982	TCTGACAGGCTTTGGCACTTCTTGGATTTCTTTCTTTCACATTCCTGTCCGGGCACTTCTTC	1041	
Db	980	GCTGTGTGGCTTCGGCTTACTTGGGATCTCTTTCTTTCCTTCCTGTCCGGGCACTTCTTC	1039	
QY	1042	TCAGGTTTTCGATTTAAAGTATACAGAAACACCGCCAGAAACACTTTGAGAAAAAGAG	1101	
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QY	1102	TAACCAAGCTGCAACCTCATTCAGTGTGTTTGGGCTAGTTACGAGGCTGATGAGAAATCT	1161	
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Db	1862	AGGAAGGCCCGGAGAGAGGCGACAAAGGGCCCTTCGACGGGAGGTGTGATGAATTC	1921
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Db	1922	ACCATATATGGGAGCGCGTGTCAAGAGTGGAGAAAGCAGTGCAGTCCATCGACGACAAGCTG	1881
OY	1834	GACTGCTTACTACATCTATCAACAGAGTCCCTTGGAAAAAGGTCTGCGCTCAGCCCTCGCT	1893
Db	1982	GACCTGCTGTGGGCTTCTATATGCGCTGCTGC-----GCTTGGGACCTTGGGCAAGC	2035
OY	1894	TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGATCTGACATCAAAACCCCT	1953
Db	2036	CTGGGCGCGGTGCAAGTGCCTGTTGTGACCCCGCAATCACTCGAGTACACAGACCCCT	2095
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Db	2096	GTGGACCAAGAGACATCTCGTCTCGCACAGAA	2129
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LOCUS	AX456863	2335 bp	DNA linear
DEFINITION	Sequence 4 from Patent WO0232960.		
ACCESSION	AX456863		
VERSION	AX456863.1	GI:21715730	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Argentiari,T.M. and Sheldon,J.H.		
JOURNAL	Method of selecting compounds for modulation of bladder function		
FEATURES	Patent: WO 0232960-A 4 25-APR-2002;		
	Wyeth (US)		
	Location/Qualifiers		

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QY 1894 TTGGCTTCAATCCAGATCCAGCTTTTGAATGTAAGACAGATCTGACTATCAAGCCCT 1953
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Db 2096 GTGATAGCAAGAGATCTTGGGCTTCCGACAAA 2129

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RESULT 19
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LOCUS Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA,
DEFINITION complete cds.
ACCESSION AF105202
VERSION AF105202.1 GI:4262522
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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REFERENCE
1 (bases 1 to 2335)
AUTHORS Kubisch,C., Schroeder,B.C., Friedrich,T., Luejohann,B.,
El-Amraoui,A., Marlin,S., Petit,C. and Jentsch,T.J.
TITLE KCNQ4, a novel potassium channel expressed in sensory outer hair
JOURNAL cells, is mutated in dominant deafness
MEDLINE Cell 96 (3), 437-446 (1999)
PUBMED 99148276
10025409
REFERENCE
2 (bases 1 to 2335)
AUTHORS Kubisch,C., Schroeder,B.C., Friedrich,T., Luejohann,B. and
Jentsch,T.J.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1998) Zentrum fuer Molekulare Neurobiologie
Hamburg (ZMNH), University of Hamburg, Martinstrasse 85, Hamburg
20246, Germany
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ORIGIN
Query Match 17.7%: Score 492; DB 9; Length 2335;
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Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;
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 QY 1834 GACTGCTTACTAGACATCTTATCAACAGTCTTCTGGAAGAGCTCTGCTCAGCCCTGCT 1893
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 QY 1894 TTGCGTTCATTCAGATCCAGACCTTTTGAATGTAAGACAGACATGATGATCAAGCCCT 1953
 Db 2036 CGGGGCGCGTCAAGTGGCGCTGTTGACCGCCGACATGACCTCGATACACAGCCCT 2095
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 Db 2096 GTGACACAGAGGACATCTCGTCCGACAGAA 2129

RESULT 20

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DEFINITION Mus musculus mRNA for alternative splicing: see accession between
 AB000497 and AB000504.
 ACCESSION AB000497.1 GI:4176399

VERSION mk02.4; alternative splicing.
 KEYWORDS Mus musculus cDNA to mRNA.
 SOURCE Mus musculus

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)
 Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
 Sasai, H. and Nishii, Y.

TITLE KQT2, a new putative potassium channel family produced by
 alternative splicing. Isolation, genomic structure, and alternative
 splicing of the putative potassium channels

JOURNAL Recept. Channels 5 (5), 255-271 (1998)
 MEDLINE 98330948
 REFERENCE 2 (bases 1 to 2827)
 Watanabe, H.

JOURNAL Direct Submission
 Submitted (14-JAN-1997) Hirofuka Watanabe, Japan Tobacco, Inc.,
 Pharmaceutical Basic Research Lab.; 6-2, Umeagoka, Aoba-ku,
 Yokohama, Kanagawa 227, Japan (E-mail: watanabe@etcl.jti.co.jp,
 Tel: 045-972-5741)

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 VERSION mKOT2.3; alternative splicing.
 KEYWORDS Mus musculus cDNA to mRNA.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (sites)
 AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasaki,H. and Nishi,Y.
 TITLE KOT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
 JOURNAL Recept. Channels 5 (5), 255-271 (1998)
 MEDLINE 98330948
 REFERENCE 2 (bases 1 to 2899)
 AUTHORS Watanabe,H.
 TITLE Direct Submission
 JOURNAL Submitted (14-JAN-1997) Hirota Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umeogaki, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)

FEATURES
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polyA_site
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 Query Match 17.1%; Score 474.8; DB 10; Length 2899;
 Best Local Similarity 57.9%; Pred. No. 4.8e-92;
 Matches 925; Conservative 0; Mismatches 607; Indels 66; Gaps 2;

169 GGCCTGCTACTGCTGGGACCCGCGGACGCTGCGGCGCGGCGGCTGAGG 228
 153 GGGTGTGTGGGGCTGGACCCCGCGCGCTGCTCCACAGCGAGCGCGCTATCATC 212
 QY 229 GAGAGCGCGCGGGGAAACAGGCGGCGCGGAGAGCGCTCTGGGGAAGCCGCTCTAC 288
 Db 213 GCGGGCTCCGAGGCCCGCAAGCGCGGACGTTTGAAGCAAGCGGAGCGGCGCGG 272
 QY 289 ACGAGTAGCCAGAGCTGCGGCGCAACGTCAGTACCGCGGCGGAGCAAGTAC 348
 Db 273 GAGCGCGGGAAGCCCGGAGGCAAGCGCTCTACCGGAGCGAGATTCCTCTAC 332
 QY 349 AACGTGCTGAGAGACCCCGCGGCTGCTCATCTACACGCTTCTGTTCTCT 408
 Db 333 AACGTGCTAGAGCGCGCGCGGCGGCTGCTCATCTACACGCTTCTGTTCT 392
 QY 409 GCTCTTGTGCTGATTTGCTAGTGTCTTACATCTCCGAGAGCAACAAATTGGCC 468
 Db 393 GCTCTTGTGCTGCTTGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 452
 QY 469 TCAAGTTGCTCTGATCTGAGTTCGTGATGATTCGCTCTTGTGAGTTCAATC 528
 Db 453 GAGGCGCGCTCTCATCTTGAATCTGATCTGATCTGATCTGATCTGATCTGATCT 512
 QY 529 ATTGATCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
 Db 513 GTAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 QY 589 TTGCTGTAAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
 Db 573 TTGCTGTAAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 QY 649 GTTCTGCAAAAACCTGATATATTTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
 Db 633 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 QY 709 CTGAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
 Db 693 TTGCAATCTTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 QY 769 TCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
 Db 753 TCGGTAGTCTACGCTCAGCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812

QY	469	TCAGTGTCCCTTATCTCGTGGAGTTCGATATGTTGCGTTTGTTGGAGTTTCATC	528
Db	409	GAGGGGGCCCTTACTATCTCGAATAATCGTACTATGCTGGGTGGAGTACTTC	468
QY	529	ATTGCAATCTGTGTGCGGGTTGCTGTTGTGATATAGAGATGGCAAGAACTGAGG	588
Db	469	GTCGGGATCTGGGCGCAGAGGCTGCTCTCGCCGCTACGCTGGATGGAGGGGGCTCAAG	528
QY	589	TTTGTGGAAGCCCTTCTGTATATAGATACCATGTGTTATGCGTTCAATAGCAGTT	648
Db	529	TTTGGCCGGAACCGTTCTGTGTGATGACATCATGCTGTCATCGCCTCCATTTGCGGTG	588
QY	649	GTTTCTGCAAAAACTCAGGCTAATATTTTGGCCAGCTCTACACAGAAATGTCGGTTTC	708
Db	589	CTGGCCGCGGCTCCAGGGCAACGCTTTGCCAATCTCGCTCCGAGGCTGGGCTTC	648
QY	709	CTTACAGATTCCTCCGATGCTGGCGCATGGAACCCGAGGGAGGCACTTGGAAATTACTGGGT	768
Db	649	CTTCAGATTTCTGCGGATGATCCGCAATGGACCGGCGGGGAGGCACTTGGAACTCTGGGCG	708
QY	769	TCAGTGTATATGCTACAGCAAGAAATTAATACAGCTTGGAATAGATATTTTGGTT	828
Db	709	TCGTGGTCTATGCGCCACAGCAAGGAGCTGGCTACGTGCTGATCATCGGCTTCTTGTG	768
QY	829	CTTATTTTTCGTCTTTCCTTGTCTATCTGTGTGGAAAGAGATGCCAATAAAGATTTTCT	888
Db	769	CTATCTCTGGGCTGTGCTGCTGTTACTGTGACAGAAAGGGGAGAACGACACTTTTAC	828
QY	889	ACATATSCAGATGCTCTGTGGGGGGGCAAAATTAATTAATGCAACTATTTGGTATAGAGAC	948
Db	829	ACCTAGCGGATGCACTGTGTTGGGGCCGTGATACGCTGACCCACATTTGGTTACGGGGAC	888
QY	949	AAAATCCCTTAACCTTGGCTGGGAAGATTTGCTTTCGACAGGCTTGGCACTCTTGGCAAT	1008
Db	889	AAATACCCCCAGACTGGAAAGGACGAGGCTCTTGGGCAACCTTACCTTCATGGGTGTC	948
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Db	949	TCCTTCTTCGCGCTCGCTGACAGGCAATCTTGGGGTCTGGGTTTCCCTGAAGGTTACAGAG	1008
QY	1069	CAACACCGCCAGAAACAATTGAGAAAAGAAAGAACCCAGCTGCCAACTCATTCAGAGT	1128
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Db	1069	GCTGTGAGATTTACGCGCACCACTTCGCGCACAGACCTGCACTCCAGCTGACAGTAC	1128
QY	1153	---GAAAAATCTGTTTCCATTCGAAACCTGGAAAGC-----	1183
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QY	1184	-----CACACTTGAAGGCTTGCACACCTGCG	1209
Db	1189	CTGCTGAGGAACCTCAAGAGTAAATCTGAGCTCGCTTTACGAAAGAACCCCGCGCGAG	1248
QY	1210	AGCCCTACCAATCAAGAGCTAAGTTTATAGAGCAGATGCGATGGCTAGCCCCAGGGGG	1269
Db	1249	CCGTCTCCAAAGCAAGAAAGTCAAGTTTGAAGATCTGTGT--CTTCTCCACCCCCCGAGGC	1305
QY	1270	CAGAGTATTAAAGACCGCAAGACCTCTAGTAG-----GTGACAGAGAGTCCCAAGACAC	1323
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QY	1324	GACATCACAGCCAGGGGAGTCCCAACCAATGCAAGAAAGCTGAGGCTTCAAGACCGA	1383
Db	1366	GACCAAGACCTCCAGAGCAACCCCGAGAAAGGTGCCCCAAGAGCTGTGGGAGACCGC	1425
QY	1384	ACCCGCTCCGCGCTGCTGCGCGCTCAAAAAGTTTTCAGCCAAAACCAAGTATAGATGCT	1443
Db	1426	AGCCGGGCAAGCAGGCTTTCGCTATCAAGAGGTGCGCGCTCACGCGCAGAACTCAGAAAGAA	1485

QY	1444	GACACAGCCCTTGGCACTGATGATATATATGAAAGATGCCAGTGTGATATCA	150	
Db	1486	G---CAAGCCTCCCGGAGAGGACATTTGGATGACAAAGACTGCCCTGCGAGTTTGG	154	
QY	1504	GTGGGAAGACCTTACCCACCACCTTAAACTGTCAATTCGACATTCAGAAATTAATTT	156	
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QY	1564	CATGTTCGAAACGGAAGTTTAAGGAAACATTAACGTCATATGATGATAAAGATGCATT	162	
Db	1603	CTGGTGTCCAAACCGGAAGTTCAAGGAGAGGCTTCCGGCCCTTACAGCTGATGACGTCATC	166	
QY	1624	GAAACATATTTCTGCTGTTCATCTGGACATGTTGTGTAGATTAAAGCCTTCAACACGT	168	
Db	1663	GAGCAGTACTCACCGGCGCACCTGGACATGCTGTCCGAATTAAGAGCCTGCAATGCCAGA	172	
QY	1684	GTGATTCAAATTCCTTGGAAAAGGCGAAATTCACATCAGATTAAGAAAGCCGAGAGAAATA	174	
Db	1723	GTGGACCAAGATGTGGGGCGGGGCCACAGCATACAGGAGCAAGGA---CCGACACAAAGGC	177	
QY	1744	ACAGCAGAATCAGAGACCAACAGACATCTCACTATCTCTGCTCGGGTGTCTCAAGTTGAA	180	
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QY	1804	AAACAGGTACACTCCATAGATTCCAAGCTGGACTGCTTACTAGACATCTATCAACAG	1860	
Db	1840	AAGCAGGCTTGTTCATGAGAGAAAGCTGACCTTCTGTGTAATATCTACATCGAG	1896	
RESULT 25	AF074247	3195 bp	linear	PRI 16-FEB-2001
LOCUS	AF074247			
DEFINITION		Human sapiens neuronal delayed-rectifier voltage-gated potassium		
ACCESSION	AF074247			
VERSION	AF074247.1	GI:3294576		
KEYWORDS				
SOURCE				
ORGANISM		Human sapiens.		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		1 (bases 1 to 3195)		
JOURNAL		Iannotti,C.A., Dargis,P.G., Christian,E.P. and Aiyar,J.		
REFERENCE		The expression pattern of KCNQ2 splice variants in neuronal		
AUTHORS		proliferation and differentiation		
TITLE		Abstr. Soc. Neurosci. (1998) In press		
JOURNAL		2 (bases 1 to 3195)		
REFERENCE		Smith,J.S., Iannotti,C.A., Dargis,P., Christian,E.P. and Aiyar,J.		
AUTHORS		Differential expression of kcng2 splice variants: implications to		
TITLE		current function during neuronal development		
JOURNAL		J. Neurosci. 21 (4), 1096-1103 (2001)		
REFERENCE				
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Db 1924 CAAGGA---CCGACCAAGGCGCCGCGAGGAGCTGCCAGAGACCCACACATAT 1980
 QY 1782 CGGTCGGGTGTCGACGCTGGAAGAAACAGTACGTATGATCCAGCTGAGTGCCT 1841
 Db 1981 GGGACGGCTCGGGAGGTGGAAGAGCGTCTTCATGAGAGAGAGAGAGAGAGAG 2040
 QY 1842 ACTAGACATCTATCAACAG 1860
 Db 2041 GGTGATATCTACATGACAG 2059

RESULT 26
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 LOCUS Rattus norvegicus potassium channel (KCNO2) mRNA, complete cds.
 DEFINITION AF087453
 VERSION AF087453.2 GI:15795325
 KEYWORDS
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 4165)
 Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
 Cloning and sequencing of the Rattus norvegicus potassium channel
 KCNO2
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4165)
 AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-1998) University of Marburg, Inst. for
 Physiology, Deutschnaust. 2, Marburg 35037, Germany
 REFERENCE 3 (bases 1 to 4165)
 AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-2001) University of Marburg, Inst. for
 Physiology, Deutschnaust. 2, Marburg 35037, Germany
 REMARK Sequence update by submitter
 COMMENT On Sep 27, 2001 this sequence version replaced gi:3641299.
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 KLGSVYASKEVLTAMVIGFICLILASFLYLAKEGNDHFEDYADLMGLITLY
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BASE COUNT 866 a 1194 c 1203 g 902 t

Query Match 16.2%; Score 448.4; DB 10; Length 4165;

Best Local Similarity 56.1%; Pred. No. 2,6e-86;
 Matches 1023; Conservative 0; Mismatches 666; Indels 135; Gaps 4;

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 Db 189 GCGTTGGTGGGCTGAGACCCCGGCGCGCCGACCTCCACTCCGCGAGCGCGCTACTCATC 248
 QY 229 GAGAGCCCGCGGCGCAAGCAGGGGGCCCGATGAGCTGTGGGAGACCGCTCTTAC 288
 Db 249 GCGGGCTCGAGGCGCCCAAGCGCGGCGGCGCTTTGAGCAAGCGCGGAGCGGCGGCG 308
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 QY 589 TTTGCTGGAAG 648
 Db 609 TTTGCTGGAAG 668
 QY 649 GTTCTGCAAAAACATCAGGAGTATATATTTTCCACATCTGCTGCTGCTGCTGCTGCTG 708
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 QY 709 CTACAGATCTCTGCGATGCTGCGCATAGACCGGAGGAGGAGGAGGAGGAGGAGGAGG 768
 Db 729 TTACAAATCTTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 788
 QY 769 TCAGTGGTTTATGCTACACAGCAAGATTAATACAGCTTGTATAGATAGATTTTGGTT 828
 Db 789 TCGGTGCTTACGCTACAGCAAGAGAGCTGTATGCTGTATGCTGTATGCTGTATGCTGT 848
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 QY 1009 TCTTTCTTGTGACTTCTGCGCGCATTTCTTGTGAGGCTTGTGATCTTAAAGATCAAGAA 1068
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 QY 1069 CAACAGCGCGCAAG 1128
 Db 1089 CAGATCGGCAAAAACATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
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 QY 1150 GATGAGAAATCTGTTTCACTTACCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209

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Oy	1210	AGCC-----	1213
Db	1269	AGACTATTTCGGCTCTGAAACAGCTGGAGATCTGAGGAAATCTCAAGCAATCTGGA	1328
Oy	1214	-----CTACCAATCAGAAAGTATTAAG	1239
Db	1329	CTCACCTTCAGGAAGAGCCACAGCCAGACCATCAACAGTCAAGAGGCAATCTGAA	1388
Oy	1240	GAGCGAG---TGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGACAAAGCTCA	1296
Db	1389	GATCTGTGTCTTCACAGCCCCGAGGGGTGGCTGGCAAGGGGAAGGGGTCTCCCAAGGCC	1448
Oy	1297	GTCAGTACAGAGAGTCCCCAACACCGACATCAACAGCCGAGGGCAGTCCCAACAAAGT	1356
Db	1449	CAGACGCTCCGGGGGTCCCCACATGGGATCAGAGTCTGCATGACAGCCCAACAGAGTG	1508
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Db	1629	AACAAGAGCTGTAACTCGAGTTGTGACAGGAAGATCTTACCCCTGGCTCAAAAGTACG	1688
Oy	1537	ATTGAGCTATCAGAAATTAATGAATTTTCATGTTGCCAAACAGGAAGTTAAGGAACATTA	1596
Db	1689	ATCAGACCTGTGTGTATGCTGGCTTCTTGGTATCTTAAGGAAAGTTCAAGAGAGTCTG	1748
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Db	1749	CGCCCATATGACGTGATGATGTATGATGACAGTACTCGGCCGACACTTGGATATGTTG	1808
Oy	1657	TGTAGAAATTAAGCCTTCAAAACAGCTGTGATCAAAATTTCTTGGAAAAGGCCAAATCACA	1716
Db	1809	TCCGGAATCAAGACCTGCACTGCCAGATGAGACAGATTTGGGGGCGGCCCAACATA	1868
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Oy	1837	TGCCTACTAGACATCTATCAACAG	1860
Db	1986	TTCTGTGTGAGCATCTACACACAG	2009
RESULT 27			
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LOCUS	A94975	2565 bp	DNA
DEFINITION	Sequence 2 from Patent WO931232.		
ACCESSION	A94975		
VERSION	A94975.1 GI:6779161		
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2565)		
AUTHORS	Christian,E.P., and Aiyar,J.		
TITLE	HUMAN BRAIN DERIVED KMO2 POTASSIUM CHANNEL		
JOURNAL	Patent: WO 9931232-A 2 24-JUN-1999;		
FEATURES	ZENECA LTD (GB)		
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Query Match	16.18;	Score 447;	DB 6;	Length 2565;
Best Local Similarity	56.88;	Pred. No. 4.9e-86;		
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349	AAGCTGTGAGAGAGACCCCGCGGCTGGCGGCTGATCTACACAGCTTTCGTTTCTCTT	408		
247	AAGCTGTGAGAGCGCGCGGGGCTGGGCGTTCATCTACACGCGCTACCTGTTCTCTCG	306		
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547	CTGGCGCGCGCTCCCAAGGCAACCTCTTTGGCAATCTGCGCTCGGAGCCCTGCTTC	606		
709	CTAAGATCCCTCCGATGTGGGATGAGACGCAAGAGGGAGGACCTTGGAAATTAAGTGT	768		
607	CTGAGATCTGCGGATATCTGCAATGGACCGCGGGGAGGACCTGGAAGCTGCTGGCC	666		
769	TCACTGTTTATGTGCACAGCAAGAAATTAATCACAGCTTGATACATAGATTTTGGTT	828		
667	TCTGTGTCTATGCCCACAGCAAGAGAGCTGTACCTGCTGTACATCGGCTTCTTGT	726		
829	CTTATTTTGTCTTCTCTTCTCTATCTGGTGGAAAGATGCCAATAAAGATTTTCT	888		
727	CTCATTCGGGCTCTGCTCTGTGTATCTGGCAGAAAGGGGAGAACGACACTTTTGAC	786		
889	ACATATGAGATGCTCTGATGGGGACAAATTAATTAACAATTTGGCTATGAGAC	948		
787	ACCTAAGGGATGCACTCTGTGGGGCCGTGATCAGCTGACCAATTTGGCTACGGGAG	846		
949	AAAACCTCCCTAATCTTGGCTGGGAAGATTCCTTCTGACAGGCTTTTGACATCTCTTGAT	1008		
847	AAGTATCCCGACCTCGCAAGCGAGGCTCTTGGCAGCAACTTCACTCCCTATCGGTGC	906		
1009	TCTTCTTTGCACTTCTGCGCGGCAATTTGGCTCAGGTTTTCATTAAGTACAGAA	1068		
907	TCTTCTTTCGCGCTGCTGACGACATCTTGGGGTCTGGGTTTCCCTGAAGGTTCAAGAG	966		
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RESULT 28
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 VERSION
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 SOURCE Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 5927)

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AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Cloning and Sequencing of the Rattus norvegicus potassium channel
        KCNQ3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5927)
AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) University of Marburg, Inst. for
        Physiology, Deutschauststr. 2, Marburg 35037, Germany
        3 (bases 1 to 5927)
AUTHORS Derst,C., Preisig-Mueller,R., Hennighausen,A. and Daut,J.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) University of Marburg, Inst. for
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REMARK Sequence update by submitter
COMMENT On Sep 27, 2001 this sequence version replaced gi:3641301.
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ACCESSION
AB000494
VERSION
AB000494.1 GI:4176393
KEYWORDS
mKOT2.1; alternative splicing.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
Sasai, H. and Nishii, Y.
KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the alternative potassium channels
Recept. Channels 5 (5), 255-271 (1998)
98330948
2 (bases 1 to 2935)
Watanabe, H.
Direct Submission
Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
Pharmaceutical Basic Research Lab., 6-2, Umeogoka, Aoba-ku,
Yokohama, Kanagawa 227, Japan (E-mail: watanabe@ctrl.jti.co.jp,
Tel: 045-972-5741)

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VERSION A94974.1 GI:6779160
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 REFERENCE 1 (sites)
 AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,

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 Db 573 TTGCGAGAGAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632

Db	612	CTGGGGCCGACGAGGCTGCCTGCTGCCGGTACCGTGGCTGGAGGGGGGGGCTCAAGTTGTGCCG	671
QY	597	AAAGCCCTTGTGTATTACATACCAATTGTTCTTATGGCTTCAATACGAGTGTGTTTGC	656
Db	672	GAAACCGTTTGTGTGATTTGACATCAATGAGTGCATCGCTCCATTCGCGGTGGCGCG	731
QY	657	AAAAACTCAGGGAATATTTTTTGGCACGTCTGCACCTGAGAAAGTCGCTTCCACAGAT	716
Db	732	CGGCTCCAGGGCAAGCTCTTTGGCAATCTGGCCCTCGAGCCTGGCGTTCGCGMAT	791
QY	717	CTTCCGCAATGGTGGCATGACCGAAGGGGAGGACATTTGAAATTAAGTTCAGTGGT	776
Db	792	TCAGCGGATATATCCGATGAGACCGGGGGAGGACCTGGAAGCTGCTGGGCTCTGTG	851
QY	777	TTATGCTCAGCAGGAATTAATCACAAGCTGGTGTACATAGAAATTTTGGTCTTATTT	836
Db	852	CTATGCCACAGCAAGAGAGCTGGTCACCTGGCTGTACATGGCTTCTTGTCTCATCT	911
QY	837	TTTGCTTTTCTTGTCTATCTGTGGAAAGAGATGCCAATTAAGTTTCTACATATGC	896
Db	912	GGGCTCTTCTTCTGGTGTACTTGGAGAGAAAGGGGGAAGACACCACTTTGACACCTACG	971
QY	897	AGATAGCTCTGGTGGGGGACAAATTAATTGACAACTATGGCTATGGAGACAAAACCTCC	956
Db	972	GGATGCACTCTGGTGGGGGCTGATCAGCTGACAGCTGACCACTTGTGCTACGGGGCAAGTACC	1031
QY	957	CTTACTTGGCTGGGAAGATTTGCTTTCGACAGGCTTTCGACCTCTGGCATTTCTTCTT	1016
Db	1032	CACAGACCTGGAAACGCGAGGCTCTCTGGGGCAACCTCATCCCTCATCGGTCTCTCTT	1091
QY	1017	TGCACCTTCGCGCGGCAATTCCTGGCTCAGCTTTTGGCAATTAAGTACAAAGAACACCG	1076
Db	1092	CGGCTCTCTGCAAGCATCTTGGGGGCTGTGGGTTTGCCTGAAGTTGACGAGCAGACAG	1151
QY	1077	CCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCCAAGCTCATTCAGTGTGGCG	1138
Db	1152	GCAGAACACTTTGAGAAAGAGCGGGAACCCGCGACAGAGCTGATCCAGTGGCGCTGGAG	1211
QY	1137	TAGTTACGC 1145	
Db	1212	ATTCTACGC 1220	
RESULT	36		
LOCUS	DB2346	1425 bp	linear
DEFINITION	Homo sapiens mRNA for HNSPC, complete cds.		PRI 18-MAR-1995
ACCESSION	DB2346		
VERSION	DB2346.1	GI:1841341	
KEYWORDS	HNSPC.		
SOURCE	Homo sapiens Neuroblastoma cell_line:IMR-32	cDNA to mRNA, clone:HNSPC.	
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.		
AUTHORS	1 (Stiles)		
TITLE	Yokoyama, M., Nishi, Y., Yoshii, J., Okubo, K. and Matsubara, K.		
JOURNAL	Identification and cloning of neuroblastoma-specific and nerve tissue-specific genes through compiled expression profiles		
MEDLINE	DNA Res. 3 (5), 311-320 (1996)		
REFERENCE	97191543		
AUTHORS	2 (bases 1 to 1425)		
TITLE	Yokoyama, M.		
JOURNAL	Direct Submission		
DEFINITION	Submitted (21-DEC-1995) Masahiro Yokoyama, Japan Tobacco, Inc., Pharmaceutical Frontier Research Laboratories: 13-2 Fukuura 1-chome, Kanazawa-ku, Yokohama, Kanagawa 236-0004, Japan (E-mail:masahiro.yokoyama@fms.jti.co.jp, Tel:045-786-7693, Fax:045-786-7692)		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:9606"		

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OY	777	TTATGCTCACA	GCAAGCAATTAATCACA	GCTTGGTACATAGAAATTTTGGTCTTAATTT	836
Db	852	CTATGCGCCAC	GAGCAAGGAGCTGTCAC	TGCTGTCATCGCTTCTTGTCTCATCT	911
OY	837	TTGCTGTTTCCT	TTCTATCTATCTG	TGTGAAAGATGCAATTAAGATTTTCTACATATGC	896
Db	912	GGCGCTGTCT	GTTCTGTATCTTGC	AGAGAGGGGAGAAACGACACTTTGACACTACGC	971
OY	897	ACATGCTCTCT	TGTTGGGCGACAATTA	CAATTGACAACATTTGGCTATGAGACAAACTCC	956
Db	972	GGATGCACTCT	TGGTGGGGCCATGATC	ACCGCTGACCACTATGCTGACGGGACAAGTACCC	1031
OY	957	CCTAATCTTGG	CTGGGAGAAATGCTTTC	TGACAGCTTTGACACCTCTGGACCTTTGCTT	1016
Db	1032	CCAGACCTGGA	CGGCGAGCGGCTCCTT	GGCGCAACCTTCAACCTCATGCTGCTCTTCTT	1091
OY	1017	TGCACCTTCT	CGCGGCAATTTCTG	GCTCAGGTTTGGCATTTAAAGTACAAAGACAACCG	1076
Db	1092	CCGCGTCCCT	CGACGGCACTTGGGGT	CTGGGTTCCCTGGAAGGTTCAGAGCAGCAGACAG	1151
OY	1077	CCAGAAACACT	TTTGAGAAAGAGAACCG	ACCACTGCAACCTCATTCAGTGTGTTGGCG	1136
Db	1152	GCAGAAACACT	TTTGAGAAAGAGCGGAC	CCGCGCAGCCTGTATCAGTGGCTGGAG	1211
OY	1137	TAGTTACGC	1145		
Db	1212	ATTCTACGC	1220		
RESULT 37					
AF033348					
LOCUS	AF033348	3232 bp	mRNA	linear	PRI 21-JAN-1998
DEFINITION	Homo sapiens potassium channel (KCNO2) mRNA, complete cds.				
ACCESSION	AF033348				
VERSION	AF033348.1	GI:2801451			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 3232)				
AUTHORS	Singh, N.A., Charlier, C., Stauffer, D., Dupont, B.R., Leach, R.J., Mellis, R., Ronen, G.M., Bjerre, I., Quattlebaum, T., Murphy, J.V., McHarg, M.L., Gagnon, D., Rosales, T.O., Peiffer, A., Anderson, V.E. and Lebert, M.				
TITLE	A novel potassium channel gene, KCNO2, is mutated in an inherited epilepsy of newborns				
JOURNAL	Nat. Genet. 18 (1), 25-29 (1998)				
MEDLINE	98085864				
PUBMED	9425895				
REFERENCE	2 (bases 1 to 3232)				
AUTHORS	Singh, N.A., Charlier, C., Stauffer, D., Dupont, B.R., Leach, R.J., Mellis, R., Ronen, R.M., Bjerre, I., Quattlebaum, T., Murphy, J.V., McHarg, M.L., Gagnon, D., Rosales, T.O., Peiffer, A., Anderson, V.E. and Lebert, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-NOV-1997) Human Genetics, University of Utah, 2030E				
FEATURES	15N Room 2100, Salt Lake City, UT 84112, USA				
Source	1.3232				
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 DB 1462 TCAGAGTTCAGCTTCTGCGAGATGCTGAGATGCGCGGAGAGACCCCTTA 1521
 QY 1529 AACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1588
 DB 1522 AGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1581
 QY 1589 AACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1648
 DB 1582 AGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1641
 QY 1649 ACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1697
 DB 1642 ACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1690

RESULT 40
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 LOCUS Homo sapiens potassium channel homolog (KCNQ3) mRNA, partial cds.
 DEFINITION AF033347 GI:2801449
 VERSION AF033347.1
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1. (bases 1 to 2755)
 Charlier, C., Singh, N.A., Ryan, S.G., Lewis, T.B., Reus, B.E.,
 Leach, R.J. and Lepelet, M.
 A pore mutation in a novel KQT-like potassium channel gene in an
 idiopathic epilepsy family
 Nat. Genet. 18 (1), 53-55 (1998)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
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 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8q24"
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 TVSGDWLLETFATIFGAEFALRIWAGCCCRKGMGRILKPAKRLMDLFIYI
 ASVPVAVGNOGNVATSLRSLFQILMLRMDRGKTKLGLSALCHSKELITVM
 YIGFLTLISFLVLYLVKEDVDEVDAGGEEMKEEFTYADALWGLTITIGDGT
 KTFEGRLIAATFSLIGVSPFALPAGILSGIALKVOEORHGFERRRPAELIOA
 AMRYATNPNRDLVATVRFESVVSFPFERRKOLBAASOKIGLIDRVLSNPRGSN
 TKGKLEPTNVAIESPSPKPKPVGLINKERPTAFKMAVYFOWSSDAGGDPVA
 EDRTGNDPFIEDMPTLTKAATRAVATILDRILYKKFKELRLRYDVADVQYSAGHL

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 TPGSMPLSTSDGISDSVWTPSNKFI*
 BASE COUNT 673 a 754 c 729 g 599 t
 ORIGIN

Query Match 15.3%; Score 425.4; DB 9; Length 2755;
 Best Local Similarity 57.2%; Pred. No. 2.4e-81;
 Matches 905; Conservative 0; Mismatches 621; Indels 57; Gaps 5;

QY 163 GCGAGCGGCTCTACTGCTGCGACACCGCGGCGCCACCGCTGCGGCGGCGGCTG 222
 DB 1 GCGAGCGTGGAGAACTCACTTGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCTG 60
 QY 223 CTGAGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 282
 DB 61 CTGCTGAGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 120
 QY 283 TCTTACAGAGTACCGAGAGCTGCC-----GCGCAACGTCAATACCGGCGGCTG 333
 DB 121 CTGCGCAAGACCGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 180
 QY 334 CAGACTACCTGTACACAGTGTGAGAGAGACCGCGGCGGCGGCGGCGGCGGCTG 393
 DB 181 CAAACTTGTATACAGAGCGGCTGAGAGAGACCGGCGGCGGCGGCGGCGGCGGCTG 240
 QY 394 TTGCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
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 QY 454 CACACAAATTTGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 513
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 QY 514 GCTTGGAGTTCATCATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
 DB 361 GGAGCCGAGTGTGCTTGGAGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 574 CAGGAGAGCTGAGTGTGCTGCGAAGCGCTTGTGTATAGATACCTGTTCTTATC 633
 DB 421 CGGGCGGAGCTGAGTGTGCTGCGAAGCGCTTGTGTATAGATACCTGTTCTTATC 480
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 DB 481 GCTTCTGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537
 QY 694 AGAGTCTCGTTCCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
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 DB 718 CCAGAGTGTGATGCCAAGAGAGAGAGATGAAGAGAGATTTGAAGACATAGAGATGTC 777
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 DB 778 CTCTGCTGGGCGCGTATCACTGCGCACCACTTGGCTATGAGAGACAAGACCAACCAAG 837
 QY 964 TGGCTGGAGAGATTTCTTCTGAGGCTTGGACCTTGGATTTCTTCTTCTTCTTCTTCTTCTTCT 1023
 DB 838 TGGAGAGCGCGCTGATTTGCGCGCACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 897

OY		102	CCTGCCGCATTCCTTGGCCACAGTTTGCAATTAAAGTACAAGAACAACACCAGCAGAAA	1083
Db		898	CCAGCGGCGATTCCTTGGGTCCGGGCTCGGCCCTCAAGGTGCAGAGAACACCCGTCAAG	957
OY		1084	CACCTTTGAAGAAAGAAGNAACCCAGCTGCGCAACTCATTCAGTGTGTTGGCGTAGTAC	1143
Db		958	CACCTTTGAGAAAGAGAGAGAGCCAGCTGCTGAGCTCATTCAGGCTGCTGGAGGTATTAT	1017
OY		1144	GCAGCTGATGAGAAATCTGTTCCATTTG-----CAACCTGGAAGCCACACTTGAAG	1194
Db		1018	GCTAACCAACCCCACAGGATTGACCTGTGGCGACATGAGATTTTATGAATCAGTGTCT	1077
OY		1195	GCCCTTGACACCCCTGAGCCCTTAACCATAGAAGCTTAAGTTTAAAGACGATGCCATG	1254
Db		1078	TCTTTTCTTCTTCTTCAGAGAAAGAACAGCTGGAGGCGCATCCAGCAAAGCTGGGTCTC	1137
OY		1255	GCTAGCCCCACAGGGCCAGAGTATTAAAGCCGACAAACCTCAGTAGGTGACAGAGGTCC	1314
Db		1138	TTGGATGGGTTTCGCTTCTTAATCTCTGTGTAGCAATACTAAAGAAAGCTATTATACC	1197
OY		1315	CCAAGCACCCGACATCACAGCCGAGGGCAGTCCACCAAAGTCCAGAGAGCTGGACCTTC	1374
Db		1198	CTCTCTGATGATGATGTCCTATGAAAGAAAGTCTCTTAAAGAAACCAAAGCCTGTGGCTTA	1257
OY		1375	AACGACCGAACCCTTCCTCGGCGCCCTCGGTGGCCCTCAAAAGTTTCAGGCCAAACCAAGT	1434
Db		1258	AACAATTAAGAGGCTTCCGACGGCCCTTCGCGATGAAAGCCCTAGCCTTTCTGGC----	1312
OY		1435	ATMGATGCTACACAGCCCTTGGCAGCTGATGATGTATGATGAAANAAGATGCCAGTGN	1494
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RESULT 41				
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LOCUS				
DEFINITION			Human mRNA for a K+ channel protein.	
ACCESSION			E13516	
VERSION			E13516.1 GI:3252321	
KEYWORDS			JP 1997J191882-A/1.	
SOURCE			Homo sapiens.	
ORGANISM			Homo sapiens.	
REFERENCE				
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
JOURNAL			(bases 1 to 1182)	
			Yokoyama,M., Nishi,Y., Matsubara,K. and Ookubo,K.	
			DNA CAPABLE OF CODING HUMAN NEW K+ CHANNEL PROTEIN AND ITS FRAGMENT	
			Patent: JP 1997J191882-A 1 29-JUL-1997;	
			JAPAN TOBACCO INC	
COMMENT				
			OS Homo sapiens (human)	
			PN JP 1997J191882-A/1	
			PD 29-JUL-1997	
			PI 16-JAN-1996 JP 1996004726	
			PT YOKOYAMA MASAHIRO, NISHI YOSHISUKE, MATSUBARA KENICHI, PI	
			OOKUBO KIMISAKU	
			PC C12N15/09,C07H21/04,C12Q1/68//C07K14/47;	
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Matches 632; Conservative	0; Mismatches 345; Indels 0; Gaps 0	
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Qy	229	GAGAGCCGCCGGGGCAAGAGGGGGCCGGATGAGCTCTGGGGAAGCGCGCTCTTAC 288
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Qy	289	ACGAGTAGCAGAGCTGCGCGGCGGCACATCAATGACCGCGGGGTGACAACTACCTGAC 348
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Qy	349	AACGTGCTGAGAGAGACCCCGCGGTGGGGGTTCATCTACACGCTTTCCTTTTCCTT 408
Db	247	AACGTCTGAGACGGCGCGCGGTGGGGGTTCATCTACACGCTTTCCTTTCCTT 306
Qy	409	GCTTTGGTGTGATTTTGTCAATGTTTACCATCTCTGACACACAATAATGGCC 468
Db	307	GTTTTCCTGCTGCTGCTGTCTGTCTGTGTTTCCACATCAAGAGATGAGAGAGCTCG 366
Qy	469	TCAAGTTGCCCTTGATCTCGAGTTCGATGATTTGCTGCTTGGTTGGAGTTTAC 528
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Qy	589	TTTGGTCAAAAGCCCTTCTGTGTATTACATTCATTTTATTCGTTCAATATGACTT 648
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Qy	709	CTACAGATCTCCGATGCGGATGAGACCGAAGGGAGGCACTTGGAAATTAAGTGGT 768
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Qy	769	TCAAGTGTATTATGTCACAGCAAGAAATTAATCAAGCTTGTGTACATAGATTTTGGTT 828
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Qy	829	CTTATTTTTCGCTTCTTCTGTATCTGTTGTAAGAAAGATGCGCAATTAAGACTTTTCT 888
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Qy	889	ACATATGACAGATCTCTGTTGGGGGACAAATTAATGCACTATTTGCTATGAGAC 948
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Db 847 AACGTACCCCGAGACCTGGAAGCGAGCGCTCTTCGCGGACCTTACCTCCTCCTGCTGTC 906
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RESULT 42
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 LOCUS DEFINITION Homo sapiens, potassium voltage-gated channel, KQT-like subfamily,
 accession BC000699.1 GI:12653820
 VERSION BC000699.1
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1314)
 Strausberg, R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgaphs-remail.nih.gov
 Tissue Procurement: ATCC
 Tissue Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nsl.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J.,
 Tlonsgon, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-R. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRRL Plate: 5 Row: n Column: 20
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 2801451.
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 53. 1234
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 subfamily, member 2"

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Query Match 15.3%; Score 425; DB 9; Length 1314;
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 QY 229 GAGAGCGCGGGGCAAGCAGGGGCGCGATGAGCTGTGGGAAGCGCTCTTAC 288
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REFERENCE	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS
1 (sites)	Nakanura, M., Watanabe, H., Kudo, Y., Yokoyama, M., Matsumoto, T., Sasaki, H. and Nishii, Y.	KOT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels	98330948	2 (bases 1 to 2014)	Watanabe, H.
3	Submitted (14-JAN-1997) Hirokawa Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umesoko, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, tel:045-972-5741)				
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QY	529	ATTCAAAATGCTGTGCGGGTGTGCTGTTGTCATATAGACGATGCAAGAGACTGAG	588		
DB	513	GTCAGATGTGGGCTGACGAGCTGTGTTCCGGTATCAGAGCGTGGAGGGGAGGCTCAAG	572		
QY	589	TTTGCTCGAAGCCCTCTGTGTATAGATACCAATGTTTATCGCTTCAATAGACAGTT	648		

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Db		633	CTGGCTGCTGTGTTCCCAAGGGCAATGTCTTTGGCCAACTCTGCGCTTGGAGCTTCGGTTC	692
Qy		709	CTACAGATCCTCCGCATGTGTGCGCATATGACCAGGAGGGAGCGACTTTGGAAATTACTGGT	768
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Qy		769	TCAGTGGTTTATGCTCAACAGCAAGGAATTAATACAAGCTTGATACATAGAGATTTTGGT	828
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LOCUS			Mus musculus mRNA for alternative splicing;see accession between	
DEFINITION			AB000494 and AB000504, complete cds.	
ACCESSION			AB000503	
VERSION			AB000503.1 GI:4176411	
KEYWORDS			mKQT2.10; alternative splicing.	
SOURCE			Mus musculus cDNA to mRNA.	
ORGANISM			Mus musculus	
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.	
			I (sites)	
TITLE			Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,	
			Sasai,H. and Nishii,Y.	
			KQT2, a new putative potassium channel family produced by	
			alternative splicing. Isolation, genomic structure, and alternative	
			splicing of the putative potassium channels	
JOURNAL			Recept. Channels 5 (5), 255-271 (1998)	
MEDLINE			98330948	
REFERENCE			2 (bases 1 to 1689)	
AUTHORS			Watanabe,H.	
TITLE			Direct Submission	
			Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,	
			Pharmaceutical Basic Research lab.; 6-2, Umeogoka, Aoba-ku,	
			Yokohama, Kanagawa 227, Japan (E-mail:watanabetercrl.jtl.co.jp,	
			Tel.:045-972-5741)	
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1689
polyA_site

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BASE COUNT      324 a 459 c 489 g 417 t
ORIGIN

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Query Match      15.1%; Score 419.4; DB 10; Length 1689;
Best Local Similarity 64.8%; Pred. No. 4.3e-80;
Matches 621; Conservative 0; Mismatches 336; Indels 0; Gaps 0;

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RESULT 46

AB000502

LOCUS AB000502 1227 bp mRNA linear ROD 23-JAN-1999

DEFINITION Mus musculus mRNA for alternative splicing:see accession between

AB000494 and AB000504, complete cds.

ACCESSION AB000502

VERSION AB000502.1 GI:4176409

KEYWORDS MKOT2.9; alternative splicing.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (sites)

Authors Nakamura, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,

Sasai, H. and Nishi, Y.

KOT2, a new putative potassium channel family produced by

alternative splicing. Isolation, genomic structure, and alternative

splicing of the putative potassium channels

Recept. Channels 5 (5), 255-271 (1998)

98330948

2 (bases 1 to 1227)

Watanabe, H.

Direct Submission

Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,

Pharmaceutical Basic Research Lab., 6-2, Umeogoka, Aoba-ku,

Yokohama, Kanagawa 227, Japan (E-mail:watanabe@cr1.jtl.co.jp,

Tel:045-972-5741)

FEATURES

Source Location/Qualifiers

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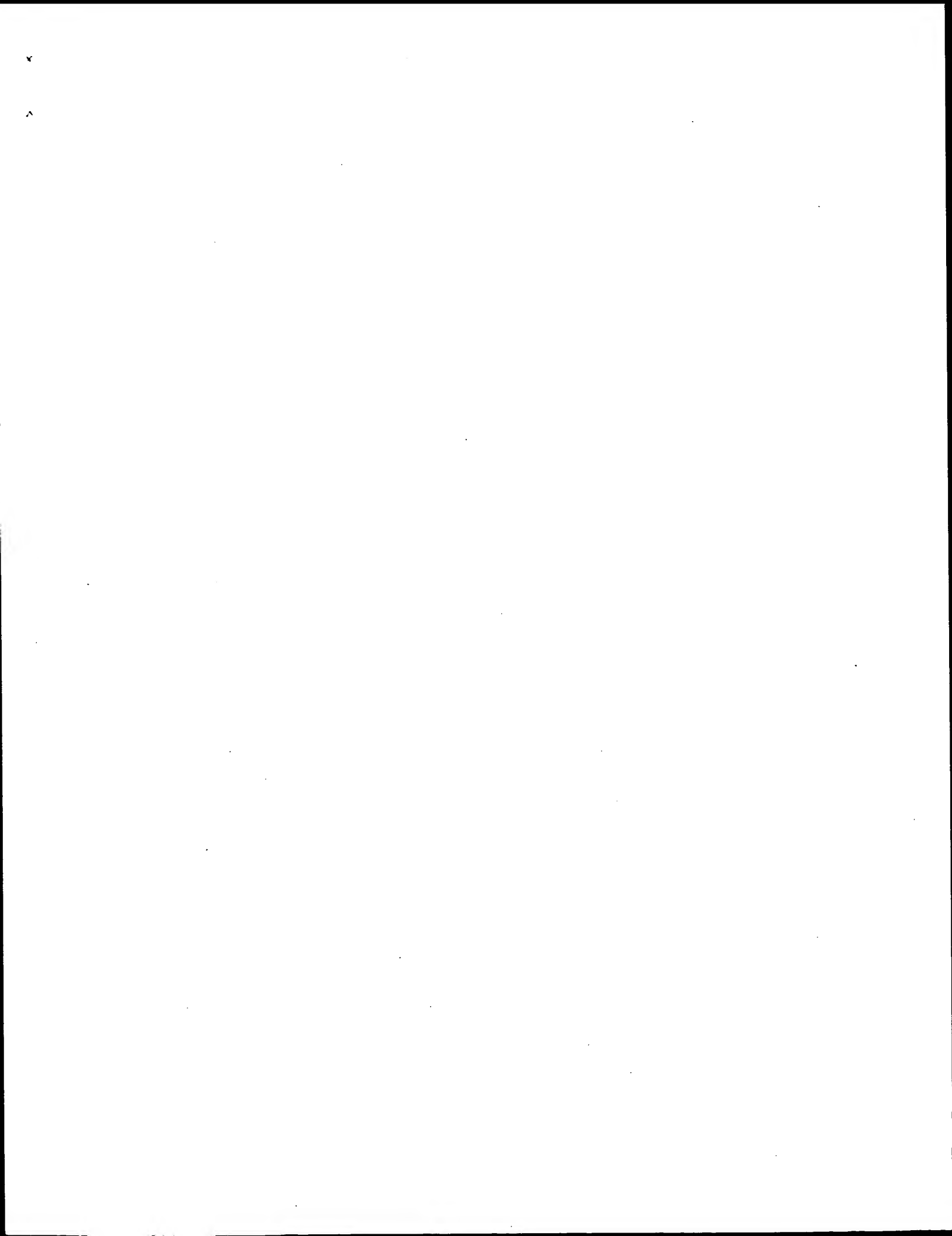
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OY	626	TTCTTATCGCTTCAATAGCAGTGTTTCTGCAAAAACCTAGGTAATATTTTGGCACGT	685
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OY	686	CTGCACCTCAGAAGCTCCGTTTCTACAGATCTCCGCACTTGGGGCATGGACGGAAGG	745
Db	699	---CCCTGGCGAGCTCGCTTCTGCGAGATCTTGGATGTGGCATATGGACCCGGAGGG	755
OY	746	GAGGCACTTGGAAATTACTGGGTTCAAGTGTTATATGCTACAGCAAGAAATTAATCAAG	805
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OY	1427	AACCACTGATAGATGTGACACAGCCCTTGGCACTGATGTATGTATGAAGAAAGAT	1486
Db	1476	GGCAGAGCTTGAAGATGCCGGGACAGGGGACCCACACGGGA-----GACAGGGGCT	1529
OY	1487	GCCAGTGTGATGTATCAGTGAAGACCTCACCCACCACTTAACATGTCATTCGAGCTA	1546
Db	1530	ACGGGAATGACTTCCATCGAACAACATGATCCCAACCTGAAAGCTGCATCCGACCGC	1589
OY	1547	TCAGAAATTAAGAAATTTTCATGTTGCAAAACGGAAGTTTAAGGAACATTAAGTCCATATG	1606

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repeat_region	8359. .8518	/note="12 repeat: matches 2352. .2507 of consensus"	
repeat_region	8896. .9177	/note="12 repeat: matches 1737. .2050 of consensus"	
repeat_region	9228. .9290	/note="12 repeat: matches 2687. .2749 of consensus"	
repeat_region	9294. .9811	/note="12 repeat: matches 1216. .1728 of consensus"	
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misc.feature	10257. .10653	/note="match: GSS: Em:AQ069885"	
repeat_region	10443. .10519	/note="MIR repeat: matches 64. .150 of consensus"	
repeat_region	10655. .10728	/note="12 repeat: matches 2065. .2122 of consensus"	
repeat_region	10729. .11038	/note="Alusx repeat: matches 1. .307 of consensus"	
repeat_region	11039. .11089	/note="12 repeat: matches 2122. .2177 of consensus"	
repeat_region	12567. .12683	/note="12 repeat: matches 2572. .2694 of consensus"	
repeat_region	12867. .13157	/note="12 repeat: matches 1995. .2283 of consensus"	
repeat_region	13380. .13920	/note="12 repeat: matches 1151. .1686 of consensus"	
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repeat_region	13982. .14216	/note="MIR repeat: matches 3. .234 of consensus"	
repeat_region	14253. .14566	/note="AluY repeat: matches 1. .310 of consensus"	
repeat_region	14592. .15509	/note="12 repeat: matches 5195. .6155 of consensus"	
repeat_region	15511. .16185	/note="12 repeat: matches 4481. .5165 of consensus"	
repeat_region	16276. .16336	/note="12 repeat: matches 2651. .2710 of consensus"	
repeat_region	16688. .16993	/note="AluSg repeat: matches 1. .305 of consensus"	
repeat_region	17161. .17455	/note="AluYo repeat: matches 1. .296 of consensus"	
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misc.feature	19429. .19831	/note="match: GSS: Em:B90569"	
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repeat_region	24456. .24578	/note="12 repeat: matches 6042. .6163 of consensus"	
repeat_region	24579. .25387	/note="12 repeat: matches 5338. .6144 of consensus"	
repeat_region	25604. .25637	/note="MER6A repeat: matches 1. .232 of consensus"	
repeat_region	26239. .26541	/note="MER2 repeat: matches 27. .340 of consensus"	
repeat_region	26544. .26707	/note="MER2 repeat: matches 476. .647 of consensus"	
repeat_region	27213. .27527		

	repeat_region	/note="Aluo repeat: matches 1..298 of consensus" 28352..28395 /note="22 copies 2 mer ta 81% conserved"
	repeat_region	29176..29316 /note="WER5B repeat: matches 172..313 of consensus"
	repeat_region	29553..29608 /note="28 copies 2 mer aa 78% conserved"
	repeat_region	29624..29663 /note="20 copies 2 mer ga 82% conserved"
	repeat_region	30427..30568 /note="LIME2 repeat: matches 5692..5945 of consensus"
	repeat_region	34962..35055 /note="MIR repeat: matches 117..201 of consensus"
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	repeat_region	41266..41537 /note="L2 repeat: matches 1681..1894 of consensus"
	repeat_region	41538..41940 /note="MLTIAI repeat: matches 1..365 of consensus"
	repeat_region	41941..42213 /note="L2 repeat: matches 1894..2176 of consensus"
	repeat_region	42354..42480 /note="MIR repeat: matches 27..155 of consensus"
	repeat_region	4518..45403 /note="LIPAV repeat: matches 5887..6141 of consensus"
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Matches 398;	Conservative 0; Mismatches 2;	Indels 0; Gaps 0;
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Dd	 4316 ATGCCCGCCACCACAGCGGAGAGAGAGAGGGCGCGCGCTGTGGTAGAAGC	43757
OY	G GGCCAGAGGGGGGGGGGGGGGGGGGGGGCTTTGGCACGGCATAAAGATCGAG	120
Dd	 4376 GGCGAGAGGGGGGGGGGGGGGGGGGGGGCTTTGGCAAGGGCATAAAGATTGGAG	44358
OY	T TCGGCGCGGGGAGAGTGTCCTCTTAACCTCGGCACCGGCGACAGGGGCGAGGGCTCTACTG	180
Dd	 4436 TTGGCGCGGGGAGAGTGTCCTCTTAACCTCGGCACCGGCGAGGGGCGAGGGCTCTACTG	44955
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Dd	 4496 CTTGGGCACCCCGCGGGCCACGCTTGGTGCGGGCGGGGTGGCTTGAGGAGAGCCCCCG	45555
OY	G GCAGAACAGGGGGGCCGATAGAGCTCTGTGGGGAAGCGCGCTTTACACAGATAGACAG	300
Dd	 4556 GCAGAACAGGGGGGCCGATAGAGCTCTGTGGGGAAGCGCGCTTTACACAGATAGACAG	46155
OY	A AGTGCGCGGCACAAGTCACTACCGGGGGGTGAGAACTACTCAACAGTGTCTGGAG	360



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 12:57:11 ; Search time 3469 Seconds
(without alignments)
12941.450 Million cell updates/sec

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Perfect score: 2772

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Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 24

Total number of hits satisfying chosen parameters: 69

Minimum DB seq length: 0
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Post-processing: Listing first 150 summaries

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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	470	17.0	547	13	BI034993
5	466	16.8	491	12	BF959488
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ALIGNMENTS

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C	11	215	7.8	267	12	BF945327	BF945327 QV2-NN004
C	12	212	7.6	266	14	BQ340178	BQ340178 QV2-NN200
C	13	179	6.5	520	17	AQ383296	AQ383296 RPTC11-13
C	14	179	6.5	659	17	AQ344243	AQ344243 RPTC11-13
C	15	158	5.7	224	12	BF954374	BF954374 QV2-NN004
C	16	144	5.2	297	14	BQ340041	BQ340041 QV2-NN004
C	17	129	4.7	268	12	BG185229	BG185229 RST4167 A
C	18	115	4.1	166	17	AQ019541	AQ019541 CIT-HSP-2
C	19	107	3.9	248	10	BE177584	BE177584 RCL1-HT059
C	20	106	3.8	267	12	BG185740	BG185740 RST4692 A
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C	22	102	3.7	160	12	BF959223	BF959223 QV2-NN004
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C	24	56	2.0	469	10	BE103175	BE103175 UT-R-BT1-
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C	26	48	1.7	434	13	BI290441	BI290441 UT-R-DK0-
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C	36	35	1.3	425	10	BE648243	BE648243 UT-M-BH2-
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C	41	31	1.1	121	12	AK020325	AK020325 Mus. muscu
C	42	26	0.9	597	10	BE549164	BE549164 UT-R-AO-2
C	43	26	0.9	622	10	BE257127	BE257127 60110867
C	44	26	0.9	749	14	BQ192564	BQ192564 UT-R-DRI-
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ACCESSION BE158938

VERSION BE158938.1 GI:8621659
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 658)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=MR0-HT0404-210>)
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 /note="Organ: head-neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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 Db 17 TGGCTATGAGACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCGACAGGCTTTGC 76
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 SOURCE human.
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 REFERENCE 1 (bases 1 to 506)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-051200-526-g09&t3=2000-12-05&t4=1>)
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 BASE COUNT 125 a 108 c 104 g 168 t 1 others

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ACCESSION	BIO33850
VERSION	BIO33850..1 GI:14440476
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 570)	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bais, G. S., Simpson, D. H., Brumstein, A. A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	

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Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV2&t2=QV2-NN2003080301-615-c09&t3=2001-03-08&t4=1>)
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/note="Organ: nervous normal; Vector: puc18; Site:1: Sma1
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESPES PCR (U.S. Letters Patent applicatio
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription o
tissue mRNA and cDNA amplification were performed under

```

BASE COUNT	135 a	122 c	131 g	182 t
ORIGIN				
Query Match	15.6%	Score 432;	DB 13;	Length 570;

Best Local Similarity 99.6%; Pred.No.1.le-210;
Matches 532; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1410	TTCTCAGCCAAAACCACTGATAGTATGCTGACACAGCCCTTGGCACTAGATGATATATGA	1475
Db	534	TTCTCAGCCAAAACCACTGATAGTATGCTGACACAGCCCTTGGCACTAGATGATATATGA	475
QY	1476	TGAAAAAGATGCGCATGTATGTATCATCGTAGGAAGACCTCACCCACACTTAAAACTGT	1535
Db	474	TGAAAAAGATGCGCATGTATGTATCATCGTAGGAAGACCTCACCCACACTTAAAACTGT	415
QY	1536	CATTGCGCATCATGATATTTGAAATTTCACTGTGCAAAAAGAGATTTAAGAAACATY	1595
Db	414	CATTGCGCATCATGATATTTGAAATTTCACTGTGCAAAAAGAGATTTAAGAAACATY	355
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QY	1656	GTGTAGAAATTAAGACCTTCAAACAACGCTTGATCAATTTCTTGAAAAAGGCAAAATAC	1715
Db	294	GTGTAGAAATTAAGACCTTCAAACAACGCTTGATCAATTTCTTGAAAAAGGCAAAATAC	235
QY	1716	ATCAGATTAAGAAGACCGAGAGAAATTAACAGACAGACATGAGACCACAGACATCTGAG	1775
Db	234	ATCAGATTAAGAAGACCGAGAGAAATTAACAGACAGACATGAGACCACAGACATCTGAG	175
QY	1776	TATCTCGGTGGGGGTCAAGGTTGAAAAACAGGTACAGTCCATAGATCAATCAACCTGGA	1835
Db	174	TATCTCGGTGGGGGTCAAGGTTGAAAAACAGGTACAGTCCATAGATCAATCAACCTGGA	115
QY	1836	CTGCGCTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCTGCTCTAGCCCTGCTTT	1895
Db	114	CTGCGCTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCTGCTCTAGCCCTGCTTT	55
QY	1896	GGGCTTCATTCAGATCCCACTTTTGATGTGGAATGGAACAGACATCTGACTATCAAG	1949
Db	54	GGGCTTCATTCAGATCCCACTTTTGATGTGGAATGGAACAGACATCTGACTATCAAG	1

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 435)	Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M., R. Nagai, M. A., da Silva, W. J., Zago, M. A., Bordin, S., Costa, F. F., Godman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brumstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496 (2000)	Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-27049822
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/RIICR Human Cancer Genome
 Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&c2=QV2-NN0045>

TITLE	JOURNAL	COMMENT
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
Contact: Simpson A.J.G.		
Laboratory of Cancer Genetics		
Ludwig Institute for Cancer Research		
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		
Tel: +55-11-2704922		
Fax: +55-11-2707001		
Email: asimpson@ludwig.org.br		
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL		
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&t2-QV2-NN0045-11100-414-108&t3-2000-11-13&t4-1)		
Seq primer: puc 18 forward		
High quality sequence stop: 517.		
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/db_xref="taxon:9606"		
/clone_lib="NN0045"		
/dev_stage="Adult"		
/note="Organ: nervous_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
low stringency conditions."		
BASE COUNT	169 a	106 c 123 g 119 t
ORIGIN		
Query Match	12.0%;	Score 332; DB 12; Length 517;
Best Local Similarity	100.0%;	Pred. No. 3.5e-159;
Matches 332; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1550	GAATTATGAAATTTTCATGTTGTCACAAACGGAAGTTTAAAGAAACATTTACGTCATATGATG 16089
DB	186	GAATTATGAAATTTTCATGTTGTCACAAACGGAAGTTTAAAGAAACATTTACGTCATATGATG 245
OY	1610	TAAAGATGTCATTTGAAACAATATTTCTGCTGGCAGTCATCGACATGTTGTGTGAATTA 16685
DB	246	TAAAGATGTCATTTGAAACAATATTTCTGCTGGCAGTCATCGACATGTTGTGTGAATTA 305
OY	1670	GCTTCAACAACGTTGTGATCAATTTCTTGGAAAAAGGCGCAATCCATCAGATTAAGA 17292
DB	306	GCTTCAACAACGTTGTGATCAATTTCTTGGAAAAAGGCGCAATCCATCAGATTAAGA 365
OY	1730	GCCGAGAAAAATTAACAGCAACATGAGCACACAGAGATCTCGATGCTGGGTGGG 1789
DB	366	GCCGAGAAAAATTAACAGCAACATGAGCACACAGAGATCTCGATGCTGGGTGGG 425
OY	1790	TGTCGAAGTTGAAAAACAGGTACAGTCCATAGATCCAAAGCTGAGCTCTACTAGACA 18445
DB	426	TGTCGAAGTTGAAAAACAGGTACAGTCCATAGATCCAAAGCTGAGCTCTACTAGACA 485
OY	1850	TCTATCAACAGGTCCTCTTGGGAAGGCTCTGCC 1881
DB	486	TCTATCAACAGGTCCTCTTGGGAAGGCTCTGCC 517
RESULT 10		
LOCUS	BF240146	908 bp mRNA linear EST 14-NOV-2000
DEFINITION	601905649P1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133293 5',	
		mRNA sequence.

Accession	Version	Keywords	Source	Organism	Reference Authors Title Journal Comment
BE240146	BF240146.1	GI:11154069	EST.	Homo sapiens	Unpublished (1999)
BE240146	BF240146.1	GI:11154069	EST.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	Contact: Robert Strausberg, Ph.D. Email: rgs@pds.nlm.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LHCMI034 row: b column: 14 High quality sequence stop: 615.
FEATURES	Source	Location/Qualifiers			
BASE COUNT	263 A 229 C 217 G 199 T				
ORIGIN					
Query Match	11.6%	Score 321; DB 12; Length 908;			
Best Local Similarity	99.8%;	Pred. No. 1.9e-15;			
Matches 441; Conservative	0; Mismatches 0; Indels 1; Gaps 1;				
OY	2103	CAGTCAACACACACAGTGCCAAATTAGTCGAAGAAGGATGGCTCAGCAGTGCGACCACCA 2162			
DB	1	CAGTCAACACACACAGTGCCAAATTAGTCGAAGAAGGATGGCTCAGCAGTGCGACCACCA 60			
OY	2163	CACCATTCGCAACCAATAAATATAGCGCACCCAGCCAGCAGCCCCAACACTTTACAGAT 2222			
DB	61	CACCATTCGCAACCAATAAATATAGCGCACCCAGCCAGCAGCCCCAACACTTTACAGAT 120			
OY	2223	CCGACCTCCTCCGCCAGCCATCAACATCTGCGCCAGGCGGACAGAAACTGTGACACCTTAACC 2282			
DB	121	CCGACCTCCTCCTCCGCCAGCCATCAACATCTGCGCCAGG - CAGAAACTGTGACACCTTAACC 179			
OY	2283	TGCAGGCTTACAGGAAGCAATTTCTGACGTCACACACTGCTGTTGCTGCTCCAGAGAAA 2342			
DB	180	TGCAGGCTTACAGGAAGCAATTTCTGACGTCACACACTGCTGTTGCTGCTCCAGAGAAA 239			
OY	2343	TGTTAGGTTGACAGTCGCAAAATTCACCAAGGACCGCTCTATGAGGAAAAAGCTTTGACAT 2402			
DB	240	TGTTAGGTTGACAGTCGCAAAATTCACCAAGGACCGCTCTATGAGGAAAAAGCTTTGACAT 299			
OY	2403	GAGAGAGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2462			
DB	300	GAGAGAGAGAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359			
OY	2463	GTCCTGCAAAACCTGATCAGGTGCACCGAGGAACTGATATACAATTTTCAGGAGTGA 2522			

Db 360 GTCTGTGCAAAACCTGATCAGGTGACCGAGCACTGATATACAACTTTCAGGGAGTGA 419

OY 2523 GTCAAGTGGCTCCAGAGGACGC 2544

Db 420 GTCAAGTGGCTCCAGAGGACGC 441

RESULT 11

BF945327/c 267 bp mRNA linear EST 22-JAN-2001

LOCUS BF945327

DEFINITION OY2-NN0045-231000-425-a01 NN0045 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF945327

VERSION BF945327.1 GI:12362602

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 267)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-231000-425-a01&t3=2000-10-23&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 19

Location/Qualifiers

1. 267

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NN0045"

/dev_stage="Adult"

/note="Organ: nervous_normal; Vector: puc18; Site:1: Smal; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 65 a 53 c 63 g 86 t

ORIGIN

Query Match 7.8%; Score 215; DB 12; Length 267;

Best Local Similarity 100.0%; Pred. No. 5.4e-99;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1373 TCAACGACGACGACCGCTTCGCGCCCTCGCTGCGCTCAAAAGTCTCAGCCAAACACAG 1432

Db 267 TCAAGGACGACGACCGCTTCGCGCCCTCGCTGCGCTCAAAAGTCTCAGCCAAACACAG 208

OY 1433 TGATAGATGCTGACACAGCCCTTGCGACATGATGATATATGATGAAGAGATGCAGT 1492

Db 207 TGATAGATGCTGACACAGCCCTTGCGACATGATGATATATGATGAAGAGATGCAGT 148

OY 1493 GTGATGATGATGAGAGACCTCACCCACCACTTAACCTGATTCAGACTATCAGAA 1552

Db 147 GTGATGATGATGAGAGACCTCACCCACCACTTAACCTGATTCAGACTATCAGAA 88

OY 1553 TTATGAATTTTCATGTTGCAAAACGGAAGTTTAAG 1587

Db 87 TTATGAATTTTCATGTTGCAAAACGGAAGTTTAAG 53

RESULT 12

BQ340178 266 bp mRNA linear EST 20-MAY-2002

LOCUS BQ340178

DEFINITION OY2-NN2004-040501-643-b02 NN2004 Homo sapiens cDNA, mRNA sequence.

ACCESSION BQ340178

VERSION BQ340178.1 GI:21000738

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 266)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN2004-040501-643-b02&t3=2001-05-04&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 266.

Location/Qualifiers

1. 266

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/organism="Homo sapiens"

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/clone_lib="NN2004"

/dev_stage="Adult"

/note="Organ: nervous_normal; Vector: puc18; Site:1: Smal; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 86 a 63 c 60 g 57 t

ORIGIN

Query Match 7.6%; Score 212; DB 14; Length 266;

Best Local Similarity 99.6%; Pred. No. 1.9e-97;

Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1687 GATCAATTTTGGAAAAGGCAAAATACATCAGATGAAGAGCGGAGAGAAATTAACA 1746

Db 4 GATCAATTTTGGAAAAGGCAAAATACATCAGATGAAGAGCGGAGAGAAATTAACA 63

OY 1747 GCGAACAATGAGACCAACAGAGATGATGATGCTCGGTGGGTGTCAAGTTGAAGAA 1806

Db 64 GCGAACAATGAGACCAACAGAGATGATGATGCTCGGTGGGTGTCAAGTTGAAGAA 123

OY	1807	CAGGTACAGTCCATAGAAATCCAACTGAGTGCCTACTAGACATCTATCAACAGGTCCTT	1866
Db	124	CAGGTACAGTCCATAGAAATCCAACTGAGTGCCTACTAGACATCTATCAACAGGTCCTT	183
OY	1867	CGGAAAGGCTCTGGCTCAGCCCTGCTTGCTTCATTCAGATCCCACTTTTGAAATGT	1926
Db	184	CGGAAAGGCTCTGGCTCAGCCCTGCTTTGGCTTCATTCAGATCCCACTTTTGAAATGT	243
OY	1927	GAACGACATCTGACTATCAAG	1949
Db	244	GAACGACATCTGACTATCAAG	266

RESULT	13
LOCUS	AQ383296/c
DEFINITION	AQ383296 520 bp DNA linear GSS 21-MAY-1999 RcPcI11-138M5_TV RcPcI-11 Homo sapiens genomic clone RcPcI-11-138M5,
ACCESSION	DNA sequence.
VERSION	AQ383296
KEYWORDS	AQ383296.1 GI:4354319
SOURCE	GSS.
ORGANISM	human.
	Homo sapiens

REFERENCE AUTHORS	TITLE	JOURNAL COMMENT
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.	Use of BAC End Sequences from Library RPhi-11 for Sequence-Ready	
	Map Building	
	Unpublished (1997)	
	Other:GSS: RPhi11-130M5.TJ	

Contact: Shanying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel.: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieteredejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genomics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.htm
Seq primer: T7
Class: BAC ends.

FEATURES	Location/Qualifiers
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	/db_xref="taxon:9606"
	/clone="RPC1-11-138M5"
	/clone_1lb="RPC1-11"
	/sex="Male"
	/cell_type="Lymphocytes"
	/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI
	RC111 Human Male BAC Library"
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Best Local Similarity	100.0%;	Pred. No. 2.2e-80;		
Matches 179;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Db	380	AGATACCATGTTCTTATCGCTTCAATAGACAGTTGTTTCGCAAAAACCTCAGGTAATAT	321	
Qy	675	TTTTGCACGTGCGACCTGAGAAGTCTCGTTTCCAGAGATCTCTCGCATGGTGGGCAT	734	
Db	320	TTTTGCACGTGCGACCTGAGAAGTCTCGTTTCCAGAGATCTCTCGCATGGTGGGCAT	261	

Qy 735 GGACCGAAGGGAGGCACTTGGAAATTACTGGGTTACAGTGGTTATGCTCACAGCAAGG 793
|||||
Db 260 GGACCGAAGGGAGGCACTTGGAAATTACTGGGTTACAGTGGTTATGCTCACAGCAAGG 202

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LOCUS	A0344243
DEFINITION	RPC11-133N24.TV RPCI-11 Homo sapiens genomic clone RCI-11-133N24 DNA sequence.
ORIGINATOR	NCBI

ACCESSION	AOJ44243	
VERSION	AOJ44243.1	GI:4169139
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS

1
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P., and Venter

TITLE	Use of BAC End Sequences from Library RPCT-11 for Sequence-Read
JOURNAL	Map Building
COMMENT	Unpublished (1997)
Other-SSS:	RPCT11-133N24.TJ
	Elstner, Norman; Mart Adams

Contact: Shanying Zhao, William Reichenbach, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPEC-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACpac Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.htm
Seq primer: 77
Class: BAC ends.

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FEATURES
source
location/Qualifiers
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/db_xref="taxon:9606"
/clone="RPC1-11-13N24"
/clone_1b="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI
RPC11 Human Male BAC library"
BASE COUNT
201 a 135 c 123 g 200 t
ORIGIN
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Best Local Similarity	100.0%	Pred. No. 2.4e+80;		
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QY 615 AGATACCATGTTCTTATCGCTTCAATAGACAGTTGTTCTGCAAAAACCTCAGGTAATAT 677
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Db 375 AGATACCATGTTCTTATCGCTTCAATAGACAGTTGTTCTGCAAAAACCTCAGGTAATAT 311

QY 675 TTTTGCACGCTGCACTCAGAAATCTCCGTTCTTACAGATCCTCCGATGTTGGCAT 73
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315 TTTTGCACGCTGCACTCAGAAATCTCCGTTCTTACAGATCCTCCGATGTTGGCAT 25
Db

Qy 735 GGACCGAAGGGGAGGCACTTGGAAATTACTGGTTCACTGGTTTATGCTCACACGAAGG 793
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Db 255 GGCACCGAAGGGGAGGCACTTGGAAATTACTGGTTCACTGGTTTATGCTCACACGAAGG 197

RESULT 15				
BF954374				
LOCUS	BF954374	224 bp	mRNA	linear
				EST 22-JAN-2001

DEFINITION QV2-NN0045-131100-414-c02 NN0045 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE954374
 VERSION BE954374.1 GI:12371649
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 224)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/PCR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t=QV2-NN0045-131100-414-c02&t3=2000-11-13&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 224.
 Location/Qualifiers
 1..224
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site: 1; Smal; Site: 2; Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 69 a 58 c 46 g 51 t
 ORIGIN
 Query Match 5.7%; Score 158; DB 12; Length 224;
 Best Local Similarity 99.5%; Pred. No. 1.2e-69;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1373 TCACGACGGAACCCGCTCCGCGCTCGCTGCGCTCAAAAGTCTCAGCCAAACG 1432
 DB 16 TCACGACGGAACCCGCTCCGCGCTCGCTGCGCTCAAAAGTCTCAGCCAAACG 75
 QY 1433 TGTATATGCTGCACACGCCCTTGCGCATGTATATGATGAAAAAGATGCCACT 1492
 DB 76 TGTATATGCTGCACACGCCCTTGCGCATGTATATGATGAAAAAGATGCCACT 135
 QY 1493 GTGATATACAGTGAAGAGACCTCACCCACCACTTAAACCTCATTTGAGGTATCAGAA 1552
 DB 136 GTGATATACAGTGAAGAGACCTCACCCACCACTTAAACCTCATTTGAGGTATCAGAA 195
 QY 1553 TTATGAATTTTCATGTTGCAAAACGGAAG 1581
 DB 196 TTATGAATTTTCATGTTGCAAAACGGAAG 224
 RESULT 16 297 bp mRNA linear EST 20-MAY-2002
 BQ340041 BQ340041

DEFINITION QV2-NN0045-261200-569-b11 NN0045 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ340041
 VERSION BQ340041.1 GI:21000357
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 297)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/PCR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t=QV2-NN0045-261200-569-b11&t3=2000-12-26&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 50.
 Location/Qualifiers
 1..297
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site: 1; Smal; Site: 2; Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 82 a 73 c 69 g 73 t
 ORIGIN
 Query Match 5.2%; Score 144; DB 14; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2e-62;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1815 GTCCATAGATTCGAAGCTGAGCTGCTTACATCATTCACAGAGCTCTGGAAAG 1874
 DB 148 GTCCATAGATTCGAAGCTGAGCTGCTTACATCATTCACAGAGCTCTGGAAAG 207
 QY 1875 CTCGACCTCAGCCCTCGCTTGCTTCAATTCAGATCCACCTTTGAAATGTAAGACAG 1934
 DB 208 CTCGACCTCAGCCCTCGCTTGCTTCAATTCAGATCCACCTTTGAAATGTAAGACAG 267
 QY 1935 ATCTGACTATCAAAAGCCCTGTGGA 1958
 DB 268 ATCTGACTATCAAAAGCCCTGTGGA 291
 RESULT 17 268 bp mRNA linear EST 21-APR-2001
 BQ185229 BQ185229
 LOCUS BQ185229 268 bp mRNA linear EST 21-APR-2001
 DEFINITION RST4167 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ185229
 VERSION BQ185229.1 GI:13706916
 KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 268)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Kika,A., Hess,J., Cuthen,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 268.
Location/Qualifiers
1. .268
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 72 a 46 c 63 g 87 t
ORIGIN
Query Match 4.7%; Score 129; DB 12; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 488 TGAAGTTCGATGATTTGCTGTTGGAGTTCAATTCGAATCTGCTCGCG 547
|||||
Db 3 TGAAGTTCGATGATTTGCTGTTGGAGTTCAATTCGAATCTGCTCGCG 62
QY 548 GTTCTGTTGCGATATAGAGATGCAAGAACTGAGTTGCTCGAAAGCCCTTC 607
|||||
Db 63 GTTCTGTTGCGATATAGAGATGCAAGAACTGAGTTGCTCGAAAGCCCTTC 122
QY 608 GTGTTATAG 616
|||||
Db 123 GTGTTATAG 131
RESULT 18
AQ019541 166 bp DNA linear GSS 09-JUN-1998
LOCUS CIT-HSP-2305P7.TF CIT-HSP Homo sapiens genomic clone 2305P7, DNA
DEFINITION
ACCESSION AQ019541
VERSION AQ019541.1 GI:3198277
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 166)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2305P7.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@igf.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
Location/Qualifiers
1. .166
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2305P7"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT 34 a 31 c 56 g 45 t
ORIGIN
Query Match 4.1%; Score 115; DB 17; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.5e-47;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2225 CACCTCTCTCCAGCCATCAAGATCTGCCAGCCAGCAAACTGCAACCTAACCTG 2284
|||||
Db 166 CACCTCTCTCCAGCCATCAAGATCTGCCAGCCAGCAAACTGCAACCTAACCTG 107
QY 2285 CAGGCTTACAGGAAGCATTTCTGACGTCACACCTGCTTGTGCTCAAGAAATG 2344
|||||
Db 106 CAGGCTTACAGGAAGCATTTCTGACGTCACACCTGCTTGTGCTCAAGAAATG 47
QY 2345 TTGAGTTGACAGCAATCTCAACAGAACCGTTCTATGAGAA 2390
|||||
Db 46 TTGAGTTGACAGCAATCTCAACAGAACCGTTCTATGAGAA 1
RESULT 19
BE177584 248 bp mRNA linear EST 22-JUN-2000
LOCUS RCI-HT0597-210300-011-h01 HT0597 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BE177584
VERSION BE177584.1 GI:8656736
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 248)
Nagai,Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias,M.A., da Silva,W. Jr., Zago,M.A., Borlin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=st2-RC1-HT0597-210
300-011-h01&t3=2000-03-21&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 248.
Location/Qualifiers

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0597"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      63 a      53 c      65 g      67 t
ORIGIN
Query Match      3.9%; Score 107; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.2e-43;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2609 AAGAGACAGACACACTTTTGATGCCGACAGCCTGCAGAGGAGCTGCTTTG 2668
|||||
Db 248 AATGACAGACAGACACACTTTTGATGCCGACAGCCTGCAGAGGAGCTGCTTTG 189
|||||
OY 2669 CATGAGACTCTTAAGACTGAGAGCTGATCATCTCAGAGCACT 2715
|||||
Db 188 CATGAGACTCTTAAGACTGAGAGCTGATCATCTCAGAGCACT 142
|||||

```

RESULT 20

BG185740

LOCUS BG185740 267 bp mRNA linear EST 21-APR-2001
DEFINITION RST4652 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG185740
VERSION BG185740.1 GI:13707427
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K., Offenbacher,
J., Danzig,J., and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com

FEATURES

Source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation

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method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 73 a 45 c 62 g 87 t

ORIGIN

```

Query Match      3.8%; Score 106; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.4e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 511 TTGGTTGGAGTTCATCATTCGATCTGTGCGGGCTGCTGTTCATATAGAGA 570
|||||
Db 25 TTGGTTGGAGTTCATCATTCGATCTGTGCGGGCTGCTGTTCATATAGAGA 84
|||||
OY 571 TGGCAAGAGAGTGTGCTGCGAAGCCCTTCTGTATTAG 616
|||||
Db 85 TGGCAAGAGAGTGTGCTGCGAAGCCCTTCTGTATTAG 130
|||||

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RESULT 21

BG218030

LOCUS BG218030 335 bp mRNA linear EST 21-APR-2001
DEFINITION RST37756 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG218030
VERSION BG218030.1 GI:13744051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Kilka,A., Hess,J., Cochren,K., Lo,K., Offenbacher,
J., Danzig,J., and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com

FEATURES
Source
Location/Qualifiers
1..335
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT

88 a 61 c 77 g 108 t 1 others

ORIGIN

```

Query Match      3.8%; Score 106; DB 12; Length 335;
Best Local Similarity 100.0%; Pred. No. 7.8e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 511 TTGGTTGGAGTTCATCATTCGATCTGTGCGGGCTGCTGTTCATATAGAGA 570
|||||
Db 26 TTGGTTGGAGTTCATCATTCGATCTGTGCGGGCTGCTGTTCATATAGAGA 85
|||||
OY 571 TGGCAAGAGAGTGTGCTGCGAAGCCCTTCTGTATTAG 616
|||||
Db 86 TGGCAAGAGAGTGTGCTGCGAAGCCCTTCTGTATTAG 131
|||||

```

RESULT 22
 BE959223 160 bp mRNA linear EST 22-JAN-2001
 LOCUS QV2-NN0045-011200-502-a05 NN0045 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE959223
 ACCESSION BE959223.1 GI:12376498
 VERSION EST.
 KEYWORDS human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 160)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&tl-QV2-NN0045-
 011200-502-a05&tl3=2000-12-01&tl4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 159.
 Location/Qualifiers
 1. 160
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
 Site:2: SmaI; A mini-library was made by cloning products
 derived from ORESTIS PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 44 a 43 c 36 g 37 t

BASE COUNT
 ORIGIN
 Query Match 3.7%; Score 102; DB 12; Length 160;
 Best Local Similarity 100.0%; Pred. No. 7.4e-41;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1372 TTCAACGACGACCCGCTTCGGCCCTGCGCCCAAAAGTTTCAGCAAAACCA 1431
 |||||||
 DB 14 TTCAACGACGACCCGCTTCGGCCCTGCGCCCAAAAGTTTCAGCAAAACCA 73
 |||||||

QY 1432 GTGTAGATGCTGACACAGCCCTTGACACTGATGATATAT 1473
 |||||||
 DB 74 GTGTAGATGCTGACACAGCCCTTGACACTGATGATATAT 115
 |||||||

RESULT 23
 A1576388 300 bp mRNA linear EST 05-APR-1999
 LOCUS A1576388
 DEFINITION UT-R-Y0-vm-b-07-0-UI.s1 UT-R-Y0 Rattus norvegicus cDNA clone
 ACCESSION A1576388
 VERSION A1576388.1 GI:4560764

KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 300)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msquares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.B.
 Soares lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 37-71,
 >GC-rich#Low-complexity
 Seq primer: M13 Forward.
 Location/Qualifiers
 1. 300
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-Y0-vm-b-07-0-UI"
 /clone_lib="UI-R-Y0"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site:1: Not I; Site:2: Eco RI; The UI-R-Y0
 library is a subtracted library derived from an
 individually-tagged normalized whole-eye (minus the lens)
 library. The driver for the subtraction consisted of a
 pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
 UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
 3-5 nucleotides present between the Not I site and the
 oligo-dt track which allows identification of the library
 of origin of a clone within the mixture. The subtracted
 library (UI-R-Y0) was constructed as follows: PCR
 amplified cDNA inserts from previous library clones from
 which 3' ESTs had been derived were used as a driver in a
 hybridization with the normalized whole-eye library in
 the form of single-stranded circles. The remaining
 single-stranded circles (subtracted library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-Y0
 library. This procedure has been previously described
 (Bonaldo, Lennon and Soares, genome Research 6: 791-806,
 1996)".
 44 a 108 c 109 g 38 t 1 others

BASE COUNT
 ORIGIN
 Query Match 2.0%; Score 56; DB 9; Length 300;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 GAGAGCGCGGCGGCAAGAGGCGCGGATGAGCTGTGGGACCGGCTTC 284
 |||||||
 DB 78 GAGAGCGCGGCGGCAAGAGGCGCGGATGAGCTGTGGGACCGGCTTC 133
 |||||||

RESULT 24
 BE103175 469 bp mRNA linear EST 13-JUN-2000
 LOCUS BE103175
 DEFINITION UT-R-BT1-agx-h-11-0-UI.s1 UT-R-BT1 Rattus norvegicus cDNA clone

ACCESSION BE103175
 VERSION BE103175.1 GI:8495314
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 469)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dT track not found, Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 1-71,
 >GC-rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source
 1..469
 /location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BT1-agg-h-11-0-UI"
 /clone_1lb="UI-R-BT1"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; The library
 UI-R-BT1 is a subtracted library derived from a mixture of
 the following tissues: hippocampus, thalamus, mid-brain,
 medulla, corpus striatum, cerebral cortex and testis. For
 a detailed description of the library from which this
 clone was derived, please visit our web site at
 ratseq.eng.uiowa.edu. The subtraction has been previously
 described in (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG-SEQ=None found"

BASE COUNT 79 a 120 c 152 g 118 t

ORIGIN

Query Match 2.0%; Score 56; DB 10; Length 469;
 Best Local Similarity 100.0%; Pred. No. 4.8e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 GAGACCGCGCGGAGCAAGAGCGGCGCGATGATGACCTGCTGGGAGACCGCTCTC 284
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 78 GAGACCGCGCGGAGCAAGAGCGGCGCGATGATGACCTGCTGGGAGACCGCTCTC 133

RESULT 25
 BG501859/c 730 bp mRNA linear EST 27-MAR-2001
 LOCUS 602548558f1 NIH_MGC-61 Homo sapiens cDNA clone IMAGE:4654814 5',
 DEFINITION mRNA sequence.
 ACCESSION BG501859
 VERSION BG501859.1 GI:13463376
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 730)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgrabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHCMI443 row: d column: 15
 High quality sequence stop: 702.

FEATURES
 source
 1..730
 /location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="IMAGE:4654814"
 /clone_1lb="NIH_MGC_61"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: testis; Vector: pPCR-LIB (Clontech); Site_1:
 SfiI (ggcgagctggcc); Site_2: SfiI (ggcattatggc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGCGCGAGCGGCGGATG-3' and 3' adaptor
 sequence: 5'-CAGCGCATATGCGC-3' (30)BN-3'
 (where B = A, C, G or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 Library."

BASE COUNT 218 a 161 c 181 g 169 t 1 others

ORIGIN

Query Match 2.0%; Score 56; DB 12; Length 730;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 343 CTGTACACGCTGCTGAGAGACCGCGCGCTGCGGCTTATCATCACCGCTTTCG 398
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 71 CTGTACACGCTGCTGAGAGACCGCGCGCTGCGGCTTATCATCACCGCTTTCG 16

RESULT 26
 BI290441/c 434 bp mRNA linear EST 19-JUL-2001
 LOCUS UI-R-DK0-cfw-c-12-0-UI s1 UI-R-DK0 Rattus norvegicus cDNA clone
 DEFINITION UI-R-DK0-cfw-c-12-0-UI 3', mRNA sequence.
 ACCESSION BI290441
 VERSION BI290441.1 GI:14949018
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 434)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat brain pool library cDNA library preparation: M.B. Soares Lab clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

SOURCE

Location/Qualifiers

1. 434

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-DKO-CfW-C-12-0-UI"

/clone.lib="UI-R-DKO"

/dev_stage="ADULT"

/lab_host="DHI0B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-DKO library is a subtracted library derived from a mixture of five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%), aorta-nRBP (20%), and placenta-nRBP (20%). Each original library was constructed from a mixture of equal amounts of RNA from seven different developmental time-points: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 12, adult day 75, and adult day 200. (Exception: the aorta pool does not contain embryonic day 17 RNA and the placenta pool contains only the three embryonic stages). Each library was normalized individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CT0S), heart (C0S0S), kidney (CU0S), aorta (CW0S), and placenta (CX0S). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CT0), heart (CS0), kidney (CU0), aorta (CW0), and placenta (CX0). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG_LIB=UI-R-DKO
TAG_TISSUE=rat brain pool
TAG_SEQ=ACTTC"

BASE COUNT

82 a 97 c 109 g 145 t 1 others

ORIGIN

Query Match 1.7%; Score 48; DB 13; Length 434;
Best Local Similarity 100.0%; Pred. No. 6.2e-13;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1345 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 1392
|||||
DB 396 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 349

RESULT 27 BH307140 719 bp DNA linear GSS 30-NOV-2001
LOCUS BH307140
DEFINITION CH230-10L20-TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

ACCESSION CH230-10L20, DNA sequence.
VERSION BH307140
KEYWORDS GI:17219548
SOURCE GSS.
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 719)
Zhuo, S., Shetty, J., Shatsman, S., Tseng, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcORI segment
Unpublished (1999)
Other GSS: CH230-10L20-TV

COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or.ering.information.htm). BAC end
page: http://www.tigr.org/cdb/bac-ends/rat/bac_end_intro.html
Plate: 10 row: L column: 20
Seq primer: 17
Class: BAC ends.

FEATURES

SOURCE

Location/Qualifiers

1. 719

/organism="Rattus norvegicus"

/strain="BN/SSHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-10L20"

/clone.lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="Vector: pTARBAC2.1; site 1: EcoRI; site 2: EcoRI;
CHORI-230 Rat (BN/SSHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT

199 a 164 c 168 g 188 t

Query Match 1.7%; Score 48; DB 17; Length 719;
Best Local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1345 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 1392
|||||
DB 423 CCCACCAAGTGCAGAGAGCTGAGCTTCAACGACGACCCGCTTC 470

RESULT 28

AM049888

LOCUS

DEFINITION

UI-M-BH1-anr-g-09-0-UI-s1 NTH BMAP.MS2 Mus musculus cDNA clone
UI-M-BH1-anr-g-09-0-UI 3', mRNA sequence.

ACCESSION

AM049888

VERSION

AM049888.1

KEYWORDS

EST.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 584)

Bonaldo, M.F., Lennon, G., and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery
Genome Res. 6 (9), 791-806 (1996)

MEDLINE
 97044477
COMMENT
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 Oligo-dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.B.
 Scores Lab clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 The following repetitive elements were found in this cDNA sequence:
 37-71, >GC richlow.complexity
 Seq primer: M13 Forward
 POLYA-NO.

FEATURES
 source
 1. 584
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U1-M-BH1-anr-g-09-0-UT"
 /clone_lib="NIH_BMAP_M_S2"
 /dev_stage="27-32 days"
 /lab_host="DHI0B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI. The
 NIH_BMAP_M_S2 library is a subtracted library derived from
 NIH_BMAP_M_S1, which in turn is a subtracted library
 derived from a mixture of normalized libraries from ten
 regions of the mouse brain (cerebellum, brain stems,
 olfactory bulbs, hypothalamus, cortex, amygdala, basal
 ganglia, pineal gland, striatum, hippocampus). The driver
 used for subtraction consisted of a pool of 5,000 clones
 from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
 obtained from non-normalized and normalized mouse brain
 spinal cord libraries.
 TAG_LIB=NIH_BMAP_M_S2
 TAG_TISSUE=corpus-striatum
 TAG_SEQ=ACGGC"
 BASE COUNT 107 a 151 c 174 g 152 t
 ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 44; DB 10; Length 584;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 412 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 455
 |||
 261 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 304

RESULT 29
 BB657491 662 bp mRNA linear EST 26-OCT-2001
LOCUS
 BB657491 RIKEN full-length enriched, 12 days embryo eyeball Mus
DEFINITION
 musculus cDNA clone D230004A10 5', mRNA sequence.
ACCESSION
 BB657491 GI:16491317
VERSION
 EST.
KEYWORDS
 house mouse.
SOURCE
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 662)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

TITLE **JOURNAL** **COMMENT**

Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshitake Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9226
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh
 M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Matsuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamataka, I., Aizawa
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational analysis of full-length mouse cDNAs compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES source

1. 662
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="D230004A10"
 /clone_lib="RIKEN full-length enriched, 12 days embryo
 eyeball"
 /tissue_type="eyeball"
 /dev_stage="12 days embryo"
 /lab_host="DHI0B"
 /note="Site 1: SalI; Site 2: BamHI. cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5',
 GAGAGAGAGAGCGCCGACACTCGAGTTTTTTTTTTTNN 3']. cDNA was
 prepared by using triethanol thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGATTCGAGTTATTAATTAATTCCTCCCTCCCTCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FIC I."
 BASE COUNT 232 a 147 c 120 g 161 t 2 others
 ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 44; DB 10; Length 662;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 412 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 455
 |||
 205 TTGGTGGCTGATTTTGCAGTGTTCACCATCCCTGAGCA 248

RESULT 30
 A2443500/c 477 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M023818R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M023818 R, DNA sequence.
 A2443500
 ACCESSION A2443500.1 GI:10591541
 VERSION
 KEYWORDS
 ORGANISM house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 477)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0238 row: H column: 18
 Seq primer: CACACGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 477.
 Location/Qualifiers
 1. 477
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M023818"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 100 a 98 c 150 g 129 t
 ORIGIN
 Query Match 1.4%; Score 38; DB 17; Length 477;
 Best Local Similarity 100.0%; Pred. No. 9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2188 GCACCAAGCAGACCCCAACACTTACAGATCCC 2225
 |||||||||||||||||||||||||||||||||||||||
 Db 269 GCACCAAGCAGACCCCAACACTTACAGATCCC 232

RESULT 31
 BE647997/c 679 bp mRNA linear EST 06-SEP-2000
 LOCUS BE647997
 DEFINITION UI-M-BH1-anr-g-09-0-UI-r1 NIH_BMAP_M.S2 Mus musculus cDNA clone
 UI-M-BH1-anr-g-09-0-UI 5', mRNA sequence.
 BE647997
 ACCESSION BE647997.1 GI:9973817
 VERSION
 KEYWORDS
 ORGANISM house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 679)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 COMMENT Contact: Chln, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 CDNA library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1. 679
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH1-anr-g-09-0-UI"
 /clone_1lb="NIH_BMAP_M.S2"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_M.S2 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries."

BASE COUNT 152 a 150 c 172 g 205 t
 ORIGIN
 Query Match 1.4%; Score 38; DB 10; Length 679;
 Best Local Similarity 100.0%; Pred. No. 9.9e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1717 TCAGATTAAGAGAGCCGAGAGAAATACAGCAGACA 1754
 |||||||||||||||||||||||||||||||||||||||
 Db 429 TCAGATTAAGAGAGCCGAGAGAAATACAGCAGACA 392

RESULT 32
 A1705051/c 226 bp mRNA linear EST 03-JUN-1999
 LOCUS A1705051
 DEFINITION UI-R-G0-uj-d-05-0-UI.s2 UI-R-G0 Rattus norvegicus cDNA clone
 UI-R-G0-uj-d-05-0-UI 3', mRNA sequence.
 A1705051
 ACCESSION A1705051.1 GI:4992951

KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 226)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 53-210,
>GC_rich#low_complexity
Seq primer: M13 Forward
POLYA=NO.

FEATURES
source
Location/Qualifiers
1..226
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-G0-uj-d-05-0-UI"
/clone_lib="UI-R-G0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of 6 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806 (1996).
TAG_SEQ=None found"
BASE COUNT 22 a 103 c 77 g 24 t
ORIGIN
Query Match 1.3%; Score 35; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 35
|||||
Db 154 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 120
|||||

RESULT 33
AM122800/c 239 bp mRNA linear EST 22-OCT-1999
LOCUS UI-M-BH2.1-acy-f-08-0-UI.s1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
DEFINITION UI-M-BH2.1-acy-f-08-0-UI 3', mRNA sequence.
ACCESSION AM122800
VERSION AM122800.1 GI:6098330
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 239)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
COMMENT 97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7A90, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dt track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH_BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 53-102, >GC_rich#low_complexity
Seq primer: M13 Forward
POLYA=NO.

FEATURES
source
Location/Qualifiers
1..239
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-acy-f-08-0-UI"
/clone_lib="NIH_BMAP_M.S3.1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M.S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library (NIH_BMAP_M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=NIH_BMAP_M.S3.1
TAG_TISSUE=hypothalamus
TAG_SEQ=CGGTA
BASE COUNT 22 a 106 c 81 g 29 t 1 others
ORIGIN
Query Match 1.3%; Score 35; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 35
|||||
Db 160 ATGCCCCGCCACCGCGGAGAGAGAGAGCGCG 126
|||||

RESULT 34
AM533367/c 330 bp mRNA linear EST 06-MAR-2000
LOCUS UI-R-BU0-anb-b-01-0-UI.s1 UI-R-BU0 Rattus norvegicus cDNA clone
DEFINITION UI-R-BU0-anb-b-01-0-UI 3', mRNA sequence.

ACCESSION AM533367.1 GI:7175781
 VERSION AM533367.1
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not a site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 53-210,
 >GC_rich#low_complexity 242-310, >GC_rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES

source location/Qualifiers
 1..330
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BU0-and-b-01-0-UI"
 /clone_1db="UI-R-BU0"
 /dev_stage="adult"
 /lab_host="DHI08 (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BU0 library is a subtracted library derived from a mixture of eye and ganglia tissues. For a detailed description of the library from which this clone was derived, please visit our web site at ratat.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_Lib-UI-R-BU0
 TAG_TISUE-Eye
 TAG_SEQ-CATTG"
 BASE COUNT 33 a 134 c 130 g 32 t 1 others
 ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 330;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCCCCGCACCGCGGAGAGAGAGGCGG 35
 ||||||||||||||||||||||||||||||||||
 DB 154 ATGCCCCCGCACCGCGGAGAGAGAGGCGG 120

RESULT 35
 BE414224/c 411 bp mRNA linear EST 28-NOV-2000
 LOCUS BE414224
 DEFINITION UI-R-BU2-bon-h-03-0-UI.s1 UI-R-BU2 Rattus norvegicus cDNA clone
 UI-R-BU2-bon-h-03-0-UI 3', mRNA sequence.
 ACCESSION BE414224
 VERSION BE414224.1 GI:11402213
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.
 REFERENCE 1 (bases 1 to 411)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dt track not found. Not a site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 54-211,
 >GC_rich#low_complexity 243-313, >GC_rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES

source location/Qualifiers
 1..411
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BU2-bon-h-03-0-UI"
 /clone_1db="UI-R-BU2"
 /lab_host="DHI08 (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BU2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratat.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"
 BASE COUNT 43 a 156 c 154 g 56 t 2 others
 ORIGIN

Query Match 1.3%; Score 35; DB 12; Length 411;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCCCCGCACCGCGGAGAGAGAGGCGG 35
 ||||||||||||||||||||||||||||||||||
 DB 155 ATGCCCCCGCACCGCGGAGAGAGAGGCGG 121

RESULT 36
 BE648243 425 bp mRNA linear EST 06-SEP-2000
 LOCUS BE648243
 DEFINITION UI-M-BH2.1-acy-f-08-0-UI.t1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
 UI-M-BH2.1-acy-f-08-0-UI 5', mRNA sequence.
 ACCESSION BE648243
 VERSION BE648243.1 GI:9974064
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 425)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chin, H
 National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov
 CDNA Library Preparation: M.B. Soares Lab Clone Distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this CDNA sequence: 172-197, >GC-rich#Low_complexity 211-242, >GC-rich#Low_complexity 172-197, >GC-rich#Low_complexity 389-438, >GC-rich#Low_complexity 275-320, >GC-rich#Low_complexity Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers
 1..425
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="NIH-BMAP_M.S3.1"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The NIH-BMAP_M.S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH-BMAP_M.S3.1, NIH-BMAP_M.S2, NIH-BMAP_M.S1. The subtracted library (NIH-BMAP_M.S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH-BMAP_M.S2 clones from which 3' ESTs had been derived was used as driver in a hybridization with the NIH-BMAP_M.S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH-BMAP_M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)."

BASE COUNT

64 a 157 c 159 g 45 t

ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCCGCCACGCGGAGAGAGAGAGCGG 35
 ||||||||||||||||||||||||||||||||
 Db 282 ATGCCCGCCACGCGGAGAGAGAGAGCGCG 316

RESULT 37
 LOCUS BF523361/c 427 bp mRNA linear EST 11-DEC-2000
 DEFINITION UI-R-GO-ug-h-09-0-UI_r1 UI-R-GO Rattus norvegicus cDNA clone
 ACCESSION BF523361
 VERSION BF523361.1 GI:11631328
 KEYWORDS EST.

SOURCE

ORGANISM Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 427)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

FEATURES

source

CDNA Library Preparation: M.B. Soares Lab Clone Distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1794020
 Seq primer: M13 Forward.

Location/Qualifiers
 1..427
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone_lib="UI-R-GO-ug-h-09-0-UI"
 /clone_lib="UI-R-GO"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-GO library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of 6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806 (1996)."

BASE COUNT

125 a 92 c 108 g 102 t

ORIGIN

Query Match 1.3%; Score 35; DB 12; Length 427;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 TTGTGAGAAAGAGACCGACGTCGACCTCAT 1121
 ||||||||||||||||||||||||||||||||
 Db 111 TTGTGAGAAAGAGACCGACGTCGACCTCAT 77

RESULT 38

LOCUS BB624101 632 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB624101 RIKEN full-length enriched, adult male cortex Mus musculus
 ACCESSION BB624101
 VERSION BB624101.1 GI:16462710
 KEYWORDS EST.

QY 1 ATGCCCCGCCACGCGGAGAGAGAGAGCGG 35
 ||||||||||||||||||||||||||||||||
 Db 282 ATGCCCGCCACGCGGAGAGAGAGAGCGCG 316

SOURCE

Mus musculus

ORGANISM

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.REFERENCE 1 (bases 1 to 632)
 AUTHORS Arakawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,T., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

TITLE

JOURNAL COMMENT

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@isc.riken.go.jp,
URL: http://genome.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Tameda, T., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

source

1. location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7730402H1"
/clone_lib="RIKEN full-length enriched, adult male cortex"
/sex="male"
/tissue_type="cortex"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTATTAATTAATCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
vector: a modified pluscript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

BASE COUNT

193 a 160 c 157 g 122 t

ORIGIN

Query Match 1.3%; Score 35; DB 10; Length 632;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 TTGAGAAAGAGAGACCCAGCTGCCAACCCTCAT 1121

Db 9 TTGAGAAAGAGAGACCCAGCTGCCAACCCTCAT 43

RESULT 39

AI603318 282 bp mRNA linear EST 21-APR-1999
LOCUS
DEFINITION
UI-R-G0-ug-h-09-0-UI-s2 UI-R-G0 Rattus norvegicus cDNA clone
UI-R-G0-ug-h-09-0-UI 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Norway rat.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus norvegicus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Oligo-dt track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares lab clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
Location/Qualifiers
1. 282
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-G0-ug-h-09-0-UI"
/clone_lib="UI-R-G0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7/3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dt track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
1996."

FEATURES

source

BASE COUNT
ORIGIN
41 a 84 c 96 g 61 t
Query Match 1.2%; Score 34; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 CAACGTCTGGAGAGACCCGCGCTGGCGCTTC 381
197 CAACGTCTGGAGAGACCCGCGCTGGCGCTTC 230

RESULT 40
BE860721 232 bp mRNA linear EST 29-SEP-2000
LOCUS
DEFINITION
UI-M-AL1-ahk-e-04-0-UI-r1 NIH_BMAP_MCO_N Mus musculus cDNA clone
UI-M-AL1-ahk-e-04-0-UI 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 232)

BASE COUNT 91 a 173 c 189 g 144 t
ORIGIN

Query Match 0.9%; Score 26; DB 10; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGCG 392
|||||
DB 10 CGCGGCTGGCGCTTCATCTACACGCG 35

RESULT 44
BE257127

LOCUS BE257127 622 bp mRNA linear EST 13-JUN-2000
DEFINITION 60110867f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349625 5',
ACCESSION BE257127
VERSION BE257127
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 622)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.linl.gov
Plate: LICM144 row: e column: 18
High quality sequence stop: 621.

FEATURES

Location/Qualifiers

1..622
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3349625"
/clone_1lb="NIH_MGC_16"
/tissue_type="retinod1astoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 93 a 205 c 207 g 117 t
ORIGIN

Query Match 0.9%; Score 26; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACACGCG 392
|||||
DB 289 CGCGGCTGGCGCTTCATCTACACGCG 314

RESULT 45
BO192564/c

LOCUS BO192564 749 bp mRNA linear EST 30-APR-2002
DEFINITION UI-R-DRI-ckz-b-18-0-UI-s1 UI-R-DRI Rattus norvegicus cDNA clone
ACCESSION BO192564
VERSION BO192564.1 GI:20368115

KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 749)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477

COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized osteoblast library cDNA library preparation: M.B. Soares
lab clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 1-23, >AT-rich#Low-complexity
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

Location/Qualifiers

1..749
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DRI-ckz-b-18-0-UI-R"
/clone_1lb="UI-R-DRI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DRI
library is a normalized Rat Osteoblast library (nRBO)
constructed in pRT37 vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag AAGATATCA between the Not I cloning site and
dH18 stretch. The Rat Osteoblast tissue was provided by
Lian & Stein of the University of Massachusetts Medical
School.
TAG LIB=UI-R-DRI
TAG_TISSUE=osteoblast
TAG_SEQ=AAGATATCA"

BASE COUNT 200 a 158 c 147 g 242 t 2 others
ORIGIN

Query Match 0.9%; Score 26; DB 14; Length 749;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2569 GAATCCAAATGTTATACATGATGA 2594
|||||
DB 699 GAATCCAAATGTTATACATGATGA 674

RESULT 46
BF312386

LOCUS BF312386 914 bp mRNA linear EST 21-NOV-2000
DEFINITION 601898926f1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127958 5',
ACCESSION BF312386
VERSION BF312386.1 GI:11260188

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI020 row: d column: 07
High quality sequence stop: 630.
Location/Qualifiers
1. 914
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4127958"
/clone_lib="NIH-MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOT87; Site:1: XhoI; Site:2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 165 a 234 c 281 g 214 t
ORIGIN
Query Match 0.9%; Score 26; DB 12; Length 914;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 367 CGCGGCTGGGCGTTCATCTACACGC 392
|||||
DB 31 CGCGGCTGGGCGTTCATCTACACGC 56
RESULT 47
BF317072 920 bp mRNA linear EST 21-NOV-2000
LOCUS 601903470F1 NIH-MGC_19 Homo sapiens CDNA clone IMAGE:4136200 5',
DEFINITION mRNA sequence.
ACCESSION BF317072
VERSION BF317072.1 GI:11265477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI041 row: k column: 17
High quality sequence stop: 714.

FEATURES
SOURCE Location/Qualifiers
1. 920
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4136200"
/clone_lib="NIH-MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOT87; Site:1: XhoI; Site:2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT 150 a 256 c 298 g 216 t
ORIGIN
Query Match 0.9%; Score 26; DB 12; Length 920;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 367 CGCGGCTGGGCGTTCATCTACACGC 392
|||||
DB 30 CGCGGCTGGGCGTTCATCTACACGC 55
RESULT 48
CNS04101/c 942 bp DNA linear GSS 18-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence PUC-Orl end of clone
DEFINITION 074H14 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AF270459.1 GI:7992380
VERSION AF270459.1
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 942)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fitzames, C., Wincker, P., Brotlier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 942)
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Fitzames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 942)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
SOURCE Location/Qualifiers
1. 942
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="074H14"
/clone_lib="G"
/note="Genoscope sequence ID : C0B6074DD07SP1-end :
PUC-Orl"

BASE COUNT	226 a	232 c	248 g	230 t	6 others
ORIGIN					
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Best Local Similarity		100.0%;	Pred. No. 0.16;		
Matches	26;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1357	CAGAAGAGCTGAGCTTCACGACCG	1382		
DB	118	CACAAGAGCTGAGCTTCACGACCG	93		
RESULT 49					
AG082214		1019 bp	DNA	linear	GSS 03-NOV-2001
LOCUS	Pan troglodytes DNA, clone: PTB-079A15.R, genomic survey sequence.				
DEFINITION					
ACCESSION	AG082214				
VERSION	AG082214.1	GI:16634016			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes male lymphoblast DNA, clone_11b.PTB Chimpanzee Male				
ORGANISM	BAC library clone:PTB-079A15.R.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.				
TITLE	1				
JOURNAL	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,				
REFERENCE	Totoki,Y., Watanabe,H. and Sakaki,Y.				
AUTHORS	BAC end sequences of library PTB				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 1019)				
REFERENCE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,				
AUTHORS	Totoki,Y., Watanabe,H. and Sakaki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical				
REFERENCE	and Chemical Research (RIKEN), Genomic Sciences Center (GSC);				
AUTHORS	1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan				
TITLE	E-mail:chiamps@sc.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/,				
JOURNAL	Tel:81-45-503-9111, Fax:81-45-503-9170)				
REFERENCE	Clones are derived from the chimpanzee BAC library PTB This BAC end				
AUTHORS	was generated during the R&D process and may have higher chance of				
TITLE	clone tracking errors.				
JOURNAL	PRIMERS				
REFERENCE	Sequencing: M13Rev				
AUTHORS	LIBRARY				
TITLE	Vector : PKS145				
JOURNAL	R.Site 1 : SacI				
REFERENCE	R.Site 2 : SacI.				
AUTHORS	Location/Qualifiers				
TITLE	1. 1019				
JOURNAL	/organism="Pan troglodytes"				
REFERENCE	/db_xref="taxon:9598"				
AUTHORS	/clone="PTB-079A15.R"				
TITLE	/sex="male"				
JOURNAL	/cell_type="lymphoblast"				
REFERENCE	/clone_lib="PTB Chimpanzee Male BAC Library"				
AUTHORS	176 a 432 c 362 g 26 t 23 others				
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AUTHORS	Best Local Similarity		100.0%;	Pred. No. 0.17;	Length 1019;
TITLE	Matches	26;	Conservative	0;	Mismatches
JOURNAL					0;
REFERENCE					Indels
AUTHORS					0;
TITLE					Gaps
JOURNAL					0;
REFERENCE	QY	67	GCGGCGCGCGCGCGCGCGCGCGCG	92	
AUTHORS	DB	344	GCGGCGCGCGCGCGCGCGCGCGCG	369	
TITLE					
JOURNAL					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REFERENCE					
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REFERENCE					
AUTHORS					
TITLE					

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VERSION      BF311176.1  GI:11258971
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 1068)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
              Plate: L1C0M1020 row: 0 column: 11
              High quality sequence stop: 696.
              location/qualifiers
                1..1068
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                  /clone="IMAGE:4128226"
                  /clone_1lb="NIH_MGC_19"
                  /tissue_type="neuroblastoma"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally
                  cloned into EcoRI/XhoI sites using the following 5'
                  adaptor: GGCACGAG(G). Library constructed by Ling Hong
                  in the laboratory of Gerald M. Rubin (University of
                  California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies).
                  Note: this is a NIH-MGC library."
BASE COUNT   180 a      362 c      366 g      159 t      1 others
ORIGIN
Query Match 0.9%; Score 26; DB 12; Length 1068;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY          367 CGCGGCTGGGCGCTTCATCTACACGC 392
            |||||||
Db          442 CGCGGCTGGGCGCTTCATCTACACGC 467

Search completed: June 19, 2003, 16:36:22
Job time : 3483 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 11:25:16 ; Search time 6933 Seconds

(without alignments)
11636.085 Million cell updates/sec

Title: us-09-825-147-1

Sequence: 2772 1 atgccccgcacacacgcgcggg.....ctcatgtcaactgaataa 2772

Scoring table: OLIGO-MUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 24

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.ov:*
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25: em.pl:*
26: em.ro:*
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30: em.htg.hum:*
31: em.htg.in:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2772	100.0	2772	6 AX268474	AX268474 Sequence
2	2772	100.0	3111	6 AX268476	AX268476 Sequence
3	1552	56.0	3074	6 AX253254	AX253254 Sequence
4	1552	56.0	3074	6 AX456864	AX456864 Sequence
5	1552	56.0	3074	6 AF249278	AF249278 Homo sapi
6	1552	56.0	3137	6 AX056817	AX056817 Sequence
7	1552	56.0	3137	6 AF202977	AF202977 Homo sapi
8	1450	52.3	2694	6 AX325209	AX325209 Sequence
9	1297	46.8	2832	9 HSA263835	AF263835 Homo sapi
10	965	34.8	1691	9 HSA272519	AJ272519 Homo sapi
11	965	34.8	120846	9 AL365232	AL365232 Human DNA
12	347	12.5	47057	9 AL445569	AL445569 Human DNA
13	293	10.6	293	9 HSA272506	AJ272506 Homo sapi
14	270	9.7	548	6 AX318576	AX318576 Sequence
15	270	9.7	548	6 AX318764	AX318764 Sequence
16	221	8.0	821	9 HSA272515	AJ272515 Homo sapi
17	179	6.5	659	11 G58300	G58300 SHGC-104174
18	179	6.5	793	9 HSA272509	AJ272509 Homo sapi
19	179	6.5	154998	9 AL360236	AL360236 Human DNA
20	135	4.9	892	9 HSA272517	AJ272517 Homo sapi
21	133	4.8	847	9 HSA272518	AJ272518 Homo sapi
22	128	4.6	460	9 HSA272510	AJ272510 Homo sapi
23	128	4.6	834	9 HSA272508	AJ272508 Homo sapi
24	112	4.0	425	9 HSA272511	AJ272511 Homo sapi
25	110	4.0	767	9 HSA272513	AJ272513 Homo sapi
26	98	3.5	748	9 HSA272512	AJ272512 Homo sapi
27	96	3.5	561	9 HSA272507	AJ272507 Homo sapi
28	92	3.3	743	9 HSA272507	AJ272507 Homo sapi
29	70	2.5	319	11 G63779	G63779 G-104174 Ra
30	63	2.3	173373	2 AC112532	AC112532 Rattus no
31	56	2.0	158119	2 AC095944	AC095944 Rattus no
32	56	2.0	179192	2 AC095904	AC095904 Rattus no
33	56	2.0	248862	2 AC091215	AC091215 Rattus no
34	47	1.7	200	10 AF525837	AF525837 Rattus no
35	44	1.6	3108	10 AF263836	AF263836 Mus muscu
36	44	1.6	185864	2 AC131088	AC131088 Mus muscu
37	38	1.4	162123	2 AC115920	AC115920 Mus muscu
38	35	1.3	162123	2 AC115920	AC115920 Mus muscu
39	35	1.3	173373	2 AC112532	AC112532 Rattus no
40	35	1.3	213256	2 AC124139	AC124139 Mus muscu
41	35	1.3	267605	2 AC125483	AC125483 Mus muscu
42	35	1.3	331447	2 AC127359	AC127359 Mus muscu
43	29	1.0	389	11 AU049631	AU049631 Rattus no
44	29	1.0	1227	10 AB000502	AB000502 Mus muscu
45	29	1.0	1689	10 AB000503	AB000503 Mus muscu
46	29	1.0	1818	10 AB000500	AB000500 Mus muscu
47	29	1.0	2014	10 AB000501	AB000501 Mus muscu
48	29	1.0	2247	10 AB000504	AB000504 Mus muscu
49	29	1.0	2382	10 AB000498	AB000498 Mus muscu
50	29	1.0	2613	10 AF490773	AF490773 Mus muscu
51	29	1.0	2764	10 AB000497	AB000497 Mus muscu
52	29	1.0	2827	10 AB000496	AB000496 Mus muscu
53	29	1.0	2899	10 AB000495	AB000495 Mus muscu
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56	29	1.0	214572	2 AL450341	AL450341 Mouse DNA
57	26	0.9	1182	6 E13516	E13516 Human mRNA
58	26	0.9	1314	9 BC000699	BC000699 Homo sapi
59	26	0.9	1425	6 A94977	A94977 Sequence 4
60	26	0.9	1425	6 D82346	D82346 Homo sapien
61	26	0.9	2565	6 A94975	A94975 Sequence 2
62	26	0.9	2750	6 AX456861	AX456861 Sequence
63	26	0.9	2750	6 AF110020	AF110020 Homo sapi
64	26	0.9	3029	6 A94974	A94974 Sequence 1
65	26	0.9	3195	9 AF074247	AF074247 Homo sapi

Pred. No. is the number of results predicted by chance to have a

[illegible]

Db	1561	TTTCATGTTCCAAAACGGAAAGCTTTAAAGAAACATTACGTCACATATGATGTAAAAAGATGTC	1620
Qy	1621	ATTGAACAATATTCGTGTGGTCATCTGGACATGTTGTAGAAATTAAGACCTTCAANCA	1680
Db	1621	ATTGAACAATATTCGTGTGGTCATCTGGACATGTTGTGTGAATTTAAAGCCTTCAANCA	1680
Qy	1681	CCTGTGTGAATTCCTTGGAAGAGGCGAAATCCATACATATTAAGAGAGCCGAGAAA	1740
Db	1681	CGTGTGTGAATTCCTTGGAAGAGGCGAAATACATCACAATTAAGAGAGCCGAGAAA	1740
Qy	1741	ATAACAGAGAATCATGTAGACCCAGACGATCTCAGTATGCTCGGTGGTGTCAAGTT	1800
Db	1741	ATAACAGAGAATCATGTAGACCCAGACGATCTCAGTATGCTCGGTGGTGTCAAGTT	1800
Qy	1801	GAAGAAACAGTACAGTCCATAGAAATCCAGAGCTGACCTCTACTAGACATCTATCAACAG	1860
Db	1801	GAAGAAACAGTACAGTCCATAGAAATCCAACTGGACCTCTACTAGACATCTATCAACAG	1860
Qy	1861	GTCCCTTCGGAAAGGCTCTGCGCTCAGCCCTGCTGGCTTTCATTCACAGATCCCACTTTT	1920
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Qy	1921	GAATGTGAACAGACATCTGACTATCAAAAGCCTGTGTGATGACAAAGATCTTTCGGGTTCC	1980
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Qy	1981	GCACAAAAACAGTGGCTGTATTCAGATTCACATGTGTGCAACATCTCGAAGAGCCCTGCAG	2040
Db	1981	GCACAAAAACAGTGGCTGTATTCAGATTCACATGTGTGCAACATCTCGAAGAGCCCTGCAG	2040
Qy	2041	TTTCATCTCTGACGCCAAATGATGATTCAGTCCCGCAGACTTTCACGCGCTTACGCCCTACTATG	2100
Db	2041	TTTCATCTCTGACGCCAAATGATGATTCAGTCCCGCAGACTTTCACGCGCTTACGCCCTACTATG	2100
Qy	2101	CACAGTCACGACACACAGGTGGCCAAATAGTCAAAAGCGATGGCTGACGAGTGGCAGCCACC	2160
Db	2101	CACAGTCACGACACACAGGTGGCCAAATAGTCAAAAGCGATGGCTGACGAGTGGCAGCCACC	2160
Qy	2161	AACACATTCGCAAAACCAAAATTAATATGCGGCACCCCAAGCCAGAGCCCCCAACAATTTACAG	2220
Db	2161	AACACATTCGCAAAACCAAAATTAATATGCGGCACCCCAAGCCAGAGCCCCCAACAATTTACAG	2220
Qy	2221	ATCCCACTCTCTCTCCCAAGCCATCAAGATATCGCCCAAGCGAANAATCTGTGACCCCTAAC	2280
Db	2221	ATCCCACTCTCTCTCTCCCAAGCCATCAAGATATCGCCCAAGCGAANAATCTGTGACCCCTAAC	2280
Qy	2281	CCTGACAGCTTACAGAAAGCATTTCTGACGCTCACACACTGTGCTTGTTCCTCCACAGAA	2340
Db	2281	CCTGACAGCTTACAGAAAGCATTTCTGACGCTCACACACTGTGCTTGTTCCTCCACAGAA	2340
Qy	2341	AAATGTCAGGTTGCACAGTCAAATCTCACCAAGAGCCGTTCTATGAGGAAAAAGCTTTGAC	2400
Db	2341	AAATGTCAGGTTGCACAGTCAAATCTCACCAAGAGCCGTTCTATGAGGAAAAAGCTTTGAC	2400
Qy	2401	ATGGAGAGAGAAATCTGTTGCTCTCTGCTGCTCCCAATGAGTGCACCAAGAGACTTGGCCAAATCT	2460
Db	2401	ATGGAGAGAGAAATCTGTTGCTCTCTGCTGCTCCCAATGAGTGCACCAAGAGACTTGGCCAAATCT	2460
Qy	2461	TTGTCTGTGCAAAAACCTGATCAGTGCAGCCGAGGAATCAAAATTTACAGGAGGT	2520
Db	2461	TTGTCTGTGCAAAAACCTGATCAGTGCAGCCGAGGAATCAAAATTTACAGGAGGT	2520
Qy	2521	GAGTCAGTGGCTCCAGAGGCGCCCAAGATTTTACCCCAAAATGAGAGGAAATCCAAATTTG	2580
Db	2521	GAGTCAGTGGCTCCAGAGGCGCCCAAGATTTTACCCCAAAATGAGAGGAAATCCAAATTTG	2580
Qy	2581	TTTATTAACGTATGAAGAGTGGGTCGCCGAAGACAGAGACAGACACTTTTGATGCCGA	2640
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Qy	2641	CCGCAAGCCTGCCAGGAAGCTGCTTGTGATCAGACATCTCTTAAGACTCGAAGGTACAGA	2700
Db	2641	CCGCAAGCCTGCCAGGAAGCTGCTTGTGATCAGACATCTCTTAAGACTCGAAGGTACAGA	2700

LOCUS	AX268476	3111 bp	DNA	linear	PAT 29-OCT-2001
DEFINITION	Sequence 3 from Patent WO0175108.				
ACCESSION	AX268476				
VERSION	AX268476.1				
KEYWORDS	GI:16541653				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Hu, Y., Kiehe, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,				
JOURNAL	Zambrowicz, B. and Sands, A.T.				
FEATURES	Human ion channel protein and polynucleotides encoding the same				
source	Patent: WO 0175108-A 3 11-OCT-2001;				
	Lexicon Genetics Incorporated (US)				
	Location/Qualifiers				
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ORIGIN					
Query Match	100.0%; Score 2772; DB 6; Length 3111;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2772; Conservative	0; Mismatches				
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QY	61 GCGCAGACG	120			
DB	120 GCGCAGACG	179			
QY	121 TCGGGCGCGGGGAGAGGGTGTGCTGAACCTGGCAGCGCGCGCGCGCGCGCGCGCGCGCG	180			
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QY	301 AGCTGCG	360			
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QY	481 TTGATCTGAGATCTGATGATTTGTGCTTTTGGTTTGGAGTTTCAATCATTCGAATCTGG	540			
DB	540 TTGATCTGAGATCTGATGATTTGTGCTTTTGGTTTGGAGTTTCAATCATTCGAATCTGG	599			

QY 541 TCTGCGGGTTCGCTGTGTCGATATAGAGATGCGAAGAGACTGAGTTTCTCGAAG 600
DB TCTGCGGGTTCGCTGTGTCGATATAGAGATGCGAAGAGACTGAGTTTCTCGAAG 659
QY 601 CCGTCTGTGTATATAGATACCATTTGTTTATCGCTTCAATAGACAGTTTCTCGAAG 660
DB CCGTCTGTGTATATAGATACCATTTGTTTATCGCTTCAATAGACAGTTTCTCGAAG 719
QY 661 ACTCAGAGTAAATTTTGGCAGCTGTGACACTGAGAGTCTCCGTTTCTAGAGATCTC 720
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QY 721 CCGATGTGCGATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB CCGATGTGCGATGAGACCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 839
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QY 1261 CCGAGGAGGAG 1320
DB CCGAGGAGGAG 1379
QY 1321 ACCGACATCAG 1380
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QY 2581 TTTATTAAGTGAAG 2640
DB TTTATTAAGTGAAG 2699
QY 2641 CCGGAGGCTGCGAG 2700
DB CCGGAGGCTGCGAG 2759
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Db	2760	TCATCTCAGACGATTTGTATAGGCGAGAGAAAGTACAGATGCCCTCAGCTTCCATGTC	2819
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RESULT 3			
AX253254			
LOCUS	AX253254	3074 bp	DNA
DEFINITION	Sequence 1 from Patent WO0170811.		linear
ACCESSION	AX253254		PAT 10-OCT-2001
VERSION	AX253254.1	GI:16073802	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3074)		
TITLE	Lecher,C., Scherer,C., Seebom,G., Busch,A. and Steilmeyer,K. Potassium channel protein kcnq5, a target for diseases of central nervous system and cardiovascular system		
JOURNAL	Patent: WO 0170811-A 1 27-SEP-2001;		
FEATURES	Aventis Pharma Deutschland GmbH (DE)		
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
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ORIGIN			
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Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1552;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	1281	GAGCCGACAGACCTCAGTAGCTGCACAGAGGTCCCCAAGCACCGATCACAGCCGAGG	1340
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Db	1477	CATGCCACCAAGTGCAGAAAGACTGGAGGTTCAACGACCGACCCGCTTCGGCCCTC	1536
Qy	1401	GCTGCGCTCAAAAGTCTCAGCCCAAAACCAAGTGAATGCTGACACAGCCCTTGCGAC	1460
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Qy	1461	TGATGATGTAATGATGAAAAAGATGCCAGTGTATGATATAGTGAAGACCTCACCCC	1520
Db	1597	TGATGATGTAATGATGAAAAAGATGCCAGTGTATGATATAGTGAAGACCTCACCCC	1656
Qy	1521	ACGACTTAAACCTCATTCGAGCTCAGATTCAGATTTGAAATTTTCATGTTGCAAAAGGAA	1580
Db	1657	ACGACTTAAACCTCATTCGAGCTCAGATTCAGATTTGAAATTTTCATGTTGCAAAAGGAA	1716
Qy	1581	GTTTAAAGAAACATTACGTCCATATGATGTAATAAGATGTCATTTGAACAATATCTGTTG	1640
Db	1717	GTTTAAAGAAACATTACGTCCATATGATGTAATAAGATGTCATTTGAACAATATCTGTTG	1776
Qy	1641	TCATCTGGACATGTTGTGTAGAAATTAAAGCCTTCAAAACAGCTGTGATCAAAATTTCTTG	1700
Db	1777	TCATCTGGACATGTTGTGTAGAAATTAAAGCCTTCAAAACAGCTGTGATCAAAATTTCTTG	1836
Qy	1701	AAAAGGCAATTCACATCAGATTAAGAGAGCCGAGGAAATTAACAGCAGAACATGAGAC	1760
Db	1837	AAAAGGCAATTCACATCAGATTAAGAGAGCCGAGGAAATTAACAGCAGAACATGAGAC	1896
Qy	1761	CACAGACATCTCATATGCTGCTGGTGGTGCAGAGTTGAAAAACAGGTACAGTCCAT	1820

D	b		1897	CACAGCAGTCTCACTATGCTGGGTGCAGGTTGAATAAACAGGTACACTCAT	1956
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D	b		1957	ACAATCCAAGCTGGAGCTGCTACTAGACATCTATCAACAGGCTTCGGAAAGGCTCGC	2016
O	y		1881	CTCACGCCCTGGGCTTGCGTTCAATTCCAGATCCACCTTTTGAATGTGAACACATCTGA	1940
D	b		2017	GTCAGGCTCTGGCTTGGCTTCAATTCAGATCCACCCTTTTGAATGTGAACACATCTGA	2076
O	y		1941	CTATCAAAGCCCTGGTAGATGCAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTCTT	2000
D	b		2077	CTATCAAAGCCCTGGTAGATGCAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTCTT	2136
O	y		2001	ATCCAGATCACTAGTGGCCACATCTCGAGAGGCTCGAGTTCAATCTCAGCGCAATTA	2060
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D	b		2197	GTTTCAGTGGCCAGACCTTCTAGCGGTTTAGCCCTTACTATGACAGTCAAGCAACAGST	2256
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O	y		2421	GTCGTGTGTCCTCAATGGTGGCGGAAGGACTTGGGCAAACTTGTGCTGTGCAAAACCTGAT	2480
D	b		2557	GTCGTGTGTCCTCAATGGTGGCGGAAGGACTTGGGCAAACTTGTGCTGTGCAAAACCTGAT	2616
O	y		2481	CAGGTGCAAGCAGAGAACTGAATATACAACCTTCAGGAGTGAAGTCAAGTGGCTCCAAGG	2540
D	b		2617	CAGGTGCAAGCAGAGAACTGAATATACAACCTTCAGGAGTGAAGTCAAGTGGCTCCAAGG	2676
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LOCUS AX456864 3074 bp DNA linear PAT 06-JUL-2002					
DEFINITION Sequence 5 from Patent WO0232960.					
ACCESSION AX456864					

VERSION	AX56864.1	GI:21715731
KEYWORDS	human.	
SOURCE ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE TITLE	Argenteiri,T.M. and Sheldon,J.H. Methods of selecting compounds for modulation of bladder function Patent: WO 0232960-A 5 25-APR-2002;	
AUTHORS	Myeth (US)	
JOURNAL		
FEATURES	Location/Qualifiers source 1..3074 /organism="Homo sapiens" /db_xref="taxon:9606"	
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Best Local Similarity	100.0%; Pred. No. 0;	
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OY	1581 GTTTAAGGAACATTACGTCATATGATGTAAAAAGATGTCATGAACAATATTCCTCGTG	1640
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LOCUS	DEFINITION	LOCUS	DEFINITION
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LOCUS	AF249278		
DEFINITION	Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete cds.		
ACCESSION	AF249278		
VERSION	AF249278.1		
KEYWORDS	GI:9651966		
SOURCE			
ORGANISM	Homo sapiens.		
	Homo sapiens.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 3074)		
AUTHORS	Leitch,C., Scherer,C.R., Seebom,G., Derst,C., Wei,A.D., Busch,A.E.		
	and Steinmeyer,K.		
TITLE	Molecular cloning and functional expression of KCNQ5, a potassium		
JOURNAL	channel subunit that may contribute to neuronal M-current diversity		
MEDLINE	J. Biol. Chem. 275 (29), 22395-22400 (2000)		
	20357367		

PUBLISHED 10787416
REFERENCE 2 (bases 1 to 3074)
AUTHORS Lerche, C., Scherer, C.R., Seeböhm, G., Derst, C., Wei, A.D., Busch, A.E. and Stelmeyer, K.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma
FEATURES Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
LOCATIONS 1 3074
QUALIFIERS Location/Qualifiers

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ACCESSION AX056817
VERSION AX056817.1 GI:12309758
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Jentsch, T.J.

REFERENCE
AUTHORS
TITLE Novel potassium channels and genes encoding these potassium
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ACCESSION					member 5 (KCNO5) mRNA, complete cds.
VERSION					AF202977
KEYWORDS					AF202977.1 GI:7798695
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					Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE					1 (bases 1 to 3137)
AUTHORS					Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and
					Jentsch,T.J.
					KCNO5, a novel potassium channel broadly expressed in brain,
					mediates M-type currents
					J. Biol. Chem. 275 (31), 24089-24095 (2000)
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MEDLINE					10816588
PUBMED					2 (bases 1 to 3137)
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AUTHORS					Jentsch,T.J.
					Direct Submission
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AF263835
VERSION AF263835.1 GI:8132996
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DB 1335 ACCACTTAAAGTGTGATTCGAGCTATCAGATTTATGAAATTTTATGATTTGCAAAACGGAA 1394
OY 1581 GTTTAAGGAAACATTCACGCCAAACACGATGATGATGATGATGATGATGATGATGAT 1640
DB 1395 GTTTAAGGAAACATTCACGCCAAACACGATGATGATGATGATGATGATGATGATGAT 1454
OY 1641 TCATCGAGCATGTTGTGTAAGTAAAGCTTCAACAGTGTGATGATGATGATGATGATGAT 1700
DB 1455 TCATCGAGCATGTTGTGTAAGTAAAGCTTCAACAGTGTGATGATGATGATGATGATGAT 1514
OY 1701 AAAAGGCAATATACATCAGATTAAGAGACCGGAGAAATATACAGAGAAATGAGAGAC 1760
DB 1515 AAAAGGCAATATACATCAGATTAAGAGACCGGAGAAATATACAGAGAAATGAGAGAC 1574
OY 1761 CACAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
DB 1575 CACAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1634
OY 1821 AGAATCCAAAGTGCATGCTTACTAGATCTATCAACAGTCTCTCGGAAAGGCTTCG 1880
DB 1635 AGAATCCAAAGTGCATGCTTACTAGATCTATCAACAGTCTCTCGGAAAGGCTTCG 1694
OY 1881 CTGAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGATCTGA 1940
DB 1695 CTGAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGATCTGA 1754
OY 1941 CTATCAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
DB 1755 CTATCAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1814
OY 2001 ATCCAGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2060
DB 1815 ATCCAGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1874
OY 2061 GTTAGAGCCAGACTTCTAGGCTTACTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2120
DB 1875 GTTAGAGCCAGACTTCTAGGCTTACTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1934
OY 2121 GCCAATTAAGTCAAAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2180
DB 1935 GCCAATTAAGTCAAAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1994

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OY		2181	AAATCGGCGACCCCAAGCCGACGAGCCCCAACACTTTACAATGCCACCTCCTCCAGC	2240
Db		1995	AAATCGGCGACCCCAAGCCGACGAGCCCCAACACTTTACAATGCCACCTCCTCCAGC	2054
OY		2241	CATCAAGCATGTGGCCAGGCSCGAAGAAGTCTGGACGCGTAACCCTGGACGGCTTACGGAAG	2300
Db		2055	CATCAAGCATGTGGCCAGGCSCGAAGAAGTCTGGACGCGTAACCCTGGACGGCTTACGGAAG	2114
OY		2301	CATTTCATACGTCACACACCTGCGCTTGTCCTTCACGAAGAAAATGTCAGGTTGCACAGTC	2360
Db		2115	CATTTCATACGTCACACACCTGCGCTTGTCCTTCACGAAGAAAATGTCAGGTTGCACAGTC	2174
OY		2361	AAATCTCACAAAGAGACCGTTCTCATGAGGAAAAAGCTTGACATGGGAGGAGAAACTCTGTT	2420
Db		2175	AAATCTCACAAAGAGACCGTTCTCATGAGGAAAAAGCTTGACATGGGAGGAGAAACTCTGTT	2234
OY		2421	GTCCTGTCTGTCCCATGTGTCGCGAAGACTTGGCGCAAATCTTGTCTGTGTGCAAAACCGTAT	2480
Db		2235	GTCCTGTCTGTCCCATGTGTCGCGAAGACTTGGCGCAAATCTTGTCTGTGTGCAAAACCGTAT	2294
OY		2481	CAGGTGACACCGAGAGAACTGAATATPACAATTCAGGGATGAGTCAAGTGGCTCCAGAGC	2540
Db		2295	CAGGTGACACCGAGAGAACTGAATATPACAATTCAGGGATGAGTCAAGTGGCTCCAGAGC	2354
OY		2541	CAGCCAAGATTTTATACCCCAAAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAGT	2600
Db		2355	CAGCCAAGATTTTATACCCCAAAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAGT	2414
OY		2601	GGGTGCCGGAAGAGACAGAGACAGACACTTTTGATGCCGACCGACGCGCTCCACAGGAGC	2660
Db		2415	GGGTGCCGGAAGAGACAGAGACAGACACTTTTGATGCCGACCGACGCGCTCCACAGGAGC	2474
OY		2661	TGCGCTTGGCATCAGACCTCTCTAAGAGACTGGAAGGTACAGATCATCTCAGAGCATTTGTAA	2720
Db		2475	TGCGCTTGGCATCAGACCTCTCTAAGAGACTGGAAGGTACAGATCATCTCAGAGCATTTGTAA	2534
OY		2721	GGCAGAGAGAAGATPACAGATGAGCCCTCAGGTTGCTTCATGTCAACATCGAATAA	2772
Db		2535	GGCAGAGAGAAGATPACAGATGAGCCCTCAGGTTGCTTCATGTCAACATCGAATAA	2586
RESULT 10				
HSA272519				
LOCUS				
DEFINITION			HSA272519	1691 bp DNA linear PRI 21-FEB-2002
ACCESSION			AJ272519	
VERSION			AJ272519.1	GI:18873690
KEYWORDS			KCNQ5 gene; KCNQ5 protein.	
SOURCE			human.	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE			1 Kanamuru,C., Blevvert,B., Hechenberger,M., Engels,H. and	
JOURNAL			Steinlein,O.K.	
REFERENCE			The new voltage gated potassium channel KCNQ5 and earlyinfantile	
AUTHORS			convulsions	
TITLE			Unpublished	
JOURNML			2 (bases 1 to 1691)	
FEATURES			Steinlein,O.K.	
source			Direct Submission	
			Submitted (22-FEB-2000) Steinlein O.K., Institute of Human	
			Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY	
			Location/Qualifiers	
			1..1691	
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			/map="6q14"	
			286..1248	
			/gene="KCNQ5"	
			286..1248	
exon				

BASE COUNT	508 a	397 c	337 g	448 t	1 others
Query Match	34.8%;	Score 965;	DB 9;	Length 1691;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 965;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
ORIGIN	/gene="KCNQ5" /number=14 /usedin=AJ272506:KCNQ5_cds				
QY	1808	AGGTACAGTCCATAGAAATCAAGCTGAGTGCCTACTAGACATCTATCAACAGGTCCCTC	1867		
Db	284	AGGTACAGTCCATAGAAATCAAGCTGAGTGCCTACTAGACATCTATCAACAGGTCCCTC	343		
QY	1868	GGAAGGGCTGCTGCTCAGGCCCTCGCTTGGCTTCATCCAGATCCACCTTTGAAATGTG	1927		
Db	344	GGAAGGGCTGCTGCTCAGGCCCTCGCTTGGCTTCATCCAGATCCACCTTTGAAATGTG	403		
QY	1928	AACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCACAAA	1987		
Db	404	AACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCACAAA	463		
QY	1988	ACAGGGCTGCTTATCCAGATTAAGTACGTGCAACATCTTGAGAGGCTTCGACTTCATTC	2047		
Db	464	ACAGGGCTGCTTATCCAGATTAAGTACGTGCAACATCTTGAGAGGCTTCGACTTCATTC	523		
QY	2048	TGAGGCCAAATGAGTTCAGTGGCCAGACTCTTTCAGCCGGTTGAGCCCTACTATGACAGTGC	2107		
Db	524	TGAGGCCAAATGAGTTCAGTGGCCAGACTCTTTCAGCCGGTTGAGCCCTACTATGACAGTGC	583		
QY	2108	AAGCAACACAGTGGCCAAATTAGTCAAAAGGATGGCTCAGCAGTGGAGGCCACCAACACA	2167		
Db	584	AAGCAACACAGTGGCCAAATTAGTCAAAAGGATGGCTCAGCAGTGGAGGCCACCAACACA	643		
QY	2168	TTGCAAAACCAATTAATACGGCACCCAGGCCAGGCCCAACAACTTATACAGATCCGAC	2227		
Db	644	TTGCAAAACCAATTAATACGGCACCCAGGCCAGGCCCAACAACTTATACAGATCCGAC	703		
QY	2228	CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAATCTGACCTTAACCTCGCAG	2287		
Db	704	CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAATCTGACCTTAACCTCGCAG	763		
QY	2288	GCTTACAGGAAAGCATTTCTGACGTCCACACACTGCTGTTGTGCTCCCAAGAAATGTTC	2347		
Db	764	GCTTACAGGAAAGCATTTCTGACGTCCACACACTGCTGTTGTGCTCCCAAGAAATGTTC	823		
QY	2348	AGGTTGCACAGTCAAAATCTCACCAAGGACCTTCTATAGAGAAAGCTTGTGATGGGGG	2407		
Db	824	AGGTTGCACAGTCAAAATCTCACCAAGGACCTTCTATAGAGAAAGCTTGTGATGGGGG	883		
QY	2408	GAAAAATCTGTTGTCTGTCTGTCCATGGTCCGAAGGACTTGGGCAAAATCTTGTCTG	2467		
Db	884	GAAAAATCTGTTGTCTGTCTGTCCATGGTCCGAAGGACTTGGGCAAAATCTTGTCTG	943		
QY	2468	TGCAAAACCTGATCAGGTGACCGAGAGAACTGAATATACAATCTTCAAGGAGTGAGTCA	2527		
Db	944	TGCAAAACCTGATCAGGTGACCGAGAGAACTGAATATACAATCTTCAAGGAGTGAGTCA	1003		
QY	2528	GTGGCTCCAGAGGACCCAAAGATTTTACCACAAATGGAGGAAATCCAAATGTTTATA	2587		
Db	1004	GTGGCTCCAGAGGACCCAAAGATTTTACCACAAATGGAGGAAATCCAAATGTTTATA	1063		
QY	2588	CTGATGANAAGAGGTGGTCCCGAAGACAGACAGACAGCACTTTTGATGCGCACCGCAGC	2647		
Db	1064	CTGATGANAAGAGGTGGTCCCGAAGACAGACAGACAGCACTTTTGATGCGCACCGCAGC	1123		
QY	2648	CTGCCAGGGAAGCTGCTTGGATCAGACCTCTGAAGGACTGGGAAGTCAAGATCAATTC	2707		
Db	1124	CTGCCAGGGAAGCTGCTTGGATCAGACCTCTCTGAAGGACTGGGAAGTCAAGATCAATTC	1183		
QY	2708	AGAGCATTTTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCATGTCAAACTGA	2767		
Db	1184	AGAGCATTTTGAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCATGTCAAACTGA	1243		

OY 2768 AATAA 2772
 |||||
 Db 1244 AATAA 1248

RESULT 11
 AL365232
 LOCUS 120846 bp DNA linear PRI 01-MAR-2001
 DEFINITION Human DNA sequence from clone RP11-257K9 on chromosome 6, complete sequence.

ACCESSION AL365232
 KEYWORDS AL365232.24 GI:13234949
 SOURCE HTG.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 120846)

REFERENCE
 AUTHORS Williams, S.
 TITLE Direct Submision
 JOURNAL Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Mar 5, 2001 this sequence version replaced gi:13160293.

COMMENT
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at
<http://www.sanger.ac.uk/projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-257K9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-257K9 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true left end of clone RP11-257K9 is at 1 in this sequence. The true left end of clone RP1-319022 is at 120747 in this sequence. The true right end of clone RP11-380M3 is at 18652 in this sequence.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="6"
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 /clone_1id="RPCI-11.1"
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 4469..4695
 /note="MIR repeat: matches 28. .261 of consensus"
 7930..8258
 /note="MIR repeat: matches 1. .365 of consensus"
 8713..9200
 /note="MIR repeat: matches 1. .568 of consensus"

repeat_region
 9523..9826
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 repeat_region
 11464..11893
 /note="MIR repeat: matches 72. .536 of consensus"
 repeat_region
 12067..12277
 /note="MIR repeat: matches 8. .245 of consensus"
 repeat_region
 12626..12979
 /note="MIR repeat: matches 1. .371 of consensus"
 repeat_region
 13234..13542
 /note="AluY repeat: matches 3. .309 of consensus"
 repeat_region
 13931..14179
 /note="MIR repeat: matches 21. .262 of consensus"
 repeat_region
 14522..14579
 /note="L2 repeat: matches 2655. .2710 of consensus"
 repeat_region
 16405..16696
 /note="AluSg repeat: matches 1. .295 of consensus"
 repeat_region
 16697..16722
 /note="L3 copies 2 mer ga 928 conserved"
 repeat_region
 16801..17320
 /note="L1MD1 repeat: matches 5188. .5745 of consensus"
 repeat_region
 17437..17496
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 repeat_region
 17506..17660
 /note="L1MD1 repeat: matches 5753. .5906 of consensus"
 repeat_region
 17738..18052
 /note="L1MD1 repeat: matches 5908. .6223 of consensus"
 repeat_region
 18473..18730
 /note="HAI1 repeat: matches 890. .1179 of consensus"
 repeat_region
 18829..19080
 /note="HAI1 repeat: matches 797. .1052 of consensus"
 repeat_region
 19213..19412
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 repeat_region
 19507..19632
 /note="HAI1 repeat: matches 2. .133 of consensus"
 repeat_region
 21835..21924
 /note="L2 repeat: matches 2542. .2634 of consensus"
 repeat_region
 23241..23537
 /note="AluSg repeat: matches 1. .308 of consensus"
 24751..25402
 /note="CpG Island"
 /evidence="not_experimental"
 25146..25454
 /note="AluSg repeat: matches 1. .312 of consensus"
 repeat_region
 25963..26384
 /note="L1PA13 repeat: matches 5719. .6156 of consensus"
 repeat_region
 26891..27204
 /note="AluY repeat: matches 1. .311 of consensus"
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 27647..27824
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 27854..28504
 /note="L1MA4A repeat: matches 5646. .6295 of consensus"
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 28796..29115
 /note="AluSg repeat: matches 1. .310 of consensus"
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 29598..29996
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 29997..30290
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 30291..30303
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 repeat_region
 30340..30353
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 repeat_region
 30354..30668
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 30669..31120
 /note="MERS repeat: matches 396. .861 of consensus"
 repeat_region
 31872..32173
 /note="AluY repeat: matches 1. .294 of consensus"
 repeat_region
 32560..32851
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 repeat_region
 32905..33039
 /note="MIR repeat: matches 31. .159 of consensus"
 repeat_region
 33040..33341
 /note="AluY repeat: matches 1. .298 of consensus"

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 47057)
Bates, K.
Direct Submission
Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
<http://www.sanger.ac.uk/Projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/Help/Chr6>

RP11-135M8 is from the library RPCR-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>
VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-135M8. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP3-474615 is at 100 in this sequence. The true right end of clone RP11-135M8 is at 47057 in this sequence.

FEATURES

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/chromosome="6"
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/clone_lib="RPC1-11.1"
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3341..5507
/note="CpG island"
/evidence="not_experimental"
4646..4735
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5518..5553
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5732..5831
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5769..5828
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6079..6504
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7839..8140
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8359..8518
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8896..9177
/note="L2 repeat: matches 1737..2050 of consensus"
9228..9290
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9294..9811
/note="L2 repeat: matches 1216..1728 of consensus"
9851..10280
/note="L2 repeat: matches 2290..2710 of consensus"

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10443..10519
/note="MIR repeat: matches 64..150 of consensus"
10655..10728
/note="L2 repeat: matches 2065..2122 of consensus"
10729..11038
/note="AluXg repeat: matches 1..307 of consensus"
11039..11089
/note="L2 repeat: matches 2122..2177 of consensus"
12567..12683
/note="L2 repeat: matches 2572..2694 of consensus"
12867..13157
/note="L2 repeat: matches 1995..2283 of consensus"
13380..13920
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13721..14158
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14253..14566
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14592..15509
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15511..16185
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16688..16993
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24397..24429
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24456..24578
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26239..26541
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26541..26707
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27213..27527
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28352..28395
/note="22 copies 2 mer ta 81% conserved"
29176..29316
/note="MER58B repeat: matches 172..313 of consensus"
29553..29608
/note="28 copies 2 mer aa 78% conserved"
29624..29663
/note="20 copies 2 mer ga 82% conserved"
30427..30668
/note="L1ME2 repeat: matches 5692..5945 of consensus"
34982..35055
/note="MIR repeat: matches 117..201 of consensus"
36030..36161
/note="MIR repeat: matches 123..255 of consensus"
36487..36558
/note="L2 repeat: matches 2656..2749 of consensus"
37144..37239
/note="24 copies 4 mer ttct 94% conserved"
37681..38061
/note="L2 repeat: matches 1996..2395 of consensus"
39084..39361


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Db      181 TACAGAGTACCAAGCTGCGCGCAACGTCACCGGGGTGAGAACTACCTG 240
OY      346 TACACAGTGTGAGAGACCCCGCGCTGGGCTTATCTACACGCTTTGCT 398
Db      241 TACAAAGTGTGAGAGACCCCGCGCTGGGCTTATCTACACGCTTTGCT 293

RESULT 14
LOCUS   AX318576                      548 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 81 from Patent WO0177155.
ACCESSION AX318576
VERSION   AX318576.2 GI:21713342
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Fernandes,E., Vernet,C.A., Mishnu,V.S., Leach,M.D., Shinkets,R.A.,
          Zerhusen,B.D. and Kekuda,R.
          Orfx polynucleotides and polypeptides
          Patent: WO 0177155-A 81 18-OCT-2001;
          Curgan Corporation (US)
          On Jul 8, 2002 this sequence version replaced gi:17900990.
FEATURES
source    1. 548
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          /db_xref="taxon:9606"

BASE COUNT      83 a      152 c      194 g      119 t

Query Match
Best Local Similarity 100.0%; Score 270; DB 6; Length 548;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      158 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCCGCGGCGACGCTGGGCGGCGG 217
Db      95 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCCGCGGCGACGCTGGGCGGCGG 154
OY      218 GTGGCGCTGAGGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGC 277
Db      155 GTGGCGCTGAGGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGC 214
OY      278 CGCTCTTACACAGTAGTACGAGCTGCGCGGCGCAACGTAAGTACCGGGGGTGACAGA 337
Db      215 CGCTCTTACACAGTAGTACGAGCTGCGCGGCGCAACGTAAGTACCGGGGGTGACAGA 274
OY      338 ACACACGCTGACACGCTGCTGAGAGACCCGCGGCGGCTGCTACCTACACGCTTTGCG 397
Db      275 ACTACCTGTACACGCTGCTGAGAGACCCGCGGCGGCTGCTACCTACACGCTTTGCG 334
OY      398 TTTTCTCCTTGTGCTTTGCTTGTGATT 427
Db      335 TTTTCTCCTTGTGCTTTGCTTGTGATT 364

RESULT 15
LOCUS   AX318764                      548 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 269 from Patent WO0177155.
ACCESSION AX318764
VERSION   AX318764.1 GI:17901084
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Fernandes,E., Vernet,C.A., Mishnu,V.S., Leach,M.D., Shinkets,R.A.,
          Zerhusen,B.D. and Kekuda,R.
          Orfx polynucleotides and polypeptides

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JOURNAL Patent: WO 0177155-A 269 18-OCT-2001;
FEATURES Curgan Corporation (US)
source    Location/Qualifiers
          1. 548
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /note="Expressed in Bone,Osteosarcoma, Lymphoid
          tissue,Lymph node-Internal ID: FLC:2498 -
          accnos=11755212/11755212 correct-Encodes a protein in
          sequence listing 270 that is 47% similar to gi14758632
          potassium voltage-gated channel, KQT-like subfamily,
          member 4"

BASE COUNT      83 a      152 c      194 g      119 t

Query Match
Best Local Similarity 100.0%; Score 270; DB 6; Length 548;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      158 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCCGCGGCGACGCTGGGCGGCGG 217
Db      95 CCAGGGGCGGAGCGCTGCTACTGCTGTGGCAACCCGCGGCGACGCTGGGCGGCGG 154
OY      218 GTGGCGCTGAGGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGC 277
Db      155 GTGGCGCTGAGGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCTGCTGGGGAAGC 214
OY      278 CGCTCTTACACAGTAGTACGAGCTGCGCGGCGCAACGTAAGTACCGGGGGTGACAGA 337
Db      215 CGCTCTTACACAGTAGTACGAGCTGCGCGGCGCAACGTAAGTACCGGGGGTGACAGA 274
OY      338 ACTACCTGTACACGCTGCTGAGAGACCCGCGGCGGCTGCTACCTACACGCTTTGCG 397
Db      275 ACTACCTGTACACGCTGCTGAGAGACCCGCGGCGGCTGCTACCTACACGCTTTGCG 334
OY      398 TTTTCTCCTTGTGCTTTGCTTGTGATT 427
Db      335 TTTTCTCCTTGTGCTTTGCTTGTGATT 364

RESULT 16
LOCUS   HSA272515                      821 bp      DNA      linear      PRI 21-FEB-2002
DEFINITION Homo sapiens partial KCNQ5 gene, exon 10.
ACCESSION AJ272515
VERSION   AJ272515.1 GI:18873686
KEYWORDS  KCNQ5 gene; KCNQ5 protein.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE
AUTHORS   Kananura,C., Bievvert,B., Hechenberger,M., Engels,H. and
          Steinlein,O.K.
          The new voltage gated potassium channel KCNQ5 and early infantile
          convulsions
          Unpublished
          Steinlein,O.K.
          Direct Submission
          Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
          Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
          Location/Qualifiers
          1. 821
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /chromosome="6"
          /map="cg14"
          323..543
          /gene="KCNQ5"
          323..543
          /gene="KCNQ5"
          /number=10

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misc_feature      complement(40907..41435)
                   /note="match: GSS: Em:A0724407"
misc_feature      41084..41545
                   /note="match: GSS: Em:A0144356"
repeat_region     41812..42593
                   /note="MERIB repeat: matches 2..790 of consensus"
                   42775..42937
                   /note="L2 repeat: matches 2360..2521 of consensus"
repeat_region     43050..43159
                   /note="L2 repeat: matches 2624..2736 of consensus"
repeat_region     43165..43441
                   /note="L2 repeat: matches 2487..2710 of consensus"
repeat_region     44149..44406
                   /note="AluJo repeat: matches 3..293 of consensus"
misc_feature      complement(44409..44950)
                   /note="match: GSS: Em:A0316119
match: STS: Em:G59247"
repeat_region     44717..45220
                   /note="L2 repeat: matches 1686..2222 of consensus"
misc_feature      complement(46056..46290)
                   /note="match: GSS: Em:A2340331"
misc_feature      46107..46212
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misc_feature      complement(46107..46212)
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misc_feature      46113..46222
                   /note="match: GSS: Em:A0307337"
misc_feature      complement(46125..46222,85424..85552)
                   /note="match: STS: Em:G08746"
misc_feature      46125..46222
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misc_feature      complement(46129..46222,85430..85560)
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misc_feature      join(46140..46204,85438..85547)
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misc_feature      46140..46227
                   /note="match: GSS: Em:A2327331"
misc_feature      complement(46141..46204,85460..85563)
                   /note="match: STS: Em:G10403"
misc_feature      join(46142..46204,85460..85553)
                   /note="match: STS: Em:L30467"
misc_feature      complement(46144..46204,85445..85569)
                   /note="match: STS: Em:G08112"
misc_feature      complement(46145..46222,85432..85552)
                   /note="match: STS: Em:G10066"
misc_feature      join(46147..46222,85403..85552)
                   /note="match: STS: Em:L18516"
misc_feature      complement(46150..46222,85236..85570)
                   /note="match: GSS: Em:A2278393"
misc_feature      join(46150..46216,85380..85568)
                   /note="match: GSS: Em:A2436733"
misc_feature      complement(46150..46235,85455..85567)
                   /note="match: GSS: Em:A2005602"
misc_feature      complement(46150..46222,85432..85560)
                   /note="match: GSS: Em:A2035333"
misc_feature      complement(46150..46275,85289..85560)
                   /note="match: GSS: Em:A2696344"
misc_feature      join(46150..46216,85368..85555)
                   /note="match: GSS: Em:A0122775"
misc_feature      complement(46150..46216,75487..75764,85371..85531)
                   /note="match: GSS: Em:A2593167"
misc_feature      join(46150..46216,85434..85528)
                   /note="match: GSS: Em:A2850525 Em:A2850535"
misc_feature      join(46150..46216,85369..85504)
                   /note="match: GSS: Em:A0921614"
misc_feature      join(46150..46216,85358..85401)

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Query Match 6.5%; Score 179; DB 9; Length 15498;
 Best Local Similarity 100.0%; Pred. No. 7.2e-93;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

615 AGATACCATGTTCTTATCGCTTAATAGACGTTGTTCTGCAAAACTCAGGGTAATAT 674
 |||

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Db      99107 AGATACCATGTTCTTATCGCTTAATAGACGTTGTTCTGCAAAACTCAGGGTAATAT 99166
Qy      675 TTTTCCACGTTGACATGAGAGTCTCGTTTCCACACATCTCCGATGGCGCAT 734
Db      99167 TTTTCCACGTTGACATGAGAGTCTCGTTTCCACACATCTCCGATGGCGCAT 99226
Qy      735 GCACCGAAGGGAGGACGACTTGGAATTTAGTGGTTCAGTGGTTATGCTCAGACAGAG 793
Db      99227 GCACCGAAGGGAGGACGACTTGGAATTTAGTGGTTCAGTGGTTCAGTGGTTCAGACAGAG 99285

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RESULT 20
LOCUS      HSA272517
DEFINITION Homo sapiens partial KCNQ5 gene, exon 12.
VERSION    AJ272517.1 GI:18873688
KEYWORDS   KCNQ5 gene; KCNQ5 protein.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS    Kanamura,C., Bievvert,B., Hechenberger,M., Engels,H. and
            Steinlein,O.K.
TITLE      The new voltage gated potassium channel KCNQ5 and earlyinfantile
            convulsions
JOURNAL    Unpublished
REFERENCE 2 (bases 1 to 892)
AUTHORS    Steinlein,O.K.
TITLE      Direct Submission
JOURNAL    Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
            Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
FEATURES   source
            1..892
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="6"
            /map="6q14"
            343..474
            /gene="KCNQ5"
            343..474
            /gene="KCNQ5"
            /number=12
            /usedin=AJ272506;KCNQ5.Cds
BASE COUNT 276 a 138 c 154 g 324 t
ORIGIN

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Query Match 4.9%; Score 135; DB 9; Length 892;
Best Local Similarity 100.0%; Pred. No. 6.1e-67;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1548 CAGAAATTATGAAATTCATGTTGCAAAAGCAAGTTAAAGCAATTCATGATATGA 1607
Db      340 CAGAAATTATGAAATTCATGTTGCAAAAGCAAGTTAAAGCAATTCATGATATGA 399
Qy      1608 TGTAAAGATGTCATGACAAATATCTGCTGTCATCTGACATCTGTTGCTAATAATTA 1667
Db      400 TGTAAAGATGTCATGACAAATATCTGCTGTCATCTGACATCTGTTGCTAATAATTA 459
Qy      1668 AAGCCTTCAAACACG 1682
Db      460 AAGCCTTCAAACACG 474

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RESULT 21
LOCUS      HSA272518
DEFINITION Homo sapiens partial KCNQ5 gene, exon 13.
VERSION    AJ272518.1 GI:18873689
KEYWORDS   KCNQ5 gene; KCNQ5 protein.
SOURCE     human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 847)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .847
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6q14"
391. .517
/gene="KCNO5"
391. .517
/gene="KCNO5"
/number=13
/usedin=AJ272506:KCNO5_cds

BASE COUNT 286 a 135 c 128 g 297 t 1 others
ORIGIN

Query Match 4.8%; Score 133; DB 9; Length 847;
Best Local Similarity 100.0%; Pred. No. 9.2e-66;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1682 GTGTTGATCAATTTCTGGAAGGCGCAATCATCATGATAGAGAGCGGAGAGAAA 1741
|||||
DB 330 GTGTTGATCAATTTCTGGAAGGCGCAATCATCATGATAGAGAGCGGAGAGAAA 449
|||||

OY 1742 TTAACGACAGATGAGACAGACAGATCTAGTATGTCGGTGGTCAAGGTTG 1801
|||||
DB 450 TTAACGACAGATGAGACAGACAGATCTAGTATGTCGGTGGTCAAGGTTG 509
|||||

OY 1802 AAAACAGGTACA 1814
|||||
DB 510 AAAACAGGTACA 522
|||||

RESULT 22
HSA272510 HSA272510 460 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens partial KCNO5 gene, exon 5.
DEFINITION AJ272510
ACCESSION AJ272510.1 GI:18873681
VERSION KCNO5 gene; KCNO5 protein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 460)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .460
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/db_xref="taxon:9606"
/chromosome="6"

gene /map="6q14"
202. .327
/gene="KCNO5"
202. .327
exon /gene="KCNO5"
/number=5
/usedin=AJ272506:KCNO5_cds

BASE COUNT 153 a 63 c 76 g 168 t
ORIGIN

Query Match 4.8%; Score 128; DB 9; Length 460;
Best Local Similarity 100.0%; Pred. No. 8.1e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 791 AGAATTAATACAGCTTGTATAGATTTTGTCTTATTTTCTGCTTCTG 850
|||||
DB 200 AGAATTAATACAGCTTGTATAGATTTTGTCTTATTTTCTGCTTCTG 259
|||||

OY 851 TCTATCTGTGGAAGAGATGCCAATTAAGATTTTCTACATATGACATGCTCTG 910
|||||
DB 260 TCTATCTGTGGAAGAGATGCCAATTAAGATTTTCTACATATGACATGCTCTG 319
|||||

OY 911 GGGGCACA 918
|||||
DB 320 GGGGCACA 327
|||||

RESULT 23
HSA272508 HSA272508 834 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens partial KCNO5 gene, exon 3.
DEFINITION AJ272508
ACCESSION AJ272508.1 GI:18873679
VERSION KCNO5 gene; KCNO5 protein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kanamura, C., Bliervert, B., Hechenberger, M., Engels, H. and
Steinlein, O. K.
TITLE The new voltage gated potassium channel KCNO5 and early infantile
convulsions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 834)
AUTHORS Steinlein, O. K.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source
1. .834
/organism="Homo sapiens"
/db_xref="taxon:9606"
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355. .481
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355. .481
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BASE COUNT 244 a 144 c 167 g 279 t
ORIGIN

Query Match 4.8%; Score 128; DB 9; Length 834;
Best Local Similarity 100.0%; Pred. No. 8.2e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 489 GGAGTTCGATGATGTTGCTGTTGTTGATTCATTCGAATCTGTCGCGG 548
|||||
DB 354 GGAGTTCGATGATGTTGCTGTTGTTGATTCATTCGAATCTGTCGCGG 413
|||||

OY 549 TTGCTGTTGATATAGAGATGGCAAGAACTGAGTTTCTGCAAGCCCTTCTG 608
|||||

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Db      414 TTGCTGTTCGATATAGAGATGCAAGAGACTGAGGTTTCGCGAAGCCCTTCTG 473
QY      609 TGTATAG 616
        |||||
Db      474 TGTATAG 481

RESULT 24
HSA272511      HSA272511      425 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 6.
ACCESSION      AJ272511
VERSION        AJ272511.1 GI:18873682
KEYWORDS       KCNQ5 gene; KCNQ5 protein.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and
                Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
                convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 425)
AUTHORS       Steinlein,O.K.
TITLE         Direct Submision
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
                Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
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gene          151..261
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                /number="6"
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exon          151..261
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                /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    124 a      80 c      70 g      151 t
ORIGIN
Query Match   4.0%; Score 112; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.2e-53;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      919 ATTACATTGACAACTATTGGCTATGAGACAACCTCCCTAAGTGGTGGGAAGATG 978
        |||||
Db      151 ATTACATTGACAACTATTGGCTATGAGACAACCTCCCTAAGTGGTGGGAAGATG 978
QY      979 CTTTCTGAGGCTTTGCACTCCTTGGCAATTTCTTTGTCACATTCCTGCG 1030
        |||||
Db      211 CTTTCTGAGGCTTTGCACTCCTTGGCAATTTCTTTGTCACATTCCTGCG 262

RESULT 25
HSA272516      HSA272516      767 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 11.
ACCESSION      AJ272516
VERSION        AJ272516.1 GI:18873687
KEYWORDS       KCNQ5 gene; KCNQ5 protein.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and
                Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
                convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 767)
AUTHORS       Steinlein,O.K.
TITLE         Direct Submision
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
                Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source        1..767
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gene          364..463
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                /number="8"
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exon          364..463
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BASE COUNT    229 a      155 c      134 g      230 t
ORIGIN

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JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 767)
AUTHORS       Steinlein,O.K.
TITLE         Direct Submision
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
                Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY

FEATURES
source        1..767
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gene          364..463
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                /number="8"
                /usedin="AJ272506:KCNQ5_cds"

exon          364..463
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                /number="8"
                /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    229 a      155 c      134 g      230 t
ORIGIN

Query Match   4.0%; Score 110; DB 9; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1441 GCTCAGACAGCCCTTGGCAGTGATGATATGATGAAAAAGATGCCAGTGTGATGA 1500
        |||||
Db      294 GCTCAGACAGCCCTTGGCAGTGATGATATGATGAAAAAGATGCCAGTGTGATGA 1500
QY      1501 TCAGTGGAGAGACCTCAGCCAGCACTTAAACTGCATTCGAGCATTCAG 1550
        |||||
Db      354 TCAGTGGAGAGACCTCAGCCAGCACTTAAACTGCATTCGAGCATTCAG 403

RESULT 26
HSA272513      HSA272513      748 bp      DNA      linear      PRI 21-FEB-2002
LOCUS          Homo sapiens partial KCNQ5 gene, exon 8.
ACCESSION      AJ272513
VERSION        AJ272513.1 GI:18873684
KEYWORDS       KCNQ5 gene; KCNQ5 protein.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS       Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and
                Steinlein,O.K.
TITLE         The new voltage gated potassium channel KCNQ5 and earlyinfantile
                convulsions
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 748)
AUTHORS       Steinlein,O.K.
TITLE         Direct Submision
JOURNAL        Submitted (22-FEB-2000) Steinlein O.K., Institute of Human
                Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY
                Revised by author 08-MAR-2000

REMARK        Location/Qualifiers
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gene          364..463
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exon          364..463
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                /usedin="AJ272506:KCNQ5_cds"

BASE COUNT    229 a      155 c      134 g      230 t
ORIGIN

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Query Match	3.5%	Score 98:	DB 9:	Length 748:
Best Local Similarity	100.0%	Pred. No. 4.2e-45:		
Matches 98:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1123	CACTGTGTTGGCGCTAGTACGACGCTGATGAGAAATCTGTTCCATTGCACCTGGGAAG	1182	
Db	361	CACTGTGTTGGCGCTAGTACGACGCTGATGAGAAATCTGTTCCATTGCACCTGGGAAG	420	
Qy	1183	CCACTTGAAGGCGCTTGACACCTGACAGCCCTACCAA	1220	
Db	421	CCACTTGAAGGCGCTTGACACCTGACAGCCCTACCAA	458	
RESULT 27				
LOCUS	HSA272512	561 bp	DNA	linear PRI 21-FEB-2002
DEFINITION	Homo sapiens partial KCNO5 gene, exon 7.			
ACCESSION	AJ272512	GI:18873683		
VERSION	AJ272512.1	GI:18873678		
KEYWORDS	KCNO5 gene; KCNO5 protein.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 Kananura,C., Bliervert,B., Hechenberger,M., Engels,H. and			
JOURNAL	Steinlein,O.K.			
REFERENCE	The new voltage gated potassium channel KCNO5 and early infantile			
AUTHORS	convulsions			
TITLE	2 (bases 1 to 561)			
JOURNAL	Unpublished			
REFERENCE	Steinlein,O.K.			
AUTHORS	Direct Submission			
TITLE	submitted (22-FEB-2000) Steinlein O.K., Institute of Human			
JOURNAL	Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY			
FEATURES	Location/Qualifiers			
source	1..561			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/chromosome="6"			
	/map="q14"			
gene	149..244			
	/gene="KCNO5"			
exon	149..244			
	/gene="KCNO5"			
	/number=7			
	/usedin="AJ272506;KCNO5.cds			
BASE COUNT	154 a 100 c 106 g 201 t			
ORIGIN				
Query Match	3.5%	Score 96:	DB 9:	Length 561:
Best Local Similarity	100.0%	Pred. No. 6.3e-44:		
Matches 96:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Qy	1030	GGCATTCTGGCTCAGTTTTCATTAAATACAGAAACACCGCCAGAAACACTTT	1089	
Db	149	GGCATTCTGGCTCAGTTTTCATTAAATACAGAAACACCGCCAGAAACACTTT	208	
Qy	1090	GAGAAAGAGAGAACCCAGCTGCCAACCCTCATTCAG	1125	
Db	209	GAGAAAGAGAGAACCCAGCTGCCAACCCTCATTCAG	244	
RESULT 28				
LOCUS	HSA272507	743 bp	DNA	linear PRI 21-FEB-2002
DEFINITION	Homo sapiens partial KCNO5 gene, exon 2.			
ACCESSION	AJ272507	GI:18873678		
VERSION	AJ272507.1	GI:18873678		
KEYWORDS	KCNO5 gene; KCNO5 protein.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE	BASE COUNT ORIGIN	Query Match Best Local Similarity Matches	Score 92; 100.0%; 92;	DB 9; Pred. No. 1.4e-41; 0;	Length 743; 0; 0;
Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo. Kananura, C., Bleyvert, B., Hechenberger, M., Engels, H. and Steinlein, O. K. The new voltage-gated potassium channel KCNO5 and early infantile convulsions Unpublished 2 (bases 1 to 743) Steinlein, O. K. Direct Submission Submitted (22-FEB-2000) Steinlein O.K., Institute of Human Genetics, University of Bonn, Wilhelmstr. 31, Bonn, 53111, GERMANY location/Qualifiers 1. .743 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="6q14" 293. .383 /gene="KCNO5" 293. .383 /gene="KCNO5" /number=2 /usedin=AJ272506.KCNO5.cds	243 a 129 c 124 g 247 t	3.3%; 100.0%; 92;	DB 9; Pred. No. 1.4e-41; 0;	Length 743; 0; 0;			
Yy	399	TTTTCTCCTTGTCTTGTGCTGCTGATTTTGTACAGTGTCTTCTACACACCTGAGCAC	458				
Db	293	TTTCTCCTTGTCTTGTGCTGCTGATTTTGTACAGTGTCTTCTACACACCTGAGCAC	352				
Yy	459	AAATTTGGCCTCAAGTTGCTGCTGATTTTGTACAGTGTCTTCTACACACCTGAGCAC	490				
Db	353	AAATTTGGCCTCAAGTTGCTGCTGATTTTGTACAGTGTCTTCTACACACCTGAGCAC	384				
RESULT 29 663779/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	663779 G-104174 Random genomic STS Homo sapiens STS genomic, sequence tagged site. 663779 G63779.1 GI:6606596 STS. Homo sapiens. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 319) Oefner, P.J. Human random genomic STS survey, unpublished data Unpublished (1999)	319 bp DNA linear STS 20-DEC-1999					
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Contact: Peter Oefner Stanford Genome Center Stanford University 855 California Ave., Palo Alto, CA 94304, USA Tel: 6508121926 Fax: 6508121975 Email: Oefner@genome.stanford.edu Primer A: CGTGGCAAAATATATACCTGAG Primer B: AATTCATAGGTAAAGCCACAA STS size: 319 PCR Profile: Initial denaturing step of 95 degrees C for 10 min to activate Amplaq Gold (1 min for Ampliq); 14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1 min at 63						

degrees C to
56 degrees C using decrements of 0.5 degrees C, extension at 72
min:
20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
degrees C for 1
min.

Protocol:
Template: 50 ng
Primer: each 0.2 uM
Tag polymerase: 0.02 units/ul
Total Vol: 50 ul

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3
0% DMSO.

FEATURES

Source
1. .319
/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="Male and Female"
/clone_11b="Random genomic STS"
STS
primer_bind 1. .23
primer_bind complement(297. .319)
BASE COUNT 101 a 68 c 63 g 87 t
ORIGIN

Query Match 2.5%; Score 70; DB 11; Length 319;
Best Local Similarity 100.0%; Pred. No. 1,4e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 AGATACCATGTTCTTATCGCTCAATAGCAGTGTTCGCAAAACCTCAGGTAATAT 674
|||||
Db 70 AGATACCATGTTCTTATCGCTCAATAGCAGTGTTCGCAAAACCTCAGGTAATAT 11
|||||
QY 675 TTTTGGCAGC 684
|||||
Db 10 TTTTGGCAGC 1

RESULT 30
AC112532 173373 bp DNA linear HTG 13-JUL-2002
LOCUS
DEFINITION Rattus norvegicus clone CH230-20N15, *** SEQUENCING IN PROGRESS
AC112532
AC112532 *** 76 unordered pieces.
AC112532.2 GI:21731360
KEYWORDS HTG; HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 173373)
Munay D.M., Adams C., Adio-oduola B., Ali-oman F.R., Allen C.,
Albrooks S.L., Amaratunga H.C., Are J.R., Ayele M., Banks T.,
Babarika J., Benton J., Bimge K., Blankenburg K., Bonnin D.,
Bouchard J., Bowles S., Brileva M., Brown E., Brown M., Bryant N.P.,
Bunay C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
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Hernandez O., Hodgson A., Hogues M., Holloway C., Hollins B.,
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Nguyen N., Nickerson E., Nwokemwo S., Ogdu M., Okunolu G.,
Oreguene N., Oviedo R., Pace A., Payton B., Peery J., Perez L.,
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Rives M., Rojas A., Rojibokan I., Rolfe M., Ruiz S., Savery G.,
Scherer S., Scott G., Shen H., Shooshari N., Slison I.,
Sodergren E., Sonaike T., Sparks A., Stanley H., Stone H.,
Sutton A., Svatek A., Taber P., Tamerisa A., Tamerisa K., Tang H.,
Tansey J., Taylor C., Taylor T., Teitrod B., Thomas N., Thomas S.,
Usmani K., Vasquez L., Vera V., Villalton D., Vinson R., Wang Q.,
Wang S., Ward-Moore S., Warren R., Washington C., Watlington S.,
Williams G., Williamson A., Wleczyk R., Wooden S., Worley K.,
Wu C., Wu Y., Wu Y.F., Zhou J., Zorrilla S., Nelson D.,
Weinstock G. and Gibbs R.
Direct Submission
Unpublished
2 (bases 1 to 173373)
Worley K.C.
Direct Submission
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173373)
Worley K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced g1:18860118.
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GYB
Center clone name: CH230-20N15
Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 109188 bases at least Q40
Consensus quality: 114200 bases at least Q30
Consensus quality: 117733 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 76 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 1111: contig of 1111 bp in length
1112 1211: gap of unknown length
1212 2295: contig of 1084 bp in length
2296 2396: gap of unknown length
2396 3881: contig of 1486 bp in length
3881 3882: gap of unknown length
3882 5339: contig of 1358 bp in length

5340 5439: gap of unknown length
 5440 6514: contig of 1075 bp in length
 6515 6614: gap of unknown length
 6615 7965: contig of 1351 bp in length
 7966 8066: gap of unknown length
 8066 9109: contig of 1043 bp in length
 9109 9208: gap of unknown length
 9208 10720: contig of 1512 bp in length
 10720 10820: gap of unknown length
 10820 11983: contig of 1163 bp in length
 11983 12084: gap of unknown length
 12084 13248: contig of 1165 bp in length
 13248 13348: gap of unknown length
 13348 14622: contig of 1274 bp in length
 14622 14723: gap of unknown length
 14723 16124: contig of 1402 bp in length
 16124 16224: gap of unknown length
 16224 17807: contig of 1583 bp in length
 17807 17907: gap of unknown length
 17907 19351: contig of 1444 bp in length
 19351 19551: gap of unknown length
 19551 20521: contig of 1070 bp in length
 20521 20622: gap of unknown length
 20622 22110: contig of 1489 bp in length
 22110 22211: gap of unknown length
 22211 23544: contig of 1334 bp in length
 23544 23644: gap of unknown length
 23644 24936: contig of 1292 bp in length
 24936 25036: gap of unknown length
 25036 26075: contig of 1039 bp in length
 26075 26175: gap of unknown length
 26175 27870: contig of 1695 bp in length
 27870 27970: gap of unknown length
 27970 29509: contig of 1539 bp in length
 29509 29609: gap of unknown length
 29609 30869: contig of 1260 bp in length
 30869 30969: gap of unknown length
 30969 32526: contig of 1557 bp in length
 32526 32626: gap of unknown length
 32626 33967: contig of 1341 bp in length
 33967 34067: gap of unknown length
 34067 35486: contig of 1419 bp in length
 35486 35586: gap of unknown length
 35586 37661: contig of 2075 bp in length
 37661 37761: gap of unknown length
 37761 38921: contig of 1160 bp in length
 38921 39021: gap of unknown length
 39021 40306: contig of 1285 bp in length
 40306 40406: gap of unknown length
 40406 42337: contig of 1931 bp in length
 42337 42437: gap of unknown length
 42437 43989: contig of 1352 bp in length
 43989 44089: gap of unknown length
 44089 46170: contig of 2081 bp in length
 46170 46270: gap of unknown length
 46270 47616: contig of 1346 bp in length
 47616 47716: gap of unknown length
 47716 50211: contig of 2495 bp in length
 50211 50311: gap of unknown length
 50311 52092: contig of 1781 bp in length
 52092 52192: gap of unknown length
 52192 54673: contig of 2481 bp in length
 54673 54773: gap of unknown length
 54773 57487: contig of 2714 bp in length
 57487 57587: gap of unknown length
 57587 59243: contig of 1656 bp in length
 59243 59343: gap of unknown length
 59343 60913: contig of 1570 bp in length
 60913 61013: gap of unknown length
 61013 62444: contig of 1431 bp in length
 62444 62544: gap of unknown length
 62544 64889: contig of 2345 bp in length
 64889 64989: gap of unknown length

64990 67253: contig of 2264 bp in length
 67253 67353: gap of unknown length
 67353 68768: contig of 1415 bp in length
 68768 68868: gap of unknown length
 68868 71347: contig of 2479 bp in length
 71347 71447: gap of unknown length
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 74130 74131: gap of unknown length
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 75896 75996: gap of unknown length
 75996 78359: contig of 2363 bp in length
 78359 78459: gap of unknown length
 78459 80708: contig of 2249 bp in length
 80708 80808: gap of unknown length
 80808 83004: contig of 2196 bp in length
 83004 83104: gap of unknown length
 83104 84918: contig of 1814 bp in length
 84918 85018: gap of unknown length
 85018 86508: contig of 1490 bp in length
 86508 86609: gap of unknown length
 86609 89116: contig of 2508 bp in length
 89116 89216: gap of unknown length
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 92114 92214: gap of unknown length
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Query Match 2.38: Score 63; DB 2; Length 173373;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 AGATACCATGTTCTTATCGCTTCATATGACGTTGTTGCAAAAACCTACGAGTAATAT 674
 Db 67618 AGATACCATGTTCTTATCGCTTCATATGACGTTGTTGCAAAAACCTACGAGTAATAT 67677
 QY 675 TTT 677
 Db 67678 TTT 67680

RESULT 31
 AC095944
 LOCUS
 DEFINITION
 Rattus norvegicus clone CH230-10P24, *** SEQUENCING IN PROGRESS
 *** 80 unordered pieces.
 AC095944
 VERSION
 AC095944.4 GI:21729331
 KEYWORDS
 HTG; HTGS_PHASET.
 SOURCE
 Norway rat.
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
 AUTHORS
 1 (bases 1 to 158119)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbara,J., Benton,J., Blinange,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhray,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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 Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
 Moser, M., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
 Nguyen, N., Nickerson, E., Nwokwenkwo, S., Ogun, M., Nguyen, A., Nguyen, N.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G.,
 Scherer, S., Scott, G., Shen, H., Shooshitani, N., Sisson, I.,
 Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tameris, A., Tameris, K., Tang, H.,
 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, Y., Villalón, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
 Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, D., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

Unpublished
 Direct Submission
 2 (bases 1 to 158119)
 Worley, K.C.

Direct Submission
 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 158119)
 Worley, K.C.

Direct Submission
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:20975970.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information
 Center project name: GDX2
 Center clone name: CH230-10B24

----- Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 81413 bases at least Q40
 Consensus quality: 88089 bases at least Q30
 Consensus quality: 93014 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length
 * (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraft.data.html>).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 80 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1015: contig of 1015 bp in length	9571: contig of 1361 bp in length
1016	1115: gap of unknown length	9572
1116	2566: contig of 1451 bp in length	9572
2567	2666: gap of unknown length	10707: contig of 1036 bp in length
2667	4281: contig of 1615 bp in length	10807: gap of unknown length
4282	4381: gap of unknown length	12352: contig of 1545 bp in length
4382	6207: contig of 1826 bp in length	12352
6208	6307: gap of unknown length	12453
6308	8110: contig of 1803 bp in length	12453
8111	8210: gap of unknown length	13961
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		14061
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		16765
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		19248
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		20518
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Query Match 2.0%; Score 56; DB 2; Length 158119;
 Best Local Similarity 100.0%; Pred. No. 2.8e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

229 GAGAGCGCGCGGCGGAGCGGCGGATGAGCTGCTGGGAGAGCGGCTCTC 284
 Db 70903 GAGAGCGCGCGGCGGAGCGGCGGCGGATGAGCTGCTGGGAGAGCGGCTCTC 70958

RESULT 32
 AC095904/c
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-10L20, *** SEQUENCING IN PROGRESS
 AC095904 179192 bp DNA linear HTG 10-JUL-2002
 Rattus norvegicus
 *** 37 unordered pieces.
 AC095904 GI:21722989
 HTG: HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 179192)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralung,H.C., Are,J.R., Ayala,M., Banks,T.,
 Barberia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Burckett,C., Burrell,K.L., Byrd,N.C.,
 Carion,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorbett,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
 Homsi,F., Howard,S., Huber,J., Huliyil,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Kotvah,J., Kovar,C.,
 Kretovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H.,
 Lorado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 179192)
 Worley,K.C.
 Direct Submission
 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 179192)
 Worley,K.C.
 Direct Submission
 Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 10, 2002 this sequence version replaced gi:17943539.
 --- genome center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GDVD
 Center clone name: CH230-10L20
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 128957 bases at least Q40
 Consensus quality: 135269 bases at least Q30
 Consensus quality: 140867 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 57 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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 4327 5334: contig of 1008 bp in length
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 6624 6725: gap of unknown length
 6725 7791: contig of 1067 bp in length
 7791 7892: gap of unknown length
 7892 9102: contig of 1211 bp in length
 9102 9203: gap of unknown length
 9203 10526: contig of 1324 bp in length
 10526 10627: gap of unknown length
 10627 11938: contig of 1332 bp in length

11959 12058: gap of unknown length
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 14027 14126: gap of unknown length
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 24852 24951: gap of unknown length
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 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 33 AC091215/c

LOCUS

AC091215 248862 bp DNA linear HTG 24-AUG-2002

DEFINITION

Rattus norvegicus clone CH230-1A4, *** SEQUENCING IN PROGRESS ***

ACCESSION

AC091215 GI:22203886

VERSION

HTG: HTGS_PHASE1.

KEYWORDS

Norway rat.

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 248862)

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayala,M., Banks,T.,

Barbata,J., Benton,J., Bimarge,K., Blankenburg,K., Bonin,D.,

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Burck,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,D., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Kocha,S., Durbin,K.J.,

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Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Gortelli,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,

Hernandez,O., Hodson,A., Hogues,M., Hollaway,C., Hollins,B.,

Homis,F., Howard,S., Huber,D., Huliy,S., Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,

Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisgeed,H.,

Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,

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Rives,M., Rojts,A., Rojudoxani,I., Rolfe,M., Ruiz,S., Savery,G.,

Scherer,S., Scott,G., Shen,H., Shooshbari,N., Sisson,I.,

Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
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 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 248862)
 Worley, K.C.

Direct Submission
 Submitted (04-APR-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 248862)
 Worley, K.C.

Direct Submission
 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 11, 2002 this sequence version replaced gi:21953790.

Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center project name: TVAL
 Center clone name: CH230-1A4
 Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 3.1
 Chemistry: Dye-terminator Big Dye 3.1
 Assembly program: Phrap
 Consensus quality: 219010 bases at least Q40
 Consensus quality: 221770 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 51 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
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/db_xref="taxon:10116"

Query Match
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Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 GAGAGCCGCGGCGGAGGAGGCGGCGGATGAGCCTGCTGGGAGCCGCTTC 284
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RESULT 34
AF525937 200 bp mRNA linear ROD 29-JUL-2002
LOCUS Rattus norvegicus potassium voltage-gated channel KQT-like
DEFINITION subfamily member 5 (Kcnq5) mRNA, partial cds.
ACCESSION AF525937
VERSION AF525937.1 GI:22001346
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 200)
AUTHORS Liang, G., Ulfendahl, M., Jin, Z. and Jarlebark, L.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2002) Center for Hearing and Communication Research, Karolinska Institute, Bldg. M1 - ENT Research Laboratory, Stockholm SE-171 76, Sweden

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RESULT 35
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LOCUS AF263836 3108 bp mRNA linear ROD 01-JUN-2000
DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA, partial cds.
ACCESSION AF263836
VERSION AF263836.1 GI:8132998
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3108)
AUTHORS Kniazeva, M. and Han, M.
TITLE A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3108)
AUTHORS Kniazeva, M. and Han, M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA
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/dev_stage="9-11 weeks"
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BASE COUNT
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Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 251 TTGGTGTGCTGATTTTTCAGTGTTCATACATCCCTGACGA 254

RESULT 36
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LOCUS Mus musculus clone RP24-87K23, WORKING DRAFT SEQUENCE, 5 unordered pieces.
ACCESSION AC131088
VERSION AC131088.1 GI:22267867

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 185864)
 AUTHORS Birren, B., Nusbaum, C. and Lander, E.
 TITLE Mus musculus, clone RP24-87K23
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 185864)
 AUTHORS Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S.,
 Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
 Camarata, J., Chang, D., Chazaro, B., Choepel, Y., Collymore, A.,
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 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zemek, L., Zimmer, A. and Zody, W.
 TITLE Direct Submission
 COMMENT Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 ALL repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24326
 Center clone name: 87_K_23
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap, version 0.960731
 Consensus quality: 183988 bases at least Q40
 Consensus quality: 185137 bases at least Q30
 Consensus quality: 185352 bases at least Q20
 Insert size: 185000; agarose-fp
 Insert coverage: 185464; sum-of-contigs
 Quality coverage: 7.9 in Q20 bases; agarose-fp
 Quality coverage: 7.9 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 149433 TTTGCTGCTGATTTTGTCACTGTTTTCACATCCGAGCA 149476
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 DEFINITION Mus musculus clone RP24-496H1, WORKING DRAFT SEQUENCE, 9 ordered
 pieces.
 AC115920
 AC115920.3 GI:21536151
 VERSION
 KEYWORDS HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 162123)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Mus musculus, clone RP24-496H1
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 162123)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
 Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., Dearliano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gaidyna, S.,
 Gaidyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., Labrecque, K., Lamazares, R.,
 Landers, T., Lehoczeky, J., Levine, R., Marquis, N., Matthews, C.,
 Maclean, C., Macdonald, P., Major, J., Marguis, N., Meneus, L.,
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
 Mihova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Straus, K., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zemek, L., Zimmer, A. and Zody, W.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 162123)

TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162123)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalil, B., Brown, A., Camarero, J., Campopiano, A., Chang, J.,
Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Gardina, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Larocque, K.,
Lamarez, R., Landers, T., Lechoczky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melitini, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicot, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2002 this sequence version replaced 91:21431285.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L24884

Center clone name: 496_H_1

Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159226 bases at least Q40
Consensus quality: 160941 bases at least Q30
Insert size: 160000; agarose-1p
Insert size: 161323; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-1p
Quality coverage: 8.6 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 617: Contig of 617 bp in length
* 618 717: gap of 100 bp
* 718 2736: contig of 2019 bp in length
* 2737 2836: gap of 100 bp
* 2837 5807: contig of 2971 bp in length
* 5808 5907: gap of 100 bp
* 5908 19603: contig of 13696 bp in length

FEATURES
source
* 19604 19703: gap of 100 bp
* 19704 34958: contig of 15255 bp in length
* 34959 35058: gap of 100 bp
* 35059 52976: contig of 17998 bp in length
* 52977 53076: gap of 100 bp
* 53077 84088: contig of 31012 bp in length
* 84089 84188: gap of 100 bp
* 84189 121320: contig of 37032 bp in length
* 121221 121320: gap of 100 bp
* 121321 162123: contig of 40803 bp in length.
Location/Qualifiers
1. 162123
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_1bp="RP24-496H1"
/clone_1bp="RP24 Male Mouse BAC"
1. 617
/note="assembly-fragment"
/note="assembly-fragment"
718. 2736
/note="assembly-fragment"
2837. 5807
/note="assembly-fragment"
5908. 19603
/note="assembly-fragment"
19704. 34958
/note="assembly-fragment"
35059. 52976
/note="assembly-fragment"
53077. 84088
/note="assembly-fragment"
84189. 121220
/note="assembly-fragment"
121321. 162123
/note="assembly-fragment"

BASE COUNT 47823 a 32956 c 33003 g 47530 t 811 others
ORIGIN
Query Match 1.3%; Score 35; DB 2; Length 162123;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 GCACCTCCTGCGATCTCTTCTTGCACCTCCTGC 1028
|||||
Db 69313 GCACCTCCTGCGATCTCTTCTTGCACCTCCTGC 69347

RESULT 39
AC112532/c 17373 bp DNA linear HTG 13-JUN-2002
LOCUS Rattus norvegicus clone CH230-20N15, *** SEQUENCING IN PROGRESS
DEFINITION *** 76 unordered pieces.
AC112532
AC112532.2 GI:21731360
VERSION HTG: HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 17373)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,
Alsdorfs, S.L., Amaratunga, H.C., Are, J.R., Ayala, M., Banks, T.,
Barbata, J., Benton, J., Blimke, K., Blankenburg, K., Bonini, D.,
Bouck, J., Bowler, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
DeLaney, K.R., Delgado, O., Dunn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Kocha, S., Durbin, R.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J.J., Foster, P., Frantz, P.,


```

* 62545 64889: contig of 2345 bp in length
* 64890 64889: gap of unknown length
* 64990 67253: contig of 2264 bp in length
* 67254 67353: gap of unknown length
* 67354 68768: contig of 1415 bp in length
* 68769 68868: gap of unknown length
* 68869 71347: contig of 2479 bp in length
* 71348 71447: gap of unknown length
* 71448 71430: contig of 2683 bp in length
* 71431 74230: gap of unknown length
* 74231 75896: contig of 1666 bp in length
* 75897 75997: gap of unknown length
* 75997 78359: contig of 2363 bp in length
* 78360 78459: gap of unknown length
* 78460 80708: contig of 2249 bp in length
* 80709 80808: gap of unknown length
* 80809 83004: contig of 2196 bp in length
* 83005 83104: gap of unknown length
* 83105 84918: contig of 1814 bp in length
* 84919 85018: gap of unknown length
* 85019 86508: contig of 1490 bp in length
* 86509 86608: gap of unknown length
* 86609 89116: contig of 2508 bp in length
* 89117 89216: gap of unknown length
* 89217 92114: contig of 2898 bp in length
* 92115 92214: gap of unknown length
* 92215 94791: contig of 2577 bp in length
* 94792 94891: gap of unknown length
* 94892 96527: contig of 1636 bp in length

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Query Match Similarity 1.3%; Score 35; DB 2; Length 173373;

Best Local Similarity 100.0%; Pred. No. 7e-08; 0; Indels 0; Gaps 0;

OY 1087 TTTGAGAAAGAGAACCCAGCTGCCAACCTCAT 1121

Db 168064 TTTGAGAAAGAGAACCCAGCTGCCAACCTCAT 168030

```

RESULT 40
AC124139 215256 bp DNA linear HTG 10-JUN-2002
LOCUS Mus musculus clone RP24-78G8, WORKING DRAFT SEQUENCE, 16 ordered
DEFINITION
AC124139
AC124139
AC124139.1 GI:21362202
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 215256)
Bliren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-78G8
Unpublished
2 (bases 1 to 215256)
Bliren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Gardina, S., Glade, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Larocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Melidim, J.,
Mencus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicoll, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

```

TITLE JOURNAL COMMENT

Schuback, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,
Theodore, J., Tophan, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center
Center code: MIBR
Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L24309

Center clone name: 78_G-8

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 209693 bases at least Q40
Consensus quality: 212534 bases at least Q30
Consensus quality: 213305 bases at least Q20

Insert size: 194000; agarose-gel

Insert size: 213756; sum-of-contigs
Quality coverage: 6.5 in Q20 bases; agarose-gel
Quality coverage: 5.9 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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1 1419: contig of 1419 bp in length
1420 1519: gap of 100 bp
1520 2936: contig of 1417 bp in length
2937 3036: gap of 100 bp
3037 5429: contig of 2393 bp in length
5430 5529: gap of 100 bp
5530 8541: contig of 3012 bp in length
8542 8641: gap of 100 bp
8642 12670: contig of 4029 bp in length
12671 12770: gap of 100 bp
12771 17587: contig of 4817 bp in length
17588 17687: gap of 100 bp
17688 21987: contig of 4300 bp in length
21988 22087: gap of 100 bp
22088 27908: contig of 5821 bp in length
27909 28008: gap of 100 bp
28009 34487: contig of 6479 bp in length
34488 34587: gap of 100 bp
34588 42749: contig of 8162 bp in length
42750 42849: gap of 100 bp
42850 62665: contig of 19816 bp in length
62666 62765: gap of 100 bp
62766 90524: contig of 27759 bp in length
90525 90624: gap of 100 bp
90625 114652: contig of 24028 bp in length
114653 114752: gap of 100 bp
114753 143778: contig of 28026 bp in length
143779 143878: gap of 100 bp
143879 176366: contig of 32488 bp in length
176367 176466: gap of 100 bp
176467 215256: contig of 38790 bp in length.

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FEATURES source

Location/Qualifiers
1. 215256

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-78G8"
/clone_lib="RPCI-24 Male Mouse BAC"
1.1419
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/note="assembly-fragment"
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8642..12670
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62766..90524
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114753..143778
/note="assembly-fragment"
143879..176366
/note="assembly-fragment"
176467..215256
/note="assembly-fragment"
42308 c 42660 g 63922 t 1515 others
BASE COUNT 64851 a
ORIGIN
Query Match 1.3%: Score 35; DB 2; Length 215256;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCCCGCCACGCGGAGAGAGAGAGGCGG 35
|||||
Db 103522 ATGCCCGCCACGCGGAGAGAGAGAGGCGG 103556
|||||
RESULT 41
AC125483/c 267605 bp DNA linear HTG 02-JUL-2002
LOCUS
DEFINITION
Mus musculus chromosome UNK clone RP23-10919, WORKING DRAFT
AC125483
ACCESSION
VERSION
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
The sequence of Mus musculus clone
JOURNAL
Unpublished
2 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (27-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 267605)
AUTHORS
McPherson,J.D. and Waterston,R.H.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUL-2002) Genome Sequencing Center, 4444 Forest Park

```

```

COMMENT
Parkway, St. Louis, MO 63108, USA
On Jul 2, 2002 this sequence version replaced gi:21617556.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
Project Information
Center project name: M8A0109109
----- Summary Statistics -----
Sequencing vector: MJ3; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 265605 bases at least Q40
Consensus quality: 266280 bases at least Q20
Insert size: 225000; agarose-fp
Insert size: 267105; sum-of-ctiggs
Quality coverage: 13.62 in Q20 bases; agarose-fp
Quality coverage: 11.39 in Q20 bases; sum-of-ctiggs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
17494: contig of 17494 bp in length
17495: gap of unknown length
17595: contig of 25183 bp in length
42777: gap of unknown length
42878: contig of 70336 bp in length
113213: contig of 133631 bp in length
246944: contig of 133631 bp in length
247044: gap of unknown length
253029: contig of 5985 bp in length
253030: gap of unknown length
267605: contig of 14476 bp in length.
Location/Qualifiers
1.267605
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-10919"
1.17494
/note="assembly_name:Contig10"
17595..42777
/note="assembly_name:Contig11"
42878..113213
/note="assembly_name:Contig12"
113314..246944
/note="assembly_name:Contig13"
247045..253029
/note="assembly_name:Contig18"
253130..267605
/note="assembly_name:Contig19"
51673 c 50947 g 80915 t 511 others
BASE COUNT 83559 a
ORIGIN
Query Match 1.3%: Score 35; DB 2; Length 267605;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCCCGCCACGCGGAGAGAGAGAGGCGG 35
|||||
Db 201645 ATGCCCGCCACGCGGAGAGAGAGAGGCGG 201611
|||||

```

```

RESULT 42
AC127359      331447 bp      DNA      linear      HTG 11-AUG-2002
LOCUS         Mus musculus chromosome UNK clone RP23-110G23, WORKING DRAFT
DEFINITION   AC127359
SEQUENCE, 5 unordered pieces.
AC127359
AC127359.2 GI:22203899
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE       house mouse.
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 331447)
AUTHORS      McPherson,J.D. and Waterston,R.H.
TITLE        The sequence of Mus musculus clone
JOURNAL      Unpublished
2 (bases 1 to 331447)
REFERENCE    McPherson,J.D. and Waterston,R.H.
AUTHORS      Direct Submission
TITLE        Submitted (14-JUL-2002) Genome Sequencing Center, 4444 Forest Park
JOURNAL      Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 331447)
REFERENCE    McPherson,J.D. and Waterston,R.H.
AUTHORS      Direct Submission
TITLE        Submitted (11-AUG-2002) Genome Sequencing Center, 4444 Forest Park
JOURNAL      Parkway, St. Louis, MO 63108, USA
On Aug 11, 2002 this sequence version replaced gi:21747773.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project Information
Center project name: M.BA0110G23

----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 326386 bases at least Q40
Consensus quality: 328112 bases at least Q30
Insert size: 190000; agarose-fp
Insert size: 331047; sum-of-contigs
Quality coverage: 20.68 in Q20 bases; agarose-fp
Quality coverage: 11.29 in Q20 bases; sum-of-contigs

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 8418: contig of 8418 bp in length
* 8419 8518: gap of unknown length
* 8519 33246: contig of 24728 bp in length
* 33247 33346: gap of unknown length
* 33347 114857: contig of 81511 bp in length
* 114858 114957: gap of unknown length
* 114958 194684: contig of 79727 bp in length
* 194685 194784: gap of unknown length
* 194785 331447: contig of 136663 bp in length.
Location/Qualifiers
1. 331447
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
FEATURES
SOURCE

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1. 8418 /clone="RP23-110G23"
/note="assembly_name:Contig11"
misc_feature
8519. 33246 /note="assembly_name:Contig12"
misc_feature
33347. 114857 /note="assembly_name:Contig13"
misc_feature
114958. 194684 /note="assembly_name:Contig14"
misc_feature
194785. 331447 /note="assembly_name:Contig15"
BASE COUNT 99727 a 65996 c 65869 g 99449 t 406 others
ORIGIN
Query Match 1.3%; Score 35; DB 2; Length 331447;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCCCGCGACCGAGAGAGAGAGAGAGCGG 35
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Db 78646 ATGCCCCGCGACCGAGAGAGAGAGAGAGCGG 78680
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RESULT 43
AU049631/c 389 bp DNA linear STS 20-JAN-2000
LOCUS Rattus norvegicus, OTSUKA clone, 900g10, microsatellite sequence,
DEFINITION sequence tagged site.
ACCESSION AU049631.1 GI:6722802
VERSION AU049631
KEYWORDS STS.
SOURCE Rattus norvegicus (strain:Brown Norway) liver hepatocyte DNA,
clone:900g10.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (sites)
Watanabe,T.K., Hishigaki,H., Okuno,S., Mizoguchi,A., Oga,K.,
Tsujii,A., Ono,T., Yamasaki,Y., Kanemoto,N., Takahashi,E., Irie,Y.,
Nakamura,Y., Takagi,Y. and Tanigami,A.
The large-scale mapping of rat microsatellite markers
Unpublished
2 (bases 1 to 389)
REFERENCE Watanabe,T.K.
AUTHORS Direct Submission
TITLE Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
JOURNAL Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
Kawachi-cho, Tokushima, Tokushima 771-0192, Japan
(E-mail:watanabe@otsuka.gr.jp; Tel:+81-886-65-2888,
Fax:+81-886-37-1035)
Location/Qualifiers
1. 389
/organism="Rattus norvegicus"
/strain="Brown Norway"
/db_xref="taxon:10116"
/clone="900g10"
/cell_type="hepatocyte"
/tissue_type="liver"
/note="900g10F=5'-TGAGGTGTACCTGGTGCAAT-3',
900g10R=5'-CTTCTCTCCCTCCCTCCCT-3'"
FEATURES
SOURCE
BASE COUNT 142 a 107 c 70 g 70 t
ORIGIN
Query Match 1.0%; Score 29; DB 11; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 517 TTGAGTTCATCATCGAATCGATCGCTGC 545
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Db 371 TTGAGTTCATCATCGAATCGATCGCTGC 343
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RESULT 44
AB000502
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000502
VERSION AB000502.1 GI:4176409
KEYWORDS mKQT2.9; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
MEDLINE 9830948
REFERENCE 2 (bases 1 to 1227)
AUTHORS Watanabe,H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
FEATURES
source Location/Qualifiers
1. .1227
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1136
/note="mKQT2.9"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37164.1"
/db_xref="GI:4176410"
/translation="MVQSRNGGVPTSGEKKLVGVGLDGPADSTRDGAALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNAPFKLONFLYVLERPGRMAFIYHAYVFL VFSCLVLSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRIMAGCCCRYGMRGR LKFAKRPFCVIDIMVLIASIAVLAAGSGNVPATSAISRFLQILRMIRMDRGCTW KLIGSVVAHSEKELVTAWYIGFLCIILASFLVYLAEGKNDHEDPTADALMCLITLT TIGYDKXPOTWNGRLAATFTLLIGVSFPALPAGILGSGFALAKYQEOHQRHKEFRRN PAAGLIQVSRAGH"
polyA_site 1227
BASE COUNT 220 a 346 c 378 g 283 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1227;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGTGCATCTACACGCG 392
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Db 348 CCCCCGGCGTGCATCTACACGCG 376
|||||
RESULT 45
AB000503
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000503
VERSION AB000503.1 GI:4176411
KEYWORDS mKQT2.10; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T.,

Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
MEDLINE 9830948
REFERENCE 2 (bases 1 to 1689)
AUTHORS Watanabe,H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
FEATURES
source Location/Qualifiers
1. .1689
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1130
/note="mKQT2.10"
/codon_start=1
/product="alternative splicing:see accession between AB000494 and AB000504"
/protein_id="BAA37165.1"
/db_xref="GI:4176412"
/translation="MVQSRNGGVPTSGEKKLVGVGLDGPADSTRDGAALLIAG SEAPKRSVLSKPRGTGAGAGKPPKRNAPFKLONFLYVLERPGRMAFIYHAYVFL VFSCLVLSVFSTIKETKESSEGALEYLIVTVIVGVYEVIRIMAGCCCRYGMRGR LKFAKRPFCVIDIMVLIASIAVLAAGSGNVPATSAISRFLQILRMIRMDRGCTW KLIGSVVAHSEKELVTAWYIGFLCIILASFLVYLAEGKNDHEDPTADALMCLITLT TIGYDKXPOTWNGRLAATFTLLIGVSFPALPAGILGSGFALAKYQEOHQRHKEFRRN PAAGLIQVSLSPC"
polyA_site 1689
BASE COUNT 324 a 459 c 489 g 417 t
ORIGIN
Query Match 1.0%; Score 29; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 CCCCCGGCGTGCATCTACACGCG 392
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Db 348 CCCCCGGCGTGCATCTACACGCG 376
|||||
RESULT 46
AB000500
LOCUS
DEFINITION Mus musculus mRNA for alternative splicing:see accession between AB000494 and AB000504, complete cds.
ACCESSION AB000500
VERSION AB000500.1 GI:4176405
KEYWORDS mKQT2.7; alternative splicing.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura,M., Watanabe,H., Kubo,Y., Yokoyama,M., Matsumoto,T., Sasai,H. and Nishi,Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Received (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 1818)
AUTHORS Watanabe,H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsaka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab.; 6-2, Umegeoka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@ctrl.jti.co.jp, Tel:045-972-5741)
FEATURES
source Location/Qualifiers

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1. .1818
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1508
/note="mKOT2.7"
/codon_start=1
/product="alternative splicing:see accession between
AB000494 and AB000504"
/protein_id="BAA37162.1"
/db_xref="GI:4176406"
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SEAPKRGSVLSKPRTRGAGAKPRKNAFRLQNLNLYLNERPGMAFYHAYVFL
VFSCLVSVSTIKTEKSESGALYIEIYIVVEGYEVRIWAACCCRYRGR
LKFARPCVIDIMVLASIAVLAAGSOGVFAFSALRSLRFLQILMIRDRGGTW
KLGSVYVASHKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNGRLAATFLIGVFEFALPAGIAGSCFALVQEOHRRKHFRNR
PAGILOSAMRFYATLSTRDLSHTWQYRYRTVTPMYSOSOTOGASRLIPLNQLE
LIRNLSKSGILFRKPEPSPRPASSRGCCTHALLSLCIHYSWGRATMG
PCVCFVQVQVTCGIPRYTSOL"

BASE COUNT 340 a 539 c 525 g 414 t

ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCGTTCATCTACACGC 392
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348 CCCCCGGGCGTTCATCTACACGC 376

RESULT 47
AB000501 2014 bp mRNA linear ROD 23-JAN-1999
LOCUS Mus musculus mRNA for alternative splicing:see accession between
DEFINITION AB000494 and AB000504, complete cds.
ACCESSION AB000501
VERSION AB000501.1 GI:4176407
KEYWORDS mKOT2.8; alternative splicing.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
Sasai, H. and Nishi, Y.
TITLE KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
JOURNAL Received Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2014)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
Pharmaceutical Basic Research Lab., 6-2, Umeagoka, Aoba-ku,
Yokohama, Kanagawa 227, Japan (E-mail:watanabectrl.jti.co.jp,
tel:045-972-5741)
FEATURES
source
1. .2014
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1478
/note="mKOT2.8"
/codon_start=1
/product="alternative splicing:see accession between
AB000494 and AB000504"
/protein_id="BAA37163.1"
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/translation="MWKSRNGGVPGTSGEKKIKVGFVGLDPGAPDSTRDGLIAG
SEAPKRGSVLSKPRTRGAGAKPRKNAFRLQNLNLYLNERPGMAFYHAYVFL
VFSCLVSVSTIKTEKSESGALYIEIYIVVEGYEVRIWAACCCRYRGR
LKFARPCVIDIMVLASIAVLAAGSOGVFAFSALRSLRFLQILMIRDRGGTW
KLGSVYVASHKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNGRLAATFLIGVFEFALPAGIAGSCFALVQEOHRRKHFRNR
PAGILOSAMRFYATLSTRDLSHTWQYRYRTVTPMYSOSOTOGASRLIPLNQLE
LIRNLSKSGILFRKPEPSPRPASSRGCCTHALLSLCIHYSWGRATMG
PCVCFVQVQVTCGIPRYTSOL"

KLGSVYVASHKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNGRLAATFLIGVFEFALPAGIAGSCFALVQEOHRRKHFRNR
PAGILOSAMRFYATLSTRDLSHTWQYRYRTVTPMYSOSOTOGASRLIPLNQLE
LIRNLSKSGILFRKPEPSPRPASSRGCCTHALLSLCIHYSWGRATMGPCVCFVQVQV
TVCDFPRVTSOL"

BASE COUNT 379 a 584 c 576 g 475 t

ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2014;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCGTTCATCTACACGC 392
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348 CCCCCGGGCGTTCATCTACACGC 376

RESULT 48
AB000504 2247 bp mRNA linear ROD 23-JAN-1999
LOCUS Mus musculus mRNA for alternative splicing:see accession between
DEFINITION AB000494 and AB000504, complete cds.
ACCESSION AB000504
VERSION AB000504.1 GI:4176413
KEYWORDS mKOT2.11; alternative splicing.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T.,
Sasai, H. and Nishi, Y.
TITLE KOT2, a new putative potassium channel family produced by
alternative splicing. Isolation, genomic structure, and alternative
splicing of the putative potassium channels
JOURNAL Received Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2247)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc.,
Pharmaceutical Basic Research Lab., 6-2, Umeagoka, Aoba-ku,
Yokohama, Kanagawa 227, Japan (E-mail:watanabectrl.jti.co.jp,
tel:045-972-5741)
FEATURES
source
1. .2247
/organism="Mus musculus"
/db_xref="taxon:10090"
87. .1103
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KLGSVYVASHKELVTAWYIGFLCLILASFLVLAEGENDHPTVADALMWGLITL
TIGYGDYKYPOTWNGRLAATFLIGVFEFALPAGIAGSCFALVQEOHRRKHFRNR
PAGILOSAMRFYATLSTRDLSHTWQYRYRTVTPMYSOSOTOGASRLIPLNQLE
LIRNLSKSGILFRKPEPSPRPASSRGCCTHALLSLCIHYSWGRATMGPCVCFVQVQV
TVCDFPRVTSOL"

BASE COUNT 444 a 587 c 655 g 561 t

ORIGIN

polya_site
2247

Query Match 1.0%; Score 29; DB 10; Length 2247;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCGTTCATCTACACGC 392
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Db 348 CCCCCGGCTGGCGCTCATCTACCACGC 376

RESULT 49
LOCUS AB000498
DEFINITION Mus musculus mRNA for alternative splicing:see accession between
AB000494 and AB000504, complete cds.
ACCESSION AB000498
VERSION 1
KEYWORDS GI:4176401
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Nakamura, M., Watanabe, H., Kubo, Y., Yokoyama, M., Matsumoto, T., Sasai, H. and Nishi, Y.
TITLE KQT2, a new putative potassium channel family produced by alternative splicing. Isolation, genomic structure, and alternative splicing of the putative potassium channels
JOURNAL Recept. Channels 5 (5), 255-271 (1998)
MEDLINE 98330948
REFERENCE 2 (bases 1 to 2382)
AUTHORS Watanabe, H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) Hirotsuka Watanabe, Japan Tobacco, Inc., Pharmaceutical Basic Research Lab., 6-2, Umegakka, Aoba-ku, Yokohama, Kanagawa 227, Japan (E-mail:watanabe@crl.jti.co.jp, Tel:045-972-5741)

FEATURES
source location/Qualifiers
1..2382
/organism="Mus musculus"
/db_xref="taxon:10090"
87..1799
/note="mKQT2.5"
/product="alternative splicing:see accession between
AB000494 and AB000504"
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/db_xref="GI:4176402"
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LKFARKPCVVIDIMVLASIAVLAAQSOGNFAVLSLRFQILRLIMDRGRTW
KLGSVYVANSKELVTAWYIGFCLILASGLVLAEGENHFDIYALIMDRGRTW
TIGYDGYPTQWNGRLAATFTLIGVSEFPAIILGSEFALKVOEOROKHFERRN
PAAGLIOSAMRFYATNLSRFDLSHSTWYERTVVPYRLIPINOLRLKRSKSG
LTFKREPOPEPSPSPADSLDPSKVPSPISWSDGSRTRQARFKIGASRQNSE
KVPKSWSPGDRSRTROAFRIKGAASRQNSSEASLPGEDIVDNKSCNCEFTEDLTPG
LKVSTRVAVMRLVSKRKRESLRPIYDVAVLEQYSAGHLDMLSRKSLQSRSCDWR
CYLA"
2382
polyA_site
BASE COUNT 477 a 684 c 692 g 529 t
ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2382;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCTGGCGCTCATCTACCACGC 392
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Db 348 CCCCCGGCTGGCGCTCATCTACCACGC 376

RESULT 50
LOCUS AF490773
DEFINITION Mus musculus potassium channel KCNQ2 mRNA, complete cds.
ACCESSION AF490773
VERSION AF490773.1
KEYWORDS GI:20069140

SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Men, H. and Levitan, I. B.
TITLE Calmodulin is an auxiliary subunit of KCNQ channels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2613)
AUTHORS Men, H. and Levitan, I. B.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Neuroscience, University of Pennsylvania, 3450 Hamilton Walk, Philadelphia, PA 19104, USA

FEATURES
source location/Qualifiers
1..2613
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="2"
/map="between Chnra4 and Eefia2"
1..2613
/codon_start=1
/product="potassium channel KCNQ2"
/protein_id="AAM09696.1"
/db_xref="GI:20069141"
/translation="MVKSRNGGVYPTGSGEKKLVGFVGLDPGADPSTRDGALLIAG
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VFSCILVSTIKKEYKSESGALVILEVTIVYFVEYFRIMAGCCCRIGWGR
LKFARKPCVVIDIMVLASIAVLAAQSOGNFAVLSLRFQILRLIMDRGRTW
KLGSVYVANSKELVTAWYIGFCLILASGLVLAEGENHFDIYALIMDRGRTW
TIGYDGYPTQWNGRLAATFTLIGVSEFPAIILGSEFALKVOEOROKHFERRN
PAAGLIOSAMRFYATNLSRFDLSHSTWYERTVVPYRLIPINOLRLKRSKSG
LTFKREPOPEPSPSPADSLDPSKVPSPISWSDGSRTRQARFKIGASRQNSE
KVPKSWSPGDRSRTROAFRIKGAASRQNSSEASLPGEDIVDNKSCNCEFTEDLTPG
LKVSTRVAVMRLVSKRKRESLRPIYDVAVLEQYSAGHLDMLSRKSLQSRSCDWR
CYLA"
EGPGRDVAAMAPRK"
BASE COUNT 553 a 770 c 766 g 524 t
ORIGIN

Query Match 1.0%; Score 29; DB 10; Length 2613;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCTGGCGCTCATCTACCACGC 392
|||||
Db 262 CCCCCGGCTGGCGCTCATCTACCACGC 290

Search completed: June 19, 2003, 15:38:11
Job time : 6939 secs

1

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OY 1921 GAATGTGACAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCC 1980
DB 1921 GAATGTGACAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCC 1980
OY 1981 GCACAAAAACAGTGGCTGCTTATCCAGATCACTAGTCCACATCTCCAGAGGCTTGAC 2040
DB 1981 GCACAAAAACAGTGGCTGCTTATCCAGATCACTAGTCCACATCTCCAGAGGCTTGAC 2040
OY 2041 TTCAATTCGAGCCCAATAGTGTGAGTCCGAGTCTTACGCGCTTACGCTTACGCTTACG 2100
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DB 2161 AACACCATTTGCAACCAATAATAGCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2220
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DB 2221 ATCCACCTCTCTCTCCAGCCATCAAGCATCTGCGCAGGCGCAGAACTTGACACCTTAC 2280
OY 2281 CCTGACGCTTACAGAAAGCATTTTGTGACGTACCACTGCTTGTGCTTGTGCTTGTGCT 2340
DB 2281 CCTGACGCTTACAGAAAGCATTTTGTGACGTACCACTGCTTGTGCTTGTGCTTGTGCT 2340
OY 2341 AATGTTACGTTGACAGTCAATCTCACCAGAGCCGTTCTTATGAGAAAGCTTTGAC 2400
DB 2341 AATGTTACGTTGACAGTCAATCTCACCAGAGCCGTTCTTATGAGAAAGCTTTGAC 2400
OY 2401 ATGGAGGAGAAACTCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB 2401 ATGGAGGAGAAACTCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
OY 2461 TTGTCTGTGCAAAACCTGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
DB 2461 TTGTCTGTGCAAAACCTGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
OY 2521 GAGTCAAGTGTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
DB 2521 GAGTCAAGTGTGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2580
OY 2581 TTTTAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
DB 2581 TTTTAACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
OY 2641 CCGCAGGCTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
DB 2641 CCGCAGGCTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
OY 2701 TCATCTCAGAGCATTTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
DB 2701 TCATCTCAGAGCATTTTGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
OY 2761 AAATCTGAATTA 2772
DB 2761 AAATCTGAATTA 2772

```

RESULT 2

AAH43634 standard; cDNA; 3111 BP.

AAH43634:

21-JAN-2002 (first entry)

Human ion-channel forming protein coding sequence.

Ion-channel forming protein; voltage-gated potassium channel;

```

KW fetal: brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX Homo sapiens.
OS key
FH location/Qualifiers
FT CDS 59..2831
FT /*tag= a
FT /product= "Human ion-channel forming protein"
XX
XX WO200175108-A1.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US10875.
XX
XX 03-APR-2000; 2000US-194255P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
XX Sands AT;
XX
XX WPI: 2001-656987/75.
XX
XX P-PSDB: AAB47678.
XX
XX New human ion channel protein and polynucleotides encoding the protein,
XX useful in diagnosing or treating diseases, in drug screening, and in
XX clinical trial monitoring
XX
XX Disclosure: Page 37-38; 41pp; English.
XX
XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
XX The protein shares structural similarity with mammalian ion channel
XX proteins, particularly voltage-gated potassium channel proteins. The
XX protein is expressed in many human cell lines including fetal brain,
XX brain, thymus, prostate, heart and skeletal muscle. The novel protein
XX can be used in the diagnosis or treatment of diseases, in drug
XX screening, and in clinical trial monitoring. The oligonucleotides may
XX be used as hybridization probes for screening libraries, and assessing
XX gene expression patterns (particularly using a micro array or high
XX throughput chip format). The nucleic acids and novel protein can also be
XX used in the identification, selection and validation of novel molecular
XX targets for drug discovery, to screen collections of genetic material
XX from patients who have a particular medical condition, to identify
XX mutations associated with a particular disease, as a diagnostic or
XX prognostic assay, and to screen for drugs which can be used to treat
XX symptomatic or phenotypic manifestations of perturbing the normal
XX function of novel human protein. The polypeptides are further used in
XX generating antibodies.
XX
XX Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 other;
XX
XX Query Match 100.0%; Score 2772; DB 22; Length 3111;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGCCCGCCACACAGCGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
DB 60 ATGCCCGCCACACAGCGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119
OY 61 GGGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 120 GGGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 179
OY 121 TCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 180 TCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
OY 181 CTGGGCAACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 240 CTGGGCAACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
OY 241 GGCAAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

```

D	300	GGCAAGCAGGAGGGCCCGGATGAGCCGTGGGGGAAACCCGTCCTTACAGAGATGACG	359
Q	301	ACGTGCGGGGCGAAGCTCAAGTACCGGGGGGTGCAGAACTACCTGTACAACTGTGAG	360
D	360	ACCTGCGGGGCGAAGCTCAAGTACCGGGGGGTGCAGAACTACCTGTACAACTGTGAG	419
Q	361	AGACCCCGGGGCGGTTCATCTACACGCTTTGTTTCTCCTGTGCTTGGTTCG	420
D	420	AGACCCCGGGGCGGTTCATCTACACGCTTTGTTTCTCCTGTGCTTGGTTCG	479
Q	421	TTGATTTTGTAGTGTCTTCTACCATCCCTGACACACAAAATGGGCTCAAGTGGCTC	480
D	480	TTGATTTTGTAGTGTCTTCTACCATCCCTGACACACAAAATGGGCTCAAGTGGCTC	539
Q	481	TTGATCTGTAGTGTGTATGTCGCTTTGGTTGGAGTTCATCATTTGGAATCTGG	540
D	540	TTGATCTGTAGTGTGTATGTCGCTTTGGTTGGAGTTCATCATTTGGAATCTGG	599
Q	541	TTCTGGGGTGTCTGTTGTGATATAGAGAGATGGCAAGAAAGTGAAGTTGCTCGAAG	600
D	600	TTCTGGGGTGTCTGTTGTGATATAGAGAGATGGCAAGAAAGTGAAGTTGCTCGAAG	659
Q	601	CCCTCTGTGTTATAGATACCATGTCTTATCCGCTTAATAGCATGCTTTCTGCAAA	660
D	660	CCCTCTGTGTTATAGATACCATGTCTTATCCGCTTAATAGCATGCTTTCTGCAAA	719
Q	661	ACTCAGGATATATTTTGGCACGCTGCTACAGAACTCCGTTTCCATAGATCCG	720
D	720	ACTCAGGATATATTTTGGCACGCTGCTACAGAACTCCGTTTCCATAGATCCG	779
Q	721	CGCATGGTGGCATGAGCCGAGGGGAGGCACTTGGAAATTAATCTGCTGAGTGGTTAT	780
D	780	CGCATGGTGGCATGAGCCGAGGGGAGGCACTTGGAAATTAATCTGCTGAGTGGTTAT	839
Q	781	GCTCAGCAGCAAGAAATTAATCAGCTGTGACATAGATTTTGGTTCTATTTTTCG	840
D	840	GCTCAGCAGCAAGAAATTAATCAGCTGTGACATAGATTTTGGTTCTATTTTTCG	899
Q	841	TTCTTCTGTCTATCTGCTGGGAAAGAGATCCCAATAAGATTTTCTACATATGACAT	900
D	900	TTCTTCTGTCTATCTGCTGGGAAAGAGATCCCAATAAGATTTTCTACATATGACAT	959
Q	901	GCTCTGTGTGGGGACAAATTAATGACAACTTATGGCTATGAGACAAACACCCCTTA	960
D	960	GCTCTGTGTGGGGACAAATTAATGACAACTTATGGCTATGAGACAAACACCCCTTA	1019
Q	961	ACTTGGCTGGGAAGATTTGCTTTCGACAGGCTTTGCACTCTTGGCATTTCTTTTGA	1020
D	1020	ACTTGGCTGGGAAGATTTGCTTTCGACAGGCTTTGCACTCTTGGCATTTCTTTTGA	1079
Q	1021	CTTCTGCGGGCAATTTTGGCTCAGGTTTGGCAATTAAGTACAAAGAAACACCGCCAG	1080
D	1080	CTTCTGCGGGCAATTTTGGCTCAGGTTTGGCAATTAAGTACAAAGAAACACCGCCAG	1139
Q	1081	AAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGT	1140
D	1140	AAACACTTTGAGAAAGAAAGAAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGT	1199
Q	1141	TACGAGCTGATGAGAAATCTGTTCCATTTGCACTGGAAGCACAATTTGAAGCCCTTG	1200
D	1200	TACGAGCTGATGAGAAATCTGTTCCATTTGCACTGGAAGCACAATTTGAAGCCCTTG	1259
Q	1201	CACACCTGACGCCCTACCAATCAGAAAGTAAAGTAAAGAGAGAGTGGCATGGCTAG	1260
D	1260	CACACCTGACGCCCTACCAATCAGAAAGTAAAGTAAAGAGAGAGTGGCATGGCTAG	1319
Q	1261	CCCAGGGGCAAGATTAAGAGCCGACAAAGCTCATGTAGTACAGAGAGTCCCAAGC	1320
D	1320	CCCAGGGGCAAGATTAAGAGCCGACAAAGCTCATGTAGTACAGAGAGTCCCAAGC	1379
Q	1321	ACCGACATCAGAGCCGAGGGGAGTCCACCAAAAGTGCAGAAAGGTGGAGCTTCAACGAC	1380
D	1380	ACCGACATCAGAGCCGAGGGGAGTCCACCAAAAGTGCAGAAAGGTGGAGCTTCAACGAC	1439
Q	1381	CGAACCCTCCGGGCTCGCTGCGCTGCTCAAAAGTTCTACGCCAAACAGTATGAT	1440
D	1440	CGAACCCTCCGGGCTCGCTGCGCTGCTCAAAAGTTCTACGCCAAACAGTATGAT	1499
Q	1441	GCTGACACAGCCCTTGGCACTGATGATGATATATATAAAAGATGCGAGTGTGATGA	1500
D	1500	GCTGACACAGCCCTTGGCACTGATGATGATGATATATAAAAGATGCGAGTGTGATGA	1559
Q	1501	TCAGTGGAAAGACCTCCACCACCACTTAAACGTCTATTGAGCTATACGAATTAAGAA	1560
D	1560	TCAGTGGAAAGACCTCCACCACCACTTAAACGTCTATTGAGCTATACGAATTAAGAA	1619
Q	1561	TTTTCATGTTGCAAAAGGAAAGTTAAGAAACATTAAGTCCATATGATGTAAGAAATGC	1620
D	1620	TTTTCATGTTGCAAAAGGAAAGTTAAGAAACATTAAGTCCATATGATGTAAGAAATGC	1679
Q	1621	ATTGAAACATATTTCTGCTGCTCATCTGAGACATTTGTGTAATTAAGCCCTTCAACA	1680
D	1680	ATTGAAACATATTTCTGCTGCTCATCTGAGACATTTGTGTAATTAAGCCCTTCAACA	1739
Q	1681	CGTGTGATCAAAATTTTGGAAAGGGCAATACATCAATGATATAGAAAGACCCAGAGAA	1740
D	1740	CGTGTGATCAAAATTTTGGAAAGGGCAATACATCAATGATATAGAAAGACCCAGAGAA	1799
Q	1741	ATTAACAGCAAGAACATGAGACCAACAGATCTCAGTATGCTGCTGGGTGTCAAGTT	1800
D	1800	ATTAACAGCAAGAACATGAGACCAACAGATCTCAGTATGCTGCTGGGTGTCAAGTT	1859
Q	1801	GAAAAACAGTACAGTCCATAGAACATGAGTGGTGGCTACTAGACATTTTCAACAG	1860
D	1860	GAAAAACAGTACAGTCCATAGAACATGAGTGGTGGCTACTAGACATTTTCAACAG	1919
Q	1861	GTCCTTGGAAAGGCTTGCCTCAGACCCCTGCTTGGCTTCAATTCAGATTCACACCTTT	1920
D	1920	GTCCTTGGAAAGGCTTGCCTCAGACCCCTGCTTGGCTTCAATTCAGATTCACACCTTT	1979
Q	1921	GAATGTGAAGACATGACATGATTAAGAGCCCTGTGATAGCAAAAGATCTTTGGGTTCC	1980
D	1980	GAATGTGAAGACATGACATGATTAAGAGCCCTGTGATAGCAAAAGATCTTTGGGTTCC	2039
Q	1981	GCACAAAACAGTGGCTTATTCAGATCAACTAGTGGCAACATCTCGAGAGCCCTGCAG	2040
D	2040	GCACAAAACAGTGGCTTATTCAGATCAACTAGTGGCAACATCTCGAGAGCCCTGCAG	2099
Q	2041	TTCAATTCGAGGCCAAATGAATTCAGTCCCAAGATTTTCTACGCGCTTACGCCCTATAG	2100
D	2100	TTCAATTCGAGGCCAAATGAATTCAGTCCCAAGATTTTCTACGCGCTTACGCCCTATAG	2159
Q	2101	CACAGTGAAGCACAAGGTGCCAATTTAGTAAAGCCATGCTGACAGTGGGACCCAGC	2160
D	2160	CACAGTGAAGCACAAGGTGCCAATTTAGTAAAGCCATGCTGACAGTGGGACCCAGC	2219
Q	2161	AACACACTTTGCAAAACCAATTAATAGCGGACCCAGAGCCGACCCCAACTTTACAG	2220
D	2220	AACACACTTTGCAAAACCAATTAATAGCGGACCCAGAGCCGACCCCAACTTTACAG	2279
Q	2221	ATCCACCTCTCTCCAGCATATAGCATATGCCCAGAGCCAGAAACATCTCCACCTTAC	2280

QY 2461 TTGCTGTGCAAAACCTGATCGACCGAGAACTGATATACACTTTCAGGAGT 2520
 CC |||||||
 Db 2520 TTGCTGTGCAAAACCTGATCGACCGAGAACTGATATACACTTTCAGGAGT 2579
 CC |||||||
 QY 2521 GAGTCAGTGGCTCCAGAGCGAGCCAGATTTTACCCCAATGAGGAGATCCAAATTG 2580
 CC |||||||
 Db 2580 GAGTCAGTGGCTCCAGAGCGAGCCAGATTTTACCCCAATGAGGAGATCCAAATTG 2639
 CC |||||||
 QY 2581 TTTATACGTATGAAGAGTGGTCCCAAGACAGACAGACACTTTGATGCGCGA 2640
 CC |||||||
 Db 2640 TTTATACGTATGAAGAGTGGTCCCAAGACAGACAGACACTTTGATGCGCGA 2699
 CC |||||||
 QY 2641 CCGAGCGCTGCGAGGAGAGTCCCTTTGCATCAGACTCTTAAGAAGTGAAGTCA 2700
 CC |||||||
 Db 2700 CCGAGCGCTGCGAGGAGAGTCCCTTTGCATCAGACTCTTAAGAAGTGAAGTCA 2759
 CC |||||||
 QY 2701 TCATCTCAGACATTTGTAAGGCGAGAGAAATACAGATGCCCTTCAGCTTCATGTC 2760
 CC |||||||
 Db 2760 TCATCTCAGACATTTGTAAGGCGAGAGAAATACAGATGCCCTTCAGCTTCATGTC 2819
 CC |||||||
 QY 2761 AAACGAAATTA 2772
 CC |||||||
 Db 2820 AAACGAAATTA 2831
 CC |||||||
 RESULT 3
 AAS14653 standard; cDNA: 2667 BP.
 ID AAS14653 standard; cDNA: 2667 BP.
 AC AAS14653;
 XX 18-DEC-2001 (first entry)
 DT
 XX Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
 DE
 XX Human; ss; voltage-gated potassium channel; KCNQ5-2; nocturnal;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; splice variant.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..2967
 FT /*tag- a
 FT /product= "hKCNQ5-2"
 XX
 PN MO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001MO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 DR WPI: 2001-611467/70.
 DR P-PSDB; AAU09021.
 XX
 XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 XX
 PS Claim 5; Page 63-64; 78pp; English.
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acid encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel and the
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-2.
 CC
 XX
 XX Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 other;
 S0
 Query Match 90.7%; Score 2514; DB 22; Length 2667;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 106 ATGAAGATGTGAGATCGGCGGGGAGGAGTGTGCTGACAGTGGGAGCGGCGAGGAGG 165
 Db 1 ATGAAGATGTGAGATCGGCGGGGAGGAGTGTGCTGACAGTGGGAGCGGCGAGGAGG 60
 QY 166 GACGCGCTGCTACTGCTGGGACCCGCGGCGACAGCTGGTGGCGGCGGCTGCTG 225
 Db 61 GACGCGCTGCTACTGCTGGGACCCGCGGCGACAGCTGGTGGCGGCGGCTGCTG 120
 QY 226 AGGAGAGCGCGCGGCGCAAGCAGGCGGCGGAGGCTGCTGGGAGAGCGGCTGCT 285
 Db 121 AGGAGAGCGCGCGGCGCAAGCAGGCGGCGGAGGCTGCTGGGAGAGCGGCTGCT 180
 QY 286 TACAGAGTGGCAGAGAGTGGCGGCGCAAGTACAGTGGGAGGAGTGGAGTACCTG 345
 Db 181 TACAGAGTGGCAGAGAGTGGCGGCGCAAGTACAGTGGGAGGAGTGGAGTACCTG 240
 QY 346 TACAGAGTGGCAGAGAGTGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 405
 Db 241 TACAGAGTGGCAGAGAGTGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 406 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
 Db 301 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 466 GCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 525
 Db 361 GCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 526 ATCAATTCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
 Db 421 ATCAATTCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 586 AGGTTGCTGCAAGAGCCCTTCTGTATATACATACATGCTTCTTATGCTTCAATGCA 645
 Db 481 AGGTTGCTGCAAGAGCCCTTCTGTATATACATACATGCTTCTTATGCTTCAATGCA 540
 QY 646 GTTGTGTTGCAAAACTGAGGTAATTTTGGCAGCTGCTGCAAGAGTCTGCT 705
 Db 541 GTTGTGTTGCAAAACTGAGGTAATTTTGGCAGCTGCTGCAAGAGTCTGCT 600
 QY 706 TTCTTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
 Db 601 TTCTTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 766 GGTTCAGTGTATATGCTCAGCAGCAAGAAATTAATCAGCTTGTGCTACATGATTTTGG 825

D		1741	GACATCTATCAACAGGTCCTTGGAAAGGCTCTGCCCTCAGCCCTCGCTTGCTGCATTTC	1807
OY		1906	CAGATCCCACCTTTTGAATGTGAACAGACAATCTGACTATCAAAGCCCTGTGATAGCAA	1965
D		1801	CAGATCCCCACCTTTTGAATGTGAACAGACAATCTGACTATCAAAGCCCTGTGATAGCAA	1866
OY		1966	GATCTTTGGGTTCCGACAAAACAGTGGCTGCTATTCAGATCAACTAGTCCAAATC	2025
D		1861	GATCTTTGGGTTCCGACAAAACAGTGGCTGCTATTCAGATCAACTAGTCCAAATC	1920
OY		2026	TGAGAGGCGCTGCAATTCCTGAGCGCCAATGAGTTCACTGAGTCCGACTTTTAAGCG	2085
D		1921	TGAGAGGCGCTGCAATTCCTGAGCGCCAATGAGTTCACTGAGTCCGACTTTTAAGCG	1980
OY		2086	CTTAGCGCTACTATGACAGATCAAGCAACAGAGTGCATAATAGTCAAAAGCGATGCTCA	2145
D		1981	CTTAGCGCTACTATGACAGATCAAGCAACAGAGTGCATAATAGTCAAAAGCGATGCTCA	2040
OY		2146	GCAGTGGCAGCCACCACCATTTGGAACCAAAATAAATGGGACCCCAAGCCAGCACGCC	2205
D		2041	GCAGTGGCAGCCACCACCATTTGGAACCAAAATAAATGGGACCCCAAGCCAGCACGCC	2100
OY		2206	CCAAACAATTTTCAATATCCCACTCTCTCTCCCAAGCCATCAAGCATCTGCCAGCGCAA	2265
D		2101	CCAAACAATTTTCAATATCCCACTCTCTCTCCCAAGCCATCAAGCATCTGCCAGCGCAA	2160
OY		2286	ACTGTGCACCCCTAACCCCTGCAGGCTTACAGAAAGCATTTCTGAGCTGCACACCTGCTT	2325
D		2161	ACTGTGCACCCCTAACCCCTGCAGGCTTACAGAAAGCATTTCTGAGCTGCACACCTGCTT	2220
OY		2326	GTTCGCTTCAAGGAAATGTTCAGGTTGTCACAGTCAAAATCTACCAAGAACCGTTCTATG	2385
D		2221	GTTCGCTTCAAGGAAATGTTCAGGTTGTCACAGTCAAAATCTACCAAGAACCGTTCTATG	2280
OY		2386	AGGAAAGCTTTGACATGGAGGAGAANAACCTGTGTCTGTCTGTGCCATGGTGGCGAAG	2445
D		2281	AGGAAAGCTTTGACATGGAGGAGAANAACCTGTGTCTGTCTGTGTGCCATGGTGGCGAAG	2340
OY		2446	GACTTGGGGCAATCTTTGTCTGTGTGCAAAAACCTGATCAGGTGACCGGAGAACTGAATATA	2505
D		2341	GACTTGGGGCAATCTTTGTGTGTGTGCAAAAACCTGATCAGGTGACCGGAGAACTGAATATA	2400
OY		2506	CAACTTTCAGGAGTGTAGTCAAGTGGTCCAGAGGSCAGCCAAAGATTTTAAOCCCAAAATGG	2565
D		2401	CAACTTTCAGGAGTGTAGTCAAGTGGTCCAGAGGSCAGCCAAAGATTTTAAOCCCAAAATGG	2460
OY		2566	AGGGAATCCAAATGTTTATTAATCACTGATGAGAGAGTGGTCCCGAAGAGACAGACAGNC	2625
D		2461	AGGGAATCCAAATGTTTATTAATCACTGATGAGAGAGTGGTCCCGAAGAGACAGACAGNC	2520
OY		2626	ACTTTTGATCCGACCGACGAGCCCTGCCAGGGAAGCTGCTTGGATCAAGACTCTTAAGG	2685
D		2521	ACTTTTGATCCGACCGACGAGCCCTGCCAGGGAAGCTGCTTGGATCAAGACTCTTAAGG	2580
OY		2686	ACTGGAAGGTCACAGATATCTCAGAGCATTTTGAAGCAGAGAAAGTACAGATGCCCCC	2745
D		2581	ACTGGAAGGTCACAGATATCTCAGAGCATTTTGAAGCAGAGAAAGTACAGATGCCCCC	2640
OY		2746	AGCTTGCTCATGTCAAACTGAATATA	2772
D		2641	AGCTTGCTCATGTCAAACTGAATATA	2667
<hr/>				
RESULT 4				
AAH49499 standard; DNA; 3074 BP.				
<hr/>				
AAH49499;				
<hr/>				
11-DEC--2001 (first entry)				
<hr/>				
Human KCNO5 DNA.				
<hr/>				

KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
 KW anticonvulsant; excitability modulator; membrane potential; neuron;
 KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
 KW screening; central nervous system disease; cardiovascular disease; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 110..2908
 FT CDS /tag= a
 FT /product= "KCNQ5"
 DEJ0013732-A1.
 PD 27-SEP-2001.
 PD 21-MAR-2000; 2000DE-1013732.
 PR 21-MAR-2000; 2000DE-1013732.
 PA (AVENTIS PHARMA DEUT GMBH.
 PI Steinmeyer K, Lerche C, Scherer C, Seebold G, Busch AE;
 DR WPI: 2001-571700/65.
 DR P-PSDB: AAB86979.
 XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
 PT for specific modulators, potential agents for treating central nervous
 PT system and cardiovascular diseases
 PS Claim 2a: Page 9-10; 20pp: German.
 XX
 XX This invention describes a novel DNA sequence (I) encoding: (i) a
 CC polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
 CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
 CC the invention have neurological, cardiovascular and anticonvulsant
 CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
 CC channel, a key regulator of membrane potential and modulator of
 CC excitability of electrically activated cells such as neurons and
 CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
 CC are used to screen for compounds that modulate the activity of KCNQ5,
 CC potentially useful for treating central nervous system (e.g. epilepsy)
 CC and cardiovascular diseases. This sequence encodes the human
 CC potassium channel KCNQ5 protein described in the invention.
 CC
 XX Sequence 3074 BP: 788 A; 784 C; 789 G; 713 T; 0 other:
 Query Match 56.0%; Score 1552; DB 22; Length 3074;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1657 ACCACTTAAACCTGATTCAGGATATGAGATTAATTTCAATGTCGCAAAACGGAA 1716
 1581 GTTTAAGGAACATTAGCTCCATATGATGTAAATAATGTCATGGAACATATTCGCTGG 1640
 1717 GTTTAAGGAACATTAGCTCCATATGATGTAAATAATGTCATGGAACATATTCGCTGG 1776
 1641 TCATCTGACATGTTGTGTAGATTAATAAGCTTCAACACGCTGTGATCAAAATTCCTGG 1700
 1777 TCATCTGACATGTTGTGTAGATTAATAAGCTTCAACACGCTGTGATCAAAATTCCTGG 1836
 1701 AAAAGGGCAATACATCATGATTAAGAGCCGAGAGAAATTAACAGCGAATCTAGAC 1760
 1837 AAAAGGGCAATACATCATGATTAAGAGCCGAGAGAAATTAACAGCGAATCTAGAC 1896
 1761 CACAGACATCTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1820
 1897 CACAGACATCTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1956
 1821 AGAATCCAAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1880
 1957 AGAATCCAAAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2016
 1881 CTCAGCCCTCGCTTTGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGCATCTGA 1940
 2017 CTCAGCCCTCGCTTTGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGCATCTGA 2076
 1941 CTATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2000
 2077 CTATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
 2001 ATCCAGATCACTAGTGGCAACATCTGAGAGCCCTGCACTTCTTGTACGCCCAATGA 2060
 2137 ATCCAGATCACTAGTGGCAACATCTGAGAGCCCTGCACTTCTTGTACGCCCAATGA 2196
 2061 GTTCAAGTGGCAACATCTTACGCGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 2120
 2197 GTTCAAGTGGCAACATCTTACGCGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 2256
 2121 GCCAATTAGTCAAAAGGATGGCTCAGAGTGGAGCCAGCCACCAACCAATTTGCAAAACCAAT 2180
 2257 GCCAATTAGTCAAAAGGATGGCTCAGAGTGGAGCCAGCCACCAACCAATTTGCAAAACCAAT 2316
 2181 AATATCGGACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2240
 2317 AATATCGGACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2376
 2241 CATCAAGCATCTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2300
 2377 CATCAAGCATCTGCGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 2436
 2301 CATTTTGCAGTACACACCTGCTTGTGCTTCCAGAGAAATTTGCAAGTTTGCACAGTGC 2360
 2437 CATTTTGCAGTACACACCTGCTTGTGCTTCCAGAGAAATTTGCAAGTTTGCACAGTGC 2496
 2361 AATATCTCAAGAGACGCTTCTATGAGAAAGCTTGTGCAATGAGAGAGAAACCTCTGT 2420
 2497 AATATCTCAAGAGACGCTTCTATGAGAAAGCTTGTGCAATGAGAGAGAAACCTCTGT 2556
 2421 GTCTGTCTGTCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2480
 2557 GTCTGTCTGTCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2616
 2481 CAGCTGACGAGAGAACTGATTAACAACCTTACGAGAGTGTAGTGAAGTGTCCAGAGG 2540
 2617 CAGCTGACGAGAGAACTGATTAACAACCTTACGAGAGTGTAGTGAAGTGTCCAGAGG 2676
 2541 CAGCAGAGATTTTACCCCAATGAGAGAAATCCAAATTTGTTATTAATGATGAAGAGT 2600
 2677 CAGCAGAGATTTTACCCCAATGAGAGAAATCCAAATTTGTTATTAATGATGAAGAGT 2736
 2601 GGGTCCGAGAGACAGACACCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2660

Db 2103 AATAAGGACCCAGACAGACCCACACTTACAGATCCACCTCTCTCCAGC 2162
 QY 2241 CATCAACATCTGCCAGGACAGAACTGTACACCTTACCTGAGGCTTACAGAAAG 2300
 Db 2163 CATCAACATCTGCCAGGACAGAACTGTACACCTTACCTGAGGCTTACAGAAAG 2222
 QY 2301 CATTTCTGACGACGACCTGCTTGTGCTCCAGGAAATTTCAAGTTGACAGTC 2360
 Db 2223 CATTTCTGACGACGACCTGCTTGTGCTCCAGGAAATTTCAAGTTGACAGTC 2282
 QY 2361 AATTCACCAAGACGCTTCTATGAGAAAGCTTGAATGGAGAGAAACCTGT 2420
 Db 2283 AATTCACCAAGACGCTTCTATGAGAAAGCTTGAATGGAGAGAAACCTGT 2342
 QY 2421 GTCCTCTGCTCCATGGTGGCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACCTGAT 2480
 Db 2343 GTCCTCTGCTCCATGGTGGCGAAGACTTGGGCAAACTTTGTCTGTGCAAAACCTGAT 2402
 QY 2481 CAGGTGACCGAGGAGACTGATATACACTTTCAGGAGAGTACATCAGTCCAGAGG 2540
 Db 2403 CAGGTGACCGAGGAGACTGATATACACTTTCAGGAGAGTACATCAGTCCAGAGG 2462
 QY 2541 CAGCAAGATTTTATCCCAATGAGGAGATCCAAATTTTATTAAGTGAAGAGT 2600
 Db 2463 CAGCAAGATTTTATCCCAATGAGGAGATCCAAATTTTATTAAGTGAAGAGT 2522
 QY 2601 GGGTCCCGAAGAGACAGACACTTTTGTATGCCAGCCAGGCTTCCAGGAGAGC 2660
 Db 2523 GGGTCCCGAAGAGACAGACACTTTTGTATGCCAGCCAGGCTTCCAGGAGAGC 2582
 QY 2661 TGGCTTTGACATCAGCTCTTAAGACTGGAAGTCAAGATCATCTCAGAGATTGTAA 2720
 Db 2583 TGGCTTTGACATCAGCTCTTAAGACTGGAAGTCAAGATCATCTCAGAGATTGTAA 2642
 QY 2721 GGCAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAATTA 2772
 Db 2643 GGCAGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAATTA 2694
 RESULT 6
 AAC64371
 ID AAC64371 standard; cDNA; 3718 BP.
 XX AAC64371;
 AC
 XX
 DT 07-FEB-2001 (first entry)
 XX
 DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
 XX
 KW Human; KCNQ5; KC6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardiocutaneous; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200061606-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000MO-US09587.
 XX
 PR 14-APR-1999; 99US-0129274.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Petrunkin K, Caskey CT, Li W, Metzker ML;
 XX
 DR WPI: 2000-647417/62.
 DR P-PSDB: AAB24241.

XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT Inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 PS Claim 3; Fig 2; 99p; English.
 XX
 CC The present sequence encodes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q.
 CC
 SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 other;
 Query Match 54.1%; Score 1501; DB 21; Length 3718;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1221 TCAGAGCTAAGTTTAAAGGAGCGAGTCCCATGCTAGCCCGAGGCGCAGATATTA 1280
 Db 1127 TCAGAGCTAAGTTTAAAGGAGCGAGTCCCATGCTAGCCCGAGGCGCAGATATTA 1186
 QY 1281 GAGCCGCAAGCCTCAGTAGTGACAGAGAGTCCCGCAAGCAGCATCAAGCCGAGG 1340
 Db 1187 GAGCCGCAAGCCTCAGTAGTGACAGAGAGTCCCGCAAGCAGCATCAAGCCGAGG 1246
 QY 1341 CAGTCCCAAGAGTGAAGAGAGCTGAGCTTCAAGCAGCAAGCCGCTTCCGCGCTC 1400
 Db 1247 CAGTCCCAAGAGTGAAGAGAGCTGAGCTTCAAGCAGCAAGCCGCTTCCGCGCTC 1306
 QY 1401 GCTGCGCCTCAAAAGTTCTCAGCCCAAAACAGATATGATCTGTCGCAAAACGGA 1460
 Db 1307 GCTGCGCCTCAAAAGTTCTCAGCCCAAAACAGATATGATCTGTCGCAAAACGGA 1366
 QY 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 Db 1367 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
 QY 1521 ACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
 Db 1427 ACCACTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
 QY 1581 GTTTAAGGAAACATTAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 Db 1487 GTTTAAGGAAACATTAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1546
 QY 1641 TCATCTGACATGTTGTGTAGATTAAGGCTTCAACACGCTGATCAATCTTGG 1700
 Db 1547 TCATCTGACATGTTGTGTAGATTAAGGCTTCAACACGCTGATCAATCTTGG 1606
 QY 1701 AAAAGGGCAATACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAATGAGAG 1760
 Db 1607 AAAAGGGCAATACATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAATGAGAG 1666
 QY 1761 CACAGACATCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
 Db 1667 CACAGACATCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
 QY 1821 AGAATCAAGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1880
 Db 1727 AGAATCAAGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
 QY 1881 CTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGGAACAGCATCTGA 1940
 Db 1787 CTCAGCCCTGCTTGGCTTCAATCCAGATCCCACTTTTGAATGGAACAGCATCTGA 1846

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OY 1941 CTATCAAGCCCTGTGATAGCAAGATCTTGGGTTCCGACAAACAGTGGCTCTT 2000
DB 1847 CTATCAAGCCCTGTGATAGCAAGATCTTGGGTTCCGACAAACAGTGGCTCTT 1906
OY 2001 ATCCAGATCAACTAGTGTCCCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAATGA 2060
DB 1907 ATCCAGATCAACTAGTGTCCCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAATGA 1966
OY 2061 GTTCAGTGGCCAGACTTTCTAGGGCTTAGGCTTACTATGACAGTCAAGCAACAGAGT 2120
DB 1967 GTTCAGTGGCCAGACTTTCTAGGGCTTAGGCTTACTATGACAGTCAAGCAACAGAGT 2026
OY 2121 GCCAATTAGTCAAGCGATGGCTCGACAGTGGCCACCAACACATTCGCAACCAAT 2180
DB 2027 GCCAATTAGTCAAGCGATGGCTCGACAGTGGCCACCAACACATTCGCAACCAAT 2086
OY 2181 AAATPAGGCAOCCCAAGCCAGACAGCCCAACAACATTACAGATCCACCTCTCTCCAGC 2240
DB 2087 AAATPAGGCAOCCCAAGCCAGACAGCCCAACAACATTACAGATCCACCTCTCTCCAGC 2146
OY 2241 CATCAAGCATCTGCCAGGCGAGAAATCTGACCCCTAACCCTGAGGCTTACAGGAAG 2300
DB 2147 CATCAAGCATCTGCCAGGCGAGAAATCTGACCCCTAACCCTGAGGCTTACAGGAAG 2206
OY 2301 CATTTTGACGTCAACACCTGGCTTGTTCCTCCAAAGAAATGTTACAGTGGACAGTC 2360
DB 2207 CATTTTGACGTCAACACCTGGCTTGTTCCTCCAAAGAAATGTTACAGTGGACAGTC 2266
OY 2361 AAATCTCACCAGAGCCGTTCTATAGAGAAATGTTTACATGGAGAGAAATCTCTGTT 2420
DB 2267 AAATCTCACCAGAGCCGTTCTATAGAGAAATGTTTACATGGAGAGAAATCTCTGTT 2326
OY 2421 GTCTGTCTGTCCATGTGTGCGAAGACTTGGCAAAATCTTGTGTGCAAAACCTGAT 2480
DB 2327 GTCTGTCTGTCCATGTGTGCGAAGACTTGGCAAAATCTTGTGTGCAAAACCTGAT 2386
OY 2481 CAGGTGACCGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGG 2540
DB 2387 CAGGTGACCGAGAACTGAATATCAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGG 2446
OY 2541 CAGCCAAATTTTACCCCAATAGAGGAAATCCAAATGTTTAACTGATGAAGAGT 2600
DB 2447 CAGCCAAATTTTACCCCAATAGAGGAAATCCAAATGTTTAACTGATGAAGAGT 2506
OY 2601 GGGTCCCGAAGACAGACACACTTTTGTATGCGCAGCGAGCTGCCAGGGAAGC 2660
DB 2507 GGGTCCCGAAGACAGACACACTTTTGTATGCGCAGCGAGCTGCCAGGGAAGC 2566
OY 2661 TGCCCTTTCATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCTCAGACATTTGTA 2720
DB 2567 TGCCCTTTCATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCTCAGACATTTGTA 2626
OY 2721 GGCAGGAGAAATACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2772
DB 2627 GGCAGGAGAAATACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATTA 2678

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RESUL: 7
AAS14652 standard; cDNA: 2694 BP.

XX AAS14652;

XX .18-DEC-2001 (first entry)

DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.

XX Human, ss; voltage-gated potassium channel; hKCNQ5-1; nontropic;

KM cerebroprotective; neurotropic; analgesic; vision disorder;

KM central nervous system disorder; epilepsy; migraine; hearing disorder;

KM psychotic disorder; seizure; learning disorder; memory disorder;

KM stroke; pain; gene therapy; splice variant.

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XX Homo sapiens.
OS Key Location/Qualifiers
XX Key 1..2994
XX CDS /tag=a
XX FT /product="hKCNQ5-1"
XX
XX MO20010759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US09328.
XX
XX 21-MAR-2000; 2000US-190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI: 2001-611467/70.
XX
XX P-PSDB; AAU09020.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ alpha
XX subunits
XX
XX Claim 5; Page 62-63; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
XX alpha-subunit of a KCNQ potassium channel, with a subsequence having
XX 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
XX sequence and forms a KCNQ potassium channel having the characteristic of
XX voltage-gating with at least an additional KCNQ alpha-subunit. Also
XX included in the scope of the invention are the nucleic acids encoding
XX hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
XX expression vectors encoding them, antibodies against them, the use of
XX 3-dimensional computer modelling to identify molecules that bind to a
XX KCNQ containing potassium channel and modulate ion flux through the
XX channel. The KCNQ polypeptide is useful for identifying a compound that
XX increases or decreases ion flux through a potassium channel expressed in
XX an eukaryotic host cell or cell membrane. The compound (and the
XX KCNQ nucleic acid when used in gene therapy) is useful as
XX a pharmaceutical agent for treating diseases involving abnormal ion flux,
XX such as disorders of the central nervous system, such as epilepsy,
XX migraines, hearing and vision problems, psychotic disorders, seizures,
XX learning and memory disorders, stroke and pain. The antibodies are
XX useful for detecting a KCNQ5 polypeptide in a human tissue and the
XX use of a nucleotide sequence of KCNQ5 to search computer databases to
XX find variants of the sequence which are associated with disease states,
XX is useful for screening mutations of KCNQ5. The present sequence is
XX a splice variant of hKCNQ5 encoding hKCNQ5-1.
XX
XX Sequence 2694 BP: 714 A; 671 C; 669 G; 640 T; 0 other;

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Query Match 52.3%; Score 1450; DB 22; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY 1221 TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCGATGCTAGCCCAAGGGCCAGATATTAA 1280
DB 1143 TCAGAAAGCTAAGTTTAAAGAGCGAGTGGCGATGCTAGCCCAAGGGCCAGATATTAA 1202
OY 1281 GAGCCGCAAGCCTCTAGTACAGAGAGGTCCCAAGCAGCGATCAAGCCGAGG 1340
DB 1203 GAGCCGCAAGCCTCTAGTACAGAGAGGTCCCAAGCAGCGATCAAGCCGAGG 1262
OY 1341 CAGTCCCAACAAAGTCAAGAGAGTGGAGCTTCAAGCAGCAGCAGCCGCTCCG 1400
DB 1263 CAGTCCCAACAAAGTCAAGAGAGTGGAGCTTCAAGCAGCAGCAGCCGCTCCG 1322
OY 1401 GCTGGCCTCAAAAAGTTCTCAGCCAAAACAGATGATGCTGACACAGCCCTTGGCAG 1460

```

Db	1223	GCTGGCCCTCAAAAGTTCTCAGCCAAACCAACGATGATGATGCTGACACAGCCCTTGGAC	1382
Qy	1461	TGATGATGTATATGATGAAAAAGATGCCAGTGTGATGTATCACTGGAAACCTCACC	1520
Db	1383	TGATGATGTATATGATGAAAAAGATGCCAGTGTGATGTATCACTGGAAACCTCACC	1442
Qy	1521	ACCACTTAAACTGTGATCTGAGCTCTACGAATTTAATAATTCATGTGGAAAAAGAA	1580
Db	1443	ACCACTTAAACTGTGATCTGAGCTCTACGAATTTAATAATTCATGTGGAAAAAGAA	1502
Qy	1581	GTTTAAAGAAACATTACGTCCATATATATGTAAAGATGTCAATTGAACAATATTCGTGG	1640
Db	1503	GTTTAAAGAAAGTTTACGTCCATATATGTAAAGATGTCAATTGAACAATATTCGTGG	1562
Qy	1641	TCATCTGGACATGTTGTGTAGAAATTAACACCTTCAAAACGCTGTGATCAAAATCTTGG	1700
Db	1563	TCATCTGGACATGTTGTGTAGAAATTAACACCTTCAAAACGCTGTGATCAAAATCTTGG	1622
Qy	1701	AAAAAGGCAAAATCACATCAGATTAAGAAAGACCCGAGAGAAAATAACAGCAAAATGAGAC	1760
Db	1623	AAAAAGGCAAAATCACATCAGATTAAGAAAGACCCGAGAGAAAATAACAGCAAAATGAGAC	1682
Qy	1761	CACAGACGATCTTCAGTATGCTCGGTGCGGTGTAAAGTTGAAAAACAGGTCACTCCAT	1820
Db	1683	CACAGACGATCTTCAGTATGCTCGGTGCGGTGTAAAGTTGAAAAACAGGTCACTCCAT	1742
Qy	1821	AGAAATCAAGCTGGAGCTGCCCTACTAGACATATATCAACAGGCTCTCGGAAAGGCTCTAC	1880
Db	1743	AGAAATCAAGCTGGAGCTGCCCTACTAGACATATATCAACAGGCTCTCGGAAAGGCTCTAC	1802
Qy	1881	CTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCAACCTTTTGAAATGAAACAGACATCTGA	1940
Db	1803	CTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCAACCTTTTGAAATGAAACAGACATCTGA	1862
Qy	1941	CTATCAAAGCCCTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGGGCTGCTT	2000
Db	1863	CTATCAAAGCCCTGTGATAGCAAAAGATCTTGGGTTCCGACAAAACAGGGCTGCTT	1922
Qy	2001	ATCCAAATCAACTAGTCCCAACATCTCGAGAGAGCCCTGCAGTTCAATCTTGACGCCAAATGA	2060
Db	1923	ATCCAAATCAACTAGTCCCAACATCTCGAGAGAGCCCTGCAGTTCAATCTTGACGCCAAATGA	1982
Qy	2061	GTTTCAGTGCCCAAGCTTTCTACGGGCTTAAGCCCTACTATGCACGTCAAGCAACACAGT	2120
Db	1983	GTTTCAGTGCCCAAGCTTTCTACGGGCTTAAGCCCTACTATGCACGTCAAGCAACACAGT	2042
Qy	2121	GCCAAATTAATGCAAAAGCATGTGCTCAGACGTGGCAGCCACCAACACCATTTGCAAAACAAAT	2180
Db	2043	GCCAAATTAATGCAAAAGCATGTGCTCAGACGTGGCAGCCACCAACACCATTTGCAAAACAAAT	2102
Qy	2181	AAATAGGCGCACCCAGCCAGAGCCCAACAACTTTACAGATCCACCTCTCTCCAGC	2240
Db	2103	AAATAGGCGCACCCAGCCAGAGCCCAACAACTTTACAGATCCACCTCTCTCCAGC	2162
Qy	2241	CATCAACCAATCTGCCCGAGGCCAGAAACATCTGACCTTAACCCCTGACGGCTTACAGGAAG	2300
Db	2163	CATCAACCAATCTGCCCGAGGCCAGAAACATCTGACCTTAACCCCTGACGGCTTACAGGAAG	2222
Qy	2301	CATTCTGACGCTCAACCACTGCTGTTGGCTCTCCAAAGAAATGTTCAAGGTTGCACAGTC	2360
Db	2223	CATTCTGACGCTCAACCACTGCTGTTGGCTCTCCAAAGAAATGTTCAAGGTTGCACAGTC	2282
Qy	2361	AAATCTCACCAAGACCGTCTTATAGAGAAAAAGCTTTGACATGTGGAGAGAAACATCTGTT	2420
Db	2283	AAATCTCACCAAGACCGTCTTATAGAGAAAAAGCTTTGACATGTGGAGAGAAACATCTGTT	2342
Qy	2421	GTTCTGTGCTCCATAGGTGCGCAAGACATGGGCAATCTTTGTCTGTGCAAAACCTGAT	2480
Db	2343	GTTCTGTGCTCCATAGGTGCGCAAGACATGGGCAATCTTTGTCTGTGCAAAACCTGAT	2402
Qy	2481	CAGTTCGACCGAGAACTGAATATACACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAG	2540

Db	2403	CAGGTCCAGCCAGGACGCTGAATTATACAACTTTCAGGGGATGATCAAGTGGACTCCAGAGG	2462
Qy	2541	CAGCCCAAGATTTTATACCCCAATGGAGGGAATCCAAATTTGTTTATATCGATGGAAGGT	2600
Db	2463	CAGCCAAATTTTATACCCCAATGGAGGGAATCCAAATTTGTTTATATCGATGGAAGAGGT	2522
Qy	2601	GGGTCCCAAGAGACAGACAGACACTTTTGATGCCGACCGCAGCTGCGCAGGGAAGC	2660
Db	2523	GGGTCCCAAGAGACAGACAGACACTTTTGATGCCGACCGCAGCTGCGCAGGGAAGC	2582
Qy	2661	TGCGTTTGATCAGACTCTCTTAAGGACTTGGAAAGTCACAGATCATCTCAGACATTTGTAA	2720
Db	2583	TGCGTTTGATCAGACTCTCTTAAGGACTTGGAAAGTCACAGATCATCTCAGAGCATTTGTAA	2642
Qy	2721	GGCAGAGAAAAGTACAGATGGCCCTTGGCTTCATGTCAAACTGAAATAAA	2772
Db	2643	GGCAGAGAAAAGTACAGATGGCCCTCAGCTTGCCCTCATGTCAAACTGAAATAAA	2694

RESULT 8

AAD27192
ID AAD27192 standard; cDNA; 2694 BP.

AC AAD27192;

DT 09-APR-2002 (first entry)

DE Human potassium channel polypeptide, KCNQ5 cDNA

KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
stroke; stroke; stroke; stroke; stroke; stroke; stroke; stroke; stroke; stroke;

ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression; bipolar disorder; sleep disorder; eating disorder; kw

addiction; myokymia; Alzheimer's disease; age-associated memory loss

neurophysiological disorder; neuropsychological disorder; aslmlia;

KW synaptic transmission; electrical excitability; ss.

OS Homo sapiens

FH	Key	Location/qualifiers
EM	CDC	1 3694

```

/*tag= 3
/product= "Human KCNO5 protein"

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XX
XX
F0300103E36-21

XX
XX
05-DEC-2001XX
DE 24-MAY-2001 : 2001WO-IIS17314XX
XX
26-MAY-2000. 2000HS-207389P-XX
XX
PA (BRTM) BRISTOL-MYERS SQUIBB

XX
PI Dworetzky ST, Ramanathan CS, Trojnecki JT, Boissard CG;

Pl GIDKOII VK;
XY

DR WPL; 2002-122069/16.
DR P-PSDB; AAF16599.

XX
PT Novel potassium channel polypeptide, KCNO5 and polynucleotide encoding

it, for diagnosing, creating and identifying modifiable risk factors for treating neurological, neurophysiological and neuropsychological

PT
XX
diseases

PS CLAIM 3, FIG 1, 120PP, 009-1-00

as KCN05 and nucleic acid molecules encoding such polypeptides. KCN

polypeptides are essential for maintaining the biological activity. The compounds identified and KCNQ5 polynucleotides

CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amniotic lateral sclerosis
 CC (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety
 CC disorders, depression, bipolar disorders, sleep disorders, eating
 CC disorders, addiction, myokymia, Alzheimer's disease, age-associated
 CC memory loss, learning deficiencies, cognitive disorders and motor
 CC neuron diseases. The nucleic acid molecules of the invention are
 CC further useful for treating neuropsychological, neuropsychological
 CC disorders, asthma, neuron cell death and brain tumours. They are also
 CC used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate
 CC synaptic transmission and electrical excitability in the brain and are
 CC useful for generating antibodies. They are also useful to affinity
 CC purify biological effectors from biological materials e.g. disease
 CC tissues or cells. The present sequence is human KCNQ5 cDNA.

XX Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 other;

Query Match 52.3%; Score 1450; DB 24; Length 2694;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1221 TCAGAACCTAGTTTAAAGAGCAGTGGCGATGGCTACCCAGGGGCGAGATATTA 1280
 1143 TCAGAACCTAGTTTAAAGAGCAGTGGCGATGGCTACCCAGGGGCGAGATATTA 1202
 1281 GAGCCGCAAGCCTCAGTAGGTGACAGAGGTCCCAACGACGACATCAGCCGAGGG 1340
 1203 GAGCCGCAAGCCTCAGTAGGTGACAGAGGTCCCAACGACGACATCAGCCGAGGG 1262
 1341 CAGTCCCAACCAAGTGGAGAGGTGAGTTCACACGACGACCCGCTCCGCGCTC 1400
 1263 CAGTCCCAACCAAGTGGAGAGGTGAGTTCACACGACGACCCGCTCCGCGCTC 1322
 1401 GCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGAC 1460
 1323 GCTGCGCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGAC 1382
 1461 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 1383 TGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
 1521 ACCACTTAAAGTGTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1580
 1443 ACCACTTAAAGTGTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1502
 1581 GTTTAAGGAAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGAT 1640
 1503 GTTTAAGGAAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGAT 1562
 1641 TCATCTGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1700
 1563 TCATCTGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
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 1623 AAAAGGGCAATTCATCAGATTAAGAGAGCCGAGAGAAATTAACAGAGAAATGAGAG 1682
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 1821 AGAATCCAAAGTGGAGTGGCTTACATCAGATCAGATCAGATCAGATCAGATCAGATCAG 1880
 1743 AGAATCCAAAGTGGAGTGGCTTACATCAGATCAGATCAGATCAGATCAGATCAGATCAG 1802
 1881 CTCACCCCTCGCTTGGCTTCAATTCAGATCCACCTTTGAAATGTAACAGACATCTGA 1940
 1803 CTCACCCCTCGCTTGGCTTCAATTCAGATCCACCTTTGAAATGTAACAGACATCTGA 1862
 1941 CTATCAAAAGCCCTGGATGAGAGAAAGATCTTGGGCTCGGACAAACAGTGGCTGCTT 2000
 1863 CTATCAAAAGCCCTGGATGAGAGAAAGATCTTGGGCTCGGACAAACAGTGGCTGCTT 1922

QY 2001 ATCCAGATCACTAGTGCACCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAAATGA 2060
 DB 1923 ATCCAGATCACTAGTGCACCAACATCTCGAGAGGCTCGAGTTCATTTGACGCCAAATGA 1982
 QY 2061 GTTCACTGCCCCAAGCTTCTACGGGCTTACGCCCTACTGACAGATCAAGCAACAGGT 2120
 DB 1983 GTTCACTGCCCCAAGCTTCTACGGGCTTACGCCCTACTGACAGATCAAGCAACAGGT 2042
 QY 2121 GCCAATTAAGTCAAGAGATGGCTCAGCAGTGGCGACGCCCAACACCATTTGCAACCAAT 2180
 DB 2043 GCCAATTAAGTCAAGAGATGGCTCAGCAGTGGCGACGCCCAACACCATTTGCAACCAAT 2102
 QY 2181 AATATGAGCAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2240
 DB 2103 AATATGAGCAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2162
 QY 2241 CATCAAGCATCTGCCCCAGGCGCAAGCATCTGCAACCCCTACAGGCTTACAGGAAG 2300
 DB 2163 CATCAAGCATCTGCCCCAGGCGCAAGCATCTGCAACCCCTACAGGCTTACAGGAAG 2222
 QY 2301 CATTTCTGACGTACACCACTGCTTGTGCTCCCAAGGAATGTTAGTTGACAGATC 2360
 DB 2223 CATTTCTGACGTACACCACTGCTTGTGCTCCCAAGGAATGTTAGTTGACAGATC 2282
 QY 2361 AATCTCAACCAAGAGACCGTTCTATGAGGAATGTTGACATGAGGAGAGAACTCTGT 2420
 DB 2283 AATCTCAACCAAGAGACCGTTCTATGAGGAATGTTGACATGAGGAGAGAACTCTGT 2342
 QY 2421 GTCTGTCTGTCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2480
 DB 2343 GTCTGTCTGTCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2402
 QY 2481 CAGGTCCAGCCGAGCACTAATATACACTTTGAGGAGTGAAGTCAAGTGGCTCCAGAG 2540
 DB 2403 CAGGTCCAGCCGAGCACTAATATACACTTTGAGGAGTGAAGTCAAGTGGCTCCAGAG 2462
 QY 2541 CAGCCAAAGATTTTACCCCAAAATGAGAGCAATCCAAATGTTATATCTGATGAAGAGT 2600
 DB 2463 CAGCCAAAGATTTTACCCCAAAATGAGAGCAATCCAAATGTTATATCTGATGAAGAGT 2522
 QY 2601 GGGTCCGAGAGAGACAGACAGACACTTTGATGCGCAGCCAGCCTGCGAGGAGG 2660
 DB 2523 GGGTCCGAGAGAGACAGACAGACACTTTGATGCGCAGCCAGCCTGCGAGGAGG 2582
 QY 2661 TGCTTTGATCAGACCTCTCTAAGAGCTGAGAGTACAGATCATCTCAAGCAATTTGTA 2720
 DB 2583 TGCTTTGATCAGACCTCTCTAAGAGCTGAGAGTACAGATCATCTCAAGCAATTTGTA 2642
 QY 2721 GGCAGAGAAAGTACAGATGCGCTGAGCTTGCCTCATGTCAAACTGAATTA 2772
 DB 2643 GGCAGAGAAAGTACAGATGCGCTGAGCTTGCCTCATGTCAAACTGAATTA 2694

RESULT 9

AS14651
 ID AS14651 standard; cDNA; 3071 BP.

AS14651:

18-DEC-2001 (first entry)

XX Human cDNA for voltage gated potassium channel hKvN5.

XX Human; ss; voltage-gated potassium channel; hKvN5; nontropic;

XX cerebroprotective; neurotropic; analgesic; vision disorder;

XX central nervous system disorder; epilepsy; migraine; hearing disorder;

XX psychotic disorder; seizure; learning disorder; memory disorder;

XX stroke; pain; gene therapy.

XX Homo sapiens.

XX OS

XX PN

XX WO200170759-A1.

Db		2592	TGCCCTTTCATGACACTCCTTAAGCACTCGAAGCTACGCATCTCTGAGCATTTGTAA	2651
Oy		2721	GCCAGAGAAAATTACAGATGCCCTCAGCTTGCCCTCATGTCAAACGATAATTA	2772
Db		2652	GCCAGGAGAAATACAGATGCCCCCTCAGCTTGCCCTCATGTCAAACGATAATTA	2703
 RESULT 10 AAC64370 ID AAC64370 standard; DNA; 125910 BP.				
Xx		AAC64370;		
Xx		07-FEB-2001 (first entry)		
Dt				
Xx				
De		Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.		
Xx				
Kw		Human: KCNQ5: KCN6q; chromosome 6; voltage-gated potassium channel;		
Kw		Stargardt-like macular dystrophy; cone-rod macular dystrophy;		
Kw		Salla disease; ophthalmological; auditory; central nervous system;		
Kw		cardioactive; anticonvulsant; gastrointestinal; muscular atrophy;		
Kw		age-related macular degeneration; macular degeneration; deafness;		
Kw		epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;		
Kw		gastrointestinal disorder; ds.		
Os		Homo sapiens.		
Pn		W0200061606-A1.		
Xx				
Pd		19-OCT-2000.		
Pf		10-APR-2000; 2000WO-US09587.		
Pr		14-APR-1999; 99US-0129274.		
Pa		(MERI) MERCK & CO INC.		
Pi		Petrukhin K, Caskey CT, Li W, Metzker ML.		
Dr		WPI: 2000-647417/62.		
Xx		P-PADB; AAB24241.		
XX		Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying		
PT		inhibitors and activators which can treat e.g. Stargardt-like macular		
PT		dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -		
XX		Claim 3; Fig 1; 9ppp; English.		
Ps		The present sequence represents the human KCNQ5 (also called KCN6q) gene,		
Xx		which encodes a voltage-gated potassium channel protein. Human KCNQ5		
Cc		has ophthalmological, auditory, central nervous system (CNS),		
Cc		cardioactive, anticonvulsant, gastrointestinal and muscular active		
Cc		activities. Sequences and methods from the present invention are useful		
Cc		for identifying activators or inhibitors of KCNQ5 protein. These		
Cc		activators and inhibitors are useful for treating Stargardt-like macular		
Cc		dystrophy, cone-rod dystrophy, Salla disease, age-related macular		
Cc		degeneration, other forms of macular degeneration, deafness, epilepsy,		
Cc		and different forms of neuropsychiatric, heart, gastrointestinal, and		
Cc		muscle disorders. Stargardt-like macular dystrophy and cone-rod		
Cc		dystrophies are located at chromosome 6q.		
SQ		Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 72 other:		
Query Match		34.8%; Score 965; DB 21; Length 125910;		
Best Local Similarity		100.0%; Pred. No: 0;		
Matches		965; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY		1808 AGTGAACATCCATAGATCCAAGCTGGACTGCTACTATAGACATCTATCAACAGGTCCTTC		1867
Db		123624 AGGTACATCATAGAAATCAACAGCTGGACTGCTACTATAGACATCTATCAACAGGTCCTTC		123683
OY		1868 GGAAAGGCTCTGCCTCACCTCGCTTGGGCTTCATTCACAATCCACACTTTTGAATGTG		1927

Db	123684	GGAAAGCTCGCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCACCTTTTGAATGTG	123743
OY	1928	AACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCGGGTCCGACAAA	1987
Db	123744	AACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCGGGTCCGACAAA	123803
OY	1988	ACATGGCTCTTATCCAGATCAACTAGTGTGCACATCTCGAGAGCCCTGCAGTTCATTC	2047
Db	123804	ACATGGCTCTTATCCAGATCAACTAGTGTGCACATCTCGAGAGCCCTGCAGTTCATTC	123863
OY	2048	TGACGCCAAATGAGTTCACTGTCGCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTC	2107
Db	123864	TGACGCCAAATGAGTTCACTGTCGCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTC	123923
OY	2108	AAGCAACACAGGTGCCAATTATGTCAAAAGCGATGGCTCAGCAGTGGACCCACCAACCA	2167
Db	123924	AAGCAACACAGGTGCCAATTATGTCAAAAGCGATGGCTCAGCAGTGGACCCACCAACCA	123983
OY	2168	TTGCAAAACCAATTAATTAAGGGCACCCCAAGCAGAGGCCCAACAACCTTTACAGATCCAC	2227
Db	123984	TTGCAAAACCAATTAATTAAGGGCACCCCAAGCAGAGGCCCAACAACCTTTACAGATCCAC	124043
OY	2228	CTCCCTCTCCACGACATCAAGACATCTGCCAGGCCAGAACTCTCACCCCTAACCTCGAG	2287
Db	124044	CTCCCTCTCCACGACATCAAGACATCTGCCAGGCCAGAACTCTCACCCCTAACCTCGAG	124103
OY	2288	GCTTCACAGAAAGCAATTTCTGACGTGACCCAGCCAGCGCTGTTCCTCCACAGAAAAATGTC	2347
Db	124104	GCTTCACAGAAAGCAATTTCTGACGTGACCCAGCCAGCGCTGTTCCTCCACAGAAAAATGTC	124163
OY	2348	AGGTTGCACAGTCAAAATCTCACCAAGAGCCGTTCTATGAGAAAAAGCTTTGACATGGGAG	2407
Db	124164	AGGTTGCACAGTCAAAATCTCACCAAGAGCCGTTCTATGAGAAAAAGCTTTGACATGGGAG	124223
OY	2408	GAGAAACCTGTTGCTGTGCTGTGCCATGTGGTGGCCGAAGACTTGGCCAAATCTTTGCTGTG	2467
Db	124224	GAGAAACCTGTTGCTGTGCTGTGCCATGTGGTGGCCGAAGACTTGGCCAAATCTTTGCTGTG	124283
OY	2468	TGCAAAACCTGATCAGGTGACGACCGAGGAAGTGAATATACAACTTTCAGGAGTAGTCAAA	2527
Db	124284	TGCAAAACCTGATCAGGTGACGACCGAGGAAGTGAATATACAACTTTCAGGAGTAGTCAAA	124343
OY	2528	GTGGCTCCAGGSGAGCCCAAGTTTTATCCCAATGAGAGGAATCCAAATGTTTATAA	2587
Db	124344	GTGGCTCCAGGSGAGCCCAAGTTTTATCCCAATGAGAGGAATCCAAATGTTTATAA	124403
OY	2588	CTGATGAAAGAGTGGTCCCAAGAGACAGACAGACACTTTGATGGCCGACCGGAGC	2647
Db	124404	CTGATGAAAGAGTGGTCCCAAGAGACAGACAGACACTTTGATGGCCGACCGGAGC	124463
OY	2648	CTGCCAGGGAGAGCTGCTTTGATCAGTCACTCTCTAAGGACTGGAAAGTCAAGATCATCTC	2707
Db	124464	CTGCCAGGGAGAGCTGCTTTGATCAGTCACTCTCTAAGGACTGGAAAGTCAAGATCATCTC	124523
OY	2708	AGAGCAATTTTAAGGCGAGGAAGTAAGATAGATAGCCCTCAGCTTGCTCATGTCAAACTGA	2767
Db	124524	AGAGCAATTTTAAGGCGAGGAAGTAAGATAGATAGCCCTCAGCTTGCTCATGTCAAACTGA	124583
OY	2768	AATAA 2772	
Db	124584	AATAA 124588	
RESULT 11			
ABN24166			
ID	ABN24166	standard; cDNA; 414 BP.	
XX	ABN24166;		
AC			
XX	24-JUN-2002	(first entry)	
DT			
XX	Human ORFX polynucleotide sequence SEQ ID NO:16809.		

XX Claim 7, Fig 10A-D; 64pp; English.

PS The present sequence encodes murine KCNQ2/Kv1.1. KCNQ proteins are
 CC nervous system-specific potassium channels. In neurons, potassium
 CC channels regulate neuronal excitability, action potential shape
 CC and firing pattern, and neurotransmitter release. KCNQ modulators
 CC may be used to treat disorders such as ataxia, myokymia, seizures,
 CC Alzheimer's disease, Parkinson's disease, age-associated memory
 CC loss, learning deficiencies, motor neuron diseases, epilepsy, and
 CC stroke.

XX Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 other;

Query Match 1.0%; Score 29; DB 20; Length 2169;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

364 CCCCCGGGCTGGGCTTCATCTACACGC 392

262 CCCCCGGGCTGGGCTTCATCTACACGC 290

Result 15

AAC64379/c

AAC64379 standard; DNA: 28 BP.

AAC64379;

07-FEB-2001 (first entry)

Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:16.

XX Human: KCNQ5; KCNQ6; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; PCR primer; ss.

XX Homo sapiens.

XX WO200061606-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US09587.

XX 14-APR-1999; 99US-0129274.

XX (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCNQ6)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and

CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q. The present sequence represents
 CC a PCR primer for human KCNQ5, which is used in an example from the
 CC present invention.

XX Sequence 28 BP; 6 A; 4 C; 9 G; 9 T; 0 other;

Query Match 1.0%; Score 28; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

439 TCTACCATCCTGAGCAGACAAATTTGG 466

28 TCTACCATCCTGAGCAGACAAATTTGG 1

Result 16

AAC64381

AAC64381 standard; DNA: 26 BP.

AAC64381;

07-FEB-2001 (first entry)

Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:18.

XX Human: KCNQ5; KCNQ6; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; PCR primer; ss.

XX Homo sapiens.

XX WO200061606-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US09587.

XX 14-APR-1999; 99US-0129274.

XX (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCNQ6)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q. The present sequence represents
 CC a PCR primer for human KCNQ5, which is used in an example from the
 CC present invention.

XX Sequence 26 BP; 11 A; 0 C; 8 G; 7 T; 0 other;

Query Match 0.9%; Score 26; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1462 GATGATGATATGATGAAAAAGGATG 1487
 |||||
 1 GATGATGATATGATGAAAAAGGATG 26

RESULT 17
 AAC64383/c
 ID AAC64383 standard; DNA; 26 BP.

XX AAC64383;

XX 07-FEB-2001 (first entry)

XX Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:20.

XX Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
 Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 Salla disease; ophthalmological; auditory; central nervous system;
 cardioactive; anticonvulsant; gastrointestinal: muscular active;
 age-related macular degeneration; macular degeneration; deafness;
 epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 gastrointestinal disorder; PCR primer; ss.

XX Homo sapiens.

XX WO200061606-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000MO-US09587.

XX 14-APR-1999; 9905-0129274.

XX (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI: 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy .
 PS Example 1; Page 33; 99pp; English.

XX The present invention describes the human KCNQ5 (also called KCN6q)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardioactive, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q. The present sequence represents
 CC a PCR primer for human KCNQ5, which is used in an example from the
 CC present invention.

XX Sequence 26 BP; 4 A; 4 C; 11 G; 7 T; 0 other;

XX Query Match 0.9%; Score 26; DB 21; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.057;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1502 CAGTGAAGACCTCCACCCACACCTT 1527

XX 26 CAGTGAAGACCTCCACCCACACCTT 1

RESULT 18
 AAS14655/c
 ID AAS14655 standard; cDNA; 26 BP.

XX AAS14655;

XX 18-DEC-2001 (first entry)

XX Human voltage-gated potassium channel hKCNQ5 PCR primer #2.

XX Human; ss; voltage-gated potassium channel; KCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychologic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; PCR primer.

XX Homo sapiens.

XX WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001MO-US09328.

XX 21-MAR-2000; 2000US-190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI: 2001-611467/70.

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits .
 XX Claim 6; Page 65; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an
 CC alpha subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychologic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a PCR primer used to amplify a 1.15kb cDNA clone for hKCNQ5.

XX Sequence 26 BP; 5 A; 7 C; 6 G; 8 T; 0 other;

XX Query Match 0.9%; Score 26; DB 22; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.057;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1809 GGTACAGTCATAGATCCAGCTGG 1834

XX |||||

DB 26 GGTACAGTCCATAGATCCAGCTGG 1

RESULT 19

AS14656

ID AS14656 standard; cDNA: 26 BP.

AC AS14656;

XX

DT 18-DEC-2001 (first entry)

DE Human voltage-gated potassium channel hKCNQ5 PCR primer #3.

XX

XX Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder;

KW stroke; pain; gene therapy; PCR primer.

OS Homo sapiens.

XX

PN WO200170759-A1.

XX

PD 27-SEP-2001.

XX

PF 20-MAR-2001; 2001WO-US09328.

XX

PR 21-MAR-2000; 2000US-190954P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ;

XX

DR WPI: 2001-611467/70.

XX

PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

PT identifying a compound modulating ion flux in eukaryotic cell or cell

PT membrane expressing the protein, comprises KCNQ alpha

PT subunits

PS

XX Claim 6; Page 65; 78pp; English.

XX

PS The invention relates to an isolated polypeptide comprising an

CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid

CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha subunit. Also

CC included in the scope of the invention are the nucleic acids encoding

CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),

CC expression vectors encoding them, antibodies against them, the use of

CC 3-dimensional computer modelling to identify molecules that bind to a

CC KCNQ containing potassium channel and modulate ion flux through the

CC channel. The KCNQ polypeptide is useful for identifying a compound that

CC increases or decreases ion flux through a potassium channel expressed in

CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy) is useful as

CC a pharmaceutical agent for treating diseases involving abnormal ion flux,

CC such as disorders of the central nervous system, such as epilepsy,

CC migraines, hearing and vision problems, psychotic disorders, seizures,

CC learning and memory disorders, stroke and pain. The antibodies are

CC useful for detecting a KCNQ5 polypeptide in a human tissue and the

CC use of a nucleotide sequence of KCNQ5 to search computer databases to

CC find variants of the sequence which are associated with disease states,

CC is useful for screening mutations of KCNQ5. The present sequence is

CC a PCR primer used to amplify a 1.2kb cDNA clone containing the 3'

CC region of hKCNQ5.

XX

XX Sequence 26 BP; 13 A; 4 C; 8 G; 1 T; 0 other;

XX

Query Match 0.9%; Score 26; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1725 GAAGAGCCGAGAGAAATACGACG 1750

DB 1 GAAGAGCCGAGAGAAATACGACG 26

RESULT 20

AS14657

ID AS14657 standard; cDNA: 26 BP.

AC AS14657;

XX

DT 18-DEC-2001 (first entry)

DE Human voltage-gated potassium channel hKCNQ5 PCR primer #4.

XX

XX Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder;

KW stroke; pain; gene therapy; PCR primer.

OS Homo sapiens.

XX

PN WO200170759-A1.

XX

PD 27-SEP-2001.

XX

PF 20-MAR-2001; 2001WO-US09328.

XX

PR 21-MAR-2000; 2000US-190954P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ;

XX

DR WPI: 2001-611467/70.

XX

PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

PT identifying a compound modulating ion flux in eukaryotic cell or cell

PT membrane expressing the protein, comprises KCNQ alpha

PT subunits

PS

XX Claim 6; Page 65; 78pp; English.

XX

PS The invention relates to an isolated polypeptide comprising an

CC alpha-subunit of a KCNQ potassium channel, with a subsequence having

CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid

CC sequence and forms a KCNQ potassium channel having the characteristic of

CC voltage-gating with at least an additional KCNQ alpha subunit. Also

CC included in the scope of the invention are the nucleic acids encoding

CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),

CC expression vectors encoding them, antibodies against them, the use of

CC 3-dimensional computer modelling to identify molecules that bind to a

CC KCNQ containing potassium channel and modulate ion flux through the

CC channel. The KCNQ polypeptide is useful for identifying a compound that

CC increases or decreases ion flux through a potassium channel expressed in

CC an eukaryotic host cell or cell membrane. The compound (and the

CC KCNQ nucleic acid when used in gene therapy) is useful as

CC a pharmaceutical agent for treating diseases involving abnormal ion flux,

CC such as disorders of the central nervous system, such as epilepsy,

CC migraines, hearing and vision problems, psychotic disorders, seizures,

CC learning and memory disorders, stroke and pain. The antibodies are

CC useful for detecting a KCNQ5 polypeptide in a human tissue and the

CC use of a nucleotide sequence of KCNQ5 to search computer databases to

CC find variants of the sequence which are associated with disease states,

CC is useful for screening mutations of KCNQ5. The present sequence is

CC a PCR primer used to amplify a 1.2kb cDNA clone containing the 3'

CC region of hKCNQ5.

XX

XX Sequence 26 BP; 6 A; 6 C; 7 G; 7 T; 0 other;

XX

Query Match 0.9%; Score 26; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1949 GCCCTGTGATAGCAAGATCTTGC 1974
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 1 GCCCTGTGATAGCAAGATCTTGC 26

RESULT 21
AAT85964
ID AAT85964 standard; cDNA: 1182 BP.
XX

AC AAT85964;

DT 09-JAN-1998 (first entry)

DE Human K+ channel gene coding sequence.

KW Human; neuroblastoma; K+ channel; glioma; probe; diagnosis; detection;
XX tumour; ds.
XX

OS Homo sapiens.

PN JP09191882-A.

PD 29-JUL-1997.

PF 16-JAN-1996; 96JP-0004726.

PR 16-JAN-1996; 96JP-0004726.

XX (NISR) JAPAN TOBACCO INC.

XX WPI: 1997-429182/40.

DR P-PSDB; AAW14282.

XX DNA encoding new human K+ channel protein - useful for detecting
PT glioma(s) and tumours

PS Claim 3; Page 10-12; 14pp; Japanese.

XX This is the nucleotide sequence encoding a novel human K+ channel
CC protein which is expressed on human glioma cells. The gene was isolated
CC from a 3' directed cDNA library prepared from human neuroblastoma cell
CC line CHP134. The screen isolated a clone designated GS008740 whose
CC insert contained the coding sequence (presented here) and the 5' and 3'
CC sequences of the gene (AAT85965-6 respectively). Expression of the gene
CC was detected in neuroblastoma cell lines. Oligonucleotides derived from
CC the sequence of the K+ channel gene can be used as probes for diagnosing
CC human gliomas, and in the detection of new tumours.

XX Sequence 1182 BP; 201 A; 372 C; 364 G; 245 T; 0 other;

Query Match 0.9%; Score 26; DB 18; Length 1182;

Best Local Similarity 100.0%; Pred. No. 0.058; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

DB 265 CGCGGCTGGCGCTTCATCTACCAAGC 290

RESULT 22

ABK64418
ID ABK64418 standard; DNA: 1425 BP.

XX ABK64418;

DT 18-JUN-2002 (first entry)

DE Human benign prostatic hyperplasia gene #313.

XX Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
KW
XX

OS Homo sapiens.

PN WO200212440-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US24708.

XX 07-AUG-2000; 2000US-223323P.

PR 05-JUN-2001; 2001US-0873319.

XX (GENE-) GENE LOGIC INC.
XX (NISR) JAPAN TOBACCO INC.

PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;

DR WPI: 2002-257476/30.

XX Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -

PS Disclosure; Page 188; 44pp; English.

XX The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.

XX Sequence 1425 BP; 231 A; 462 C; 439 G; 293 T; 0 other;

Query Match 0.9%; Score 26; DB 24; Length 1425;

Best Local Similarity 100.0%; Pred. No. 0.058; Mismatches 0; Indels 0; Gaps 0;

OY 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

DB 442 CGCGGCTGGCGCTTCATCTACCAAGC 467

RESULT 23

AAK81548
ID AAK81548 standard; DNA: 2565 BP.

XX AAK81548;

DT 25-AUG-1999 (first entry)

DE Human brain-derived potassium channel DNA structural DNA.

XX Human; brain-derived potassium channel; neurophysiology;

XX cognitive disorder; behavioural disorder; psychiatric disorder;
KW neurodegenerative disorder; developmental disorder; mental retardation;
KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
XX

KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 OS Homo sapiens.
 PN MO9931232-A1.
 XX
 XX
 PD 24-JUN-1999.
 XX
 XX 11-DEC-1998; 98WO-GB03720.
 XX
 XX 13-DEC-1997; 97GB-0026339.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 XX Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 PI WPI; 1999-395178/33.
 XX
 XX New isolated potassium channel polypeptide
 PT Claim 2; Fig 2; 151pp; English.
 PS
 XX
 XX The present sequence represents brain-derived potassium channel DNA.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 SO Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other;
 QY
 QY Query Match 0.9%; Score 26; DB 20; Length 2565;
 Db Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
 265 CGCGGCTGGCGCTTCATCTACCAAGC 290
 RESULT 24
 AAX81547
 ID AAX81547 standard; cDNA; 3029 BP.
 XX
 XX AAX81547;
 AC
 XX 25-AUG-1999 (first entry)
 DT
 XX Human brain-derived potassium channel cDNA.
 DE Human brain-derived potassium channel; neurophysiology;
 XX
 XX Human; brain-derived potassium channel; neurophysiology;

KW cognitive disorder; behavioural disorder; psychiatric disorder;
 KW neurodegenerative disorder; developmental disorder; mental retardation;
 KW asthma; migraine; epilepsy; stroke; brain tumour; Huntington's disease;
 KW Lou Gehrig's; neurodegeneration; multiple sclerosis; psychosis;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW cerebellar degeneration; urinary incontinence; diabetes; asthma;
 KW premature labour; hypertension; cardiac ischemia; arrhythmia;
 KW autoimmune disease; cancer; graft rejection; inflammation; allergy;
 KW proliferative disorder; anaemia; autoimmune disease;
 KW type-1 diabetes mellitus myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; rheumatoid arthritis; ss.
 OS Homo sapiens.
 PN MO9931232-A1.
 XX
 XX
 PD 24-JUN-1999.
 XX
 XX 11-DEC-1998; 98WO-GB03720.
 XX
 XX 13-DEC-1997; 97GB-0026339.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 XX Aiyar J, Christian EP, Iannotti CA, Logsdon NJ;
 PI WPI; 1999-395178/33.
 XX
 XX P-PSDB; AAY23215.
 DR
 DR New isolated potassium channel polypeptide
 PT Example 1; Fig 1; 151pp; English.
 PS
 XX
 XX The present sequence encodes a human brain-derived potassium channel.
 CC The polynucleotides and polypeptides can be used for identifying
 CC compounds that modulate the biological activity of a potassium channel
 CC or neurophysiology. It is used as a method of treatment for patients
 CC with conditions which are mediated by the biological activity of a
 CC human potassium channel. Antagonists can be used in modulating cognitive,
 CC behavioural, psychiatric, neurodegenerative and developmental disorders
 CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
 CC and brain tumours. They can be used for treating diseases such as
 CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
 CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
 CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
 CC autoimmune diseases, cancer, graft rejections, acute and chronic
 CC inflammation, allergies, proliferative disorders, anaemias,
 CC neurodegenerative diseases with immunological components, as well as
 CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
 CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
 CC syndrome, mixed connective tissue disease, and experimental allergic
 CC encephalomyelitis (EAE).
 CC
 SO Sequence 3029 BP; 546 A; 972 C; 1004 G; 507 T; 0 other;
 QY
 QY Query Match 0.9%; Score 26; DB 20; Length 3029;
 Db Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 367 CGCGGCTGGCGCTTCATCTACCAAGC 392
 275 CGCGGCTGGCGCTTCATCTACCAAGC 300
 RESULT 25
 AAS74831
 ID AAS74831 standard; cDNA; 3195 BP.
 XX
 XX AAS74831;
 AC
 XX 13-FEB-2002 (first entry)
 DT

XX DE DNA encoding novel human diagnostic protein #10635.
 XX XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX PN W0200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HXSE-) HXSEQ INC.
 XX PT Drmanac RT, Liu C, Tang YT;
 XX DR P-PSDB; ABG10644.
 XX DR WPI; 2001-639362/73.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 1; SEQ ID No 10635; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 3195 BP; 559 A; 1048 C; 1068 G; 520 T; 0 other;
 XX
 XX Query Match 0.9%; Score 26; DB 23; Length 3195;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 367 CGCGGCTGGGCGTTCATCTACACGCG 392
 XX ||||||||||||||||||||||||||||
 XX Db 440 CGCGGCTGGGCGTTCATCTACACGCG 465
 XX
 XX RESULT 26
 XX ID AAS7057 standard; DNA; 3232 BP.
 XX AC AAS7057;
 XX XX 22-JUL-1999 (first entry)
 XX DT
 XX XX Human KCNQ2 cDNA.
 XX DE

XX XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
 KW JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; ss.
 XX OS Homo sapiens.
 XX PN Key Location/Qualifiers
 XX FT CDS 128..2746
 XX FT /*tag= a
 XX FT /product= "KCNQ2"
 XX PN W09921875-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98WO-US22375.
 XX PR 24-OCT-1997; 97US-0063147.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Charlier C, Leppert MF, Singh NA;
 XX DR WPI; 1999-312938/26.
 XX DR P-PSDB; AAY08341.
 XX PT Nucleic acid encoding potassium channels KCNQ2 and 3
 XX PS Claim 1; Page 117-122; 195pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 XX SQ Sequence 3232 BP; 577 A; 1054 C; 1061 G; 533 T; 7 other;
 XX
 XX Query Match 0.9%; Score 26; DB 20; Length 3232;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 367 CGCGGCTGGGCGTTCATCTACACGCG 392
 XX ||||||||||||||||||||||||||||
 XX Db 392 CGCGGCTGGGCGTTCATCTACACGCG 417
 XX
 XX RESULT 27
 XX ID AAS74830 standard; cDNA; 3232 BP.
 XX AC AAS74830;
 XX XX 13-FEB-2002 (first entry)
 XX DT
 XX XX DNA encoding novel human diagnostic protein #10634.
 XX DE
 XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW DE

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR P-PSDB; ABG10643.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PT Claim 1: SEQ ID NO 10634; 103pp; English.
 XX PS
 XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ
 XX Sequence 3232 BP; 576 A; 1054 C; 1061 G; 533 T; 8 other;
 Query Match 0.9%; Score 26; DB 23; Length 3232;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 367 CGCGGCTGGGCGTTTCATCTACACGC 392
 DB 392 CGCGGCTGGGCGTTTCATCTACACGC 417
 RESULT 28
 AAX57145
 ID AAX57145 standard; DNA: 3237 BP.
 XX AC AAX57145;
 XX DT 22-JUL-1999 (first entry)
 XX DE Human mutant KCNQ2 cDNA.
 XX KW KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myoclonic epilepsy;
 KW JME; Rolandic epilepsy; mutant; treatment; screening; epilepsy;
 KW detection; gene therapy; drug screening; ss.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key
 XX FT CDS Location/Qualifiers
 FT CDS 128..2920
 FT /tag= a
 FT /product= "KCNQ2"
 XX PN WO9921875-A1.
 XX PD 06-MAY-1999.
 XX PF 23-OCT-1998; 98WO-US22375.
 XX PR 24-OCT-1997; 97US-0063147.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Charlier C, Leppert MF, Singh NA;
 XX DR WPI: 1999-312938/26.
 XX DR P-PSDB; AAY08347.
 XX PT Nucleic acid encoding potassium channels KCNQ2 and 3
 XX PS
 XX CC Claim 1: Page 168-172; 195pp; English.
 XX CC This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myoclonic
 CC epilepsy (JME) or Rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as
 CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
 CC useful in rational design of drugs and therapeutically (in replacement
 CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
 CC 3 sequences can now be diagnosed early (before symptoms are manifest),
 CC and better treatment options will be available.
 XX SQ
 XX Sequence 3237 BP; 577 A; 1056 C; 1064 G; 533 T; 7 other;
 Query Match 0.9%; Score 26; DB 20; Length 3237;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 367 CGCGGCTGGGCGTTTCATCTACACGC 392
 DB 392 CGCGGCTGGGCGTTTCATCTACACGC 417
 RESULT 29
 AAX26587
 ID AAX26587 standard; DNA: 3287 BP.
 XX AC AAX26587;
 XX DT 16-JUN-1999 (first entry)
 XX DE Nucleotide sequence of human KCNQ2 (formerly known as KVLRL1).
 XX KW Human; KCNQ protein; nervous system-specific potassium channel;
 KW neuronal excitability; neurotransmitter release; KCNQ modulator;
 KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KW age-associated memory loss; learning deficiency; motor neuron disease;
 KW epilepsy; stroke; ss.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 61..2676
 XX FT /tag= a
 XX
 XX MO9907832-A1.
 XX
 XX 18-FEB-1999.
 XX
 XX 26-JUN-1998; 98MO-US13276.
 XX
 XX 12-AUG-1997; 97US-0055599.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Blonar MA, Dworetzky S, Gribkoff VK, Levesque PC;
 XX Little WA, Neubauer MG, Yang W;
 XX WPI; 1999-190047/16.
 XX P-PSDB; AAY01529.
 XX
 XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
 XX neurotransmission and neuroprotection, used to treat, e.g. ataxia
 XX
 XX Claim 5; Fig 2; 64pp; English.
 XX
 XX The present sequence encodes human KCNQ2/KvLRI. KCNQ proteins are
 XX nervous system-specific potassium channels. In neurons, potassium
 XX channels regulate neuronal excitability, action potential shape
 XX and firing pattern, and neurotransmitter release. KCNQ modulators
 XX may be used to treat disorders such as ataxia, myokymia, seizures,
 XX Alzheimer's disease, Parkinson's disease, age-associated memory
 XX loss, learning deficiencies, motor neuron diseases, epilepsy, and
 XX stroke.
 XX
 XX Sequence 3287 BP; 587 A; 1062 C; 1083 G; 555 T; 0 other.
 XX
 XX Query Match 0.9%; Score 26; DB 20; Length 3287;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
 XX |
 XX 325 CGCGGCTGGGCGTTCATCTACACGC 350
 XX
 XX RESULT 30
 XX AAS74832
 XX ID AAS74832 standard; CDNA; 7413 BP.
 XX
 XX AAS74832;
 XX
 XX 13-FEB-2002 (first entry)
 XX
 XX DNA encoding novel human diagnostic protein #10636.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 XX Homo sapiens.
 XX
 XX MO200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001MO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG10645.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX
 XX Claim 1; SEQ ID No 10636; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. AAS64197-AAS94564 represent novel human
 XX diagnostic coding sequences of the invention.
 XX Note: The sequence data for this patent did not appear in the printed
 XX specification, but was obtained in electronic format directly from WPI
 XX at ftp.wpi.int/pub/published_pct_sequences.
 XX
 XX Sequence 7413 BP; 1354 A; 2331 C; 2353 G; 1368 T; 7 other;
 XX
 XX Query Match 0.9%; Score 26; DB 23; Length 7413;
 XX Best Local Similarity 100.0%; Pred. No. 0.058;
 XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 367 CGCGGCTGGGCGTTCATCTACACGC 392
 XX |
 XX 311 CGCGGCTGGGCGTTCATCTACACGC 336
 XX
 XX RESULT 31
 XX AAC64374
 XX ID AAC64374 standard; DNA; 25 BP.
 XX
 XX AAC64374;
 XX
 XX 07-FEB-2001 (first entry)
 XX
 XX Human KCNQ5 (KCNQ5) PCR primer SEQ ID NO:11.
 XX
 XX Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
 XX Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 XX Salla disease; ophthalmological; auditory; central nervous system;
 XX cardiocative; anticonvulsant; gastrointestinal; muscular active;
 XX age-related macular degeneration; macular degeneration; deafness;
 XX epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 XX gastrointestinal disorder; PCR primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX MO200061606-A1.
 XX
 XX 19-OCT-2000.
 XX
 XX 10-APR-2000; 2000MO-US09587.
 XX
 XX 14-APR-1999; 99US-0129274.
 XX

PA (MERI) MERCK & CO INC.
 XX
 PI Petrukhin K, Caskey CT, Li W, Metzker ML;
 XX
 DR WPI: 2000-647417/62.
 XX
 PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
 PT inhibitors and activators which can treat e.g. Stargardt-like macular
 PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy -
 XX
 PS Example 1; Page 32; 99pp; English.
 XX
 CC The present invention describes the human KCNQ5 (also called KCNQ6)
 CC protein, which is a voltage-gated potassium channel protein. Human
 CC KCNQ5 has ophthalmological, auditory, central nervous system (CNS),
 CC cardiovascular, anticonvulsant, gastrointestinal and muscular active
 CC activities. Sequences and methods from the present invention are useful
 CC for identifying activators or inhibitors of KCNQ5 protein. These
 CC activators and inhibitors are useful for treating Stargardt-like macular
 CC dystrophy, cone-rod dystrophy, Salla disease, age-related macular
 CC degeneration, other forms of macular degeneration, deafness, epilepsy,
 CC and different forms of neuropsychiatric, heart, gastrointestinal, and
 CC muscle disorders. Stargardt-like macular dystrophy and cone-rod
 CC dystrophies are located at chromosome 6q. The present sequence represents
 CC a PCR primer for human KCNQ5, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 0 A; 5 C; 5 G; 15 T; 0 other;
 XX
 Query Match 0.9%; Score 25; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 399 TTTTCTCTGTCTTTGTTGCTTG 423
 DB 1 TTTTCTCTGTCTTTGTTGCTTG 25
 XX
 RESULT 32
 AAS14658/C
 ID AAS14658 standard; cDNA; 25 BP.
 XX
 AC AAS14658;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human voltage-gated potassium channel hKCNQ5 PCR primer #5.
 XX
 DE Human; ss; voltage-gated potassium channel; hKCNQ5; noctropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI: 2001-611467/70.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha

PT subunits -
 XX
 PS Claim 6; Page 65; 78pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a PCR primer used to amplify a 650bp cDNA clone containing the 5'
 CC region of hKCNQ5.
 XX
 SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 other;
 XX
 Query Match 0.9%; Score 25; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 765 GGGTTAGTGGTTTATGCTCAGAC 789
 DB 25 GGGTTAGTGGTTTATGCTCAGAC 1
 XX
 RESULT 33
 AAS14659/C
 ID AAS14659 standard; cDNA; 25 BP.
 XX
 AC AAS14659;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human voltage-gated potassium channel hKCNQ5 PCR primer #6.
 XX
 DE Human; ss; voltage-gated potassium channel; hKCNQ5; noctropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder;
 KW stroke; pain; gene therapy; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US09328.
 XX
 PR 21-MAR-2000; 2000US-190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 DR WPI: 2001-611467/70.
 XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for

Identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ alpha subunits

Claim 6; Page 65; 78pp; English.

The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a PCR primer used to amplify a 650bp cDNA clone containing the 5' region of hKCNQ5.

Sequence 25 BP; 5 A; 8 C; 8 G; 4 T; 0 other;

Query Match 0.9%; Score 25; DB 22; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

712 CAGATCCCGCCGATGTCGCGCATGG 736

25 CAGATCCCGCCGATGTCGCGCATGG 1

RESULT 34

AAC64384

ID AAC64384 standard; DNA; 24 BP.

AC AAC64384;

07-FEB-2001 (first entry)

Human KCNQ5 (KCN6q) PCR primer SEQ ID NO:21.

Human; KCNQ5; chromosome 6; voltage-gated potassium channel; Stargardt-like macular dystrophy; cone-rod macular dystrophy; Salla disease; ophthalmological; auditory; central nervous system; cardioactive; anticonvulsant; gastrointestinal; muscular active; age-related macular degeneration; macular degeneration; deafness; epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder; gastrointestinal disorder; PCR primer; ss.

Homo sapiens.

MO200061606-A1.

19-OCT-2000.

10-APR-2000; 2000MO-US09587.

14-APR-1999; 99US-0129274.

(MERI) MERCK & CO INC.

Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying PT inhibitors and activators which can treat e.g. Stargardt-like macular PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy - XX

Example 1; Page 33; 99pp; English.

The present invention describes the human KCNQ5 (also called KCN6q) protein, which is a voltage-gated potassium channel protein. Human KCNQ5 has ophthalmological, auditory, central nervous system (CNS), cardioactive, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQ5 protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of neuropsychiatric heart, gastrointestinal, and muscle disorders. Stargardt-like macular dystrophy and cone-rod dystrophies are located at chromosome 6q. The present sequence represents a PCR primer for human KCNQ5, which is used in an example from the present invention.

Sequence 24 BP; 9 A; 2 C; 4 G; 9 T; 0 other;

Query Match 0.9%; Score 24; DB 21; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1549 AGAATTATGAAATTTCATGTTGCA 1572

1 AGAATTATGAAATTTCATGTTGCA 24

Search completed: June 19, 2003, 13:42:23
Job time : 602 secs

|||||
Db 541 TCTCCGGGTTCTGTTGCGATATAGAGATGCGAAGAACTGAGGTTGCTCGAAG 600
601 CCCTTCGTGTATAGATACCATGTTGCTTATCGCTCAATACAGTGTGTTGCAAAA 660
601 CCCCTCTGTGTATATATACCATGTTGCTTATCGCTCAATACAGTGTGTTGCAAAA 660
661 ACTCAGGGAATATATTTTGGCCAGCTGCTGACAGTCTCGTTCCGTTCCACAGATCTC 720
661 ACTCAGGGAATATATTTTGGCCAGCTGCTGACAGTCTCGTTCCGTTCCACAGATCTC 720
661 ACTCAGGGAATATATTTTGGCCAGCTGCTGACAGTCTCGTTCCGTTCCACAGATCTC 720
721 CGCATGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 780
721 CGCATGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 780
721 CGCATGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 780
781 GCTCAGCAGCAAGAAATATATACACATGTTGATATGATATTTTGGTTCTATTTTTCG 840
781 GCTCAGCAGCAAGAAATATATACACATGTTGATATGATATTTTGGTTCTATTTTTCG 840
841 TCTTTCTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTATATATGAGAT 900
841 TCTTTCTGTCTATCTGTGTGAAAAAGATGCAATTAAGAGTTTCTATATATGAGAT 900
901 GCTCTCTGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 960
901 GCTCTCTGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 960
901 GCTCTCTGTGTGCGATATGACCCGAAAGGGAGGACCTTGGAAATTTACTGGGTTTCTAT 960
961 ACTTGTGTGGAATATGCTTCTGCTGAGGCTTGTGACCTGCTGAGCTTCTTCTTTTGA 1020
961 ACTTGTGTGGAATATGCTTCTGCTGAGGCTTGTGACCTGCTGAGCTTCTTCTTTTGA 1020
1021 CTTCCTGCGGCAATCTTGTGCTGAGGCTTGTGACCTGCTGAGCTTCTTCTTTTGA 1080
1021 CTTCCTGCGGCAATCTTGTGCTGAGGCTTGTGACCTGCTGAGCTTCTTCTTTTGA 1080
1081 AATCAGCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1140
1081 AATCAGCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1140
1141 TACGACCTGATGAGAAATCTGTTCCATTTGCACTGGAAGCAACACTTGAAGGCTTG 1200
1141 TACGACCTGATGAGAAATCTGTTCCATTTGCACTGGAAGCAACACTTGAAGGCTTG 1200
1201 CACACCTGAGAGCTTACCAATCAGAGCTTAAGTTTAAAGAGCAGAGCTGCTGATG 1260
1201 CACACCTGAGAGCTTACCAATCAGAGCTTAAGTTTAAAGAGCAGAGCTGCTGATG 1260
1201 CACACCTGAGAGCTTACCAATCAGAGCTTAAGTTTAAAGAGCAGAGCTGCTGATG 1260
1261 CCCAGAGGCGAGATATTAAGAGCGACAGAGCTGATAGTGAAGAGAGGAGGAGGAGG 1320
1261 CCCAGAGGCGAGATATTAAGAGCGACAGAGCTGATAGTGAAGAGAGGAGGAGGAGG 1320
1321 ACCGACATCAGAGCGAGAGGAGCTCCACAAAGTGCAGAAAGAGTGGAGCTTCAACGAG 1380
1321 ACCGACATCAGAGCGAGAGGAGCTCCACAAAGTGCAGAAAGAGTGGAGCTTCAACGAG 1380
1381 CGAAGCCGCTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1381 CGAAGCCGCTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 GCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 TCACTGGAAGACCTTCAACCCACACTTAAACTGTCATTTGAGCTATCAGATTTTATGAAA 1560
1501 TCACTGGAAGACCTTCAACCCACACTTAAACTGTCATTTGAGCTATCAGATTTTATGAAA 1560
1561 TTTTCACTGGAAGACCTTCAACCCACACTTAAACTGTCATTTGAGCTATCAGATTTTATGAAA 1620
1561 TTTTCACTGGAAGACCTTCAACCCACACTTAAACTGTCATTTGAGCTATCAGATTTTATGAAA 1620
1621 ATTGAACAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1621 ATTGAACAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

Db 1621 ATTGAACAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1681 CGTGTGATCAATTTCTGGAAGAGGCAAAATCAATCAATATAGAAAGCCGAGAGAAA 1740
Db 1681 CGTGTGATCAATTTCTGGAAGAGGCAAAATCAATCAATATAGAAAGCCGAGAGAAA 1740
Qy 1741 ATAGAGCAGAAATGAGACACAGAGATCTGATAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 ATAGAGCAGAAATGAGACACAGAGATCTGATAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Qy 1801 GAAAAACAGATACATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG 1860
Db 1801 GAAAAACAGATACATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG 1860
Qy 1861 GTCCTTGGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1861 GTCCTTGGAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy 1921 GAATGTGAACAGACATCTGATATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 1980
Db 1921 GAATGTGAACAGACATCTGATATCAAAAGCCCTGTGATAGCAAAAGATCTTTCGGGTTCC 1980
Qy 1981 GCACAAACAGTGTGCTTATTCAGATCAATAGTCCCAACATCTGAGAGGCTGAG 2040
Db 1981 GCACAAACAGTGTGCTTATTCAGATCAATAGTCCCAACATCTGAGAGGCTGAG 2040
Qy 2041 TTTATTTGAGGCGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2041 TTTATTTGAGGCGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Qy 2101 CACAGTCAAGCAACAGAGTGTGCAATATAGCAAAAGGATGCTGAGCAGTGTGAGCCACC 2160
Db 2101 CACAGTCAAGCAACAGAGTGTGCAATATAGCAAAAGGATGCTGAGCAGTGTGAGCCACC 2160
Qy 2161 AACACATTTGCAAAACCAATTAATATAGGCAACCAAGCCAGCAGCCCAACACTTTCAG 2220
Db 2161 AACACATTTGCAAAACCAATTAATATAGGCAACCAAGCCAGCAGCCCAACACTTTCAG 2220
Qy 2221 ATCCACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 ATCCACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2281 CCTGAGGCTTACAGAGAAAGCAATTTCTGAGCTGACCACTGCTGCTGCTGCTGCTGCTGCTG 2340
Db 2281 CCTGAGGCTTACAGAGAAAGCAATTTCTGAGCTGACCACTGCTGCTGCTGCTGCTGCTGCTG 2340
Qy 2341 AATGTTGAGTTGCAAGCTGCAATATCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
Db 2341 AATGTTGAGTTGCAAGCTGCAATATCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400
Qy 2401 ATGGAGAGAGAAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Db 2401 ATGGAGAGAGAAATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Qy 2461 TTTGCTGTGCAAAACCTGATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Db 2461 TTTGCTGTGCAAAACCTGATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Qy 2521 GAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 GAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Qy 2581 TTTATTAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db 2581 TTTATTAATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Qy 2641 CCGAGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
Db 2641 CCGAGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
Qy 2701 TCAATCTGAGACATTTTGAAGCAGAGAGAAATACAGATGAGGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 TCAATCTGAGACATTTTGAAGCAGAGAGAAATACAGATGAGGCTGCTGCTGCTGCTGCTGCTG 2760

1680 ATTGACAAATATTTGCTGTCATCTGACATGTTGTAGATTAAGACCTTCAACA 1739
1681 CGTGTGATCAATTTCTGGAAAAGGCAATTCACATAGATAGACAGCCGAGAGAA 1740
1740 CGTGTGATCAATTTCTGGAAAAGGCAATTCACATAGATTAAGAGCCGAGAGAA 1799
1741 ATTAAGACAGAAATGAGACACAGACATCTCAGTATGTCGGGTGCTCAAGTT 1800
1800 ATTAAGACAGAAATGAGACACAGACATCTCAGTATGTCGGGTGCTCAAGTT 1859
1801 GAAAAACAGGTACAGTCCATAGATCAAGCTGAGCTCCATAGATCAATCAACAG 1860
1860 GAAAAACAGGTACAGTCCATAGATCAAGCTGAGCTCCATAGATCAATCAACAG 1919
1861 GTCTCTGGAAAAGGCTGCTGCTGAGCCCTGCTTGGCTTATTCAGATGCCACTTTT 1920
1920 GTCTCTGGAAAAGGCTGCTGCTGAGCCCTGCTTGGCTTATTCAGATGCCACTTTT 1979
1921 GAATGTGAACAGATCTGACTATCAAGCCCTGATAGCAAGATCTTCGGGTTC 1980
1980 GAATGTGAACAGATCTGACTATCAAGCCCTGATAGCAAGATCTTCGGGTTC 2039
1981 GCACAAAACAGTGGCTCTTATCCAGATCAACTAGTCCCAATCTCGAGAGGCTTCAG 2040
2040 GCACAAAACAGTGGCTCTTATCCAGATCAACTAGTCCCAATCTCGAGAGGCTTCAG 2099
2041 TTGATCTGAGCAATGAGTGTGAGTCCAGACCTTCTAGGCTTGGCTTACTAG 2100
2100 TTGATCTGAGCAATGAGTGTGAGTCCAGACCTTCTAGGCTTGGCTTACTAG 2159
2101 CACAGTCAACACACAGTGTCCATTAATAGTCAAGCGATGGCTCAGAGTGGCAGCC 2160
2160 CACAGTCAACACACAGTGTCCATTAATAGTCAAGCGATGGCTCAGAGTGGCAGCC 2219
2161 AACACATTGCAACCAATTAATAGTGTGAGTCCAGACCTTCTAGGCTTGGCTTACTAG 2220
2220 AACACATTGCAACCAATTAATAGTGTGAGTCCAGACCTTCTAGGCTTGGCTTACTAG 2279
2221 ATCCACCTCTCTCCAGACCTATCAAGCTGAGCCAGGAGCAAGCTGAGCCCTTAC 2280
2280 ATCCACCTCTCTCCAGACCTATCAAGCTGAGCCAGGAGCAAGCTGAGCCCTTAC 2339
2281 CCTGACAGCTTACAGAAAGCATTTCTGACGTACACACCTGCTTGGCTTGGCTTCAAGAA 2340
2340 CCTGACAGCTTACAGAAAGCATTTCTGACGTACACACCTGCTTGGCTTGGCTTCAAGAA 2399
2341 AATGTTAGTGTGACAGTCAATCTCAGCAAGACCTGTTCTATAGAGAAAGCTTTGAC 2400
2400 AATGTTAGTGTGACAGTCAATCTCAGCAAGACCTGTTCTATAGAGAAAGCTTTGAC 2459
2401 ATGGAGAGAGAAATCTGTTGTCTGTCTGTCATGTCAGAGAGACTTGGCAATCT 2460
2460 ATGGAGAGAGAAATCTGTTGTCTGTCTGTCATGTCAGAGAGACTTGGCAATCT 2519
2461 TTGTTCTGTGAAAACTGATCAGGTGACCGAGAACTGAATATACAACTTTCAGGAGT 2520
2520 TTGTTCTGTGAAAACTGATCAGGTGACCGAGAACTGAATATACAACTTTCAGGAGT 2579
2521 GAGTCAAGTGGCTCAGAGGACAGCAAGATTTTACCCCAATGAGGAGATCAAAATG 2580
2580 GAGTCAAGTGGCTCAGAGGACAGCAAGATTTTACCCCAATGAGGAGATCAAAATG 2639
2581 TTTATATGATGAAAGGTGGGTCCGAAAGACAGAGACACTTGTGATGCGCA 2640
2640 TTTATATGATGAAAGGTGGGTCCGAAAGACAGAGACACTTGTGATGCGCA 2699
2641 CCGCAGCTGCGCAGAGAGAGTGCCTTTGATCAGATCAAGCTCTTAAGAGCTGAAAGTCA 2700
2700 CCGCAGCTGCGCAGAGAGAGTGCCTTTGATCAGATCAAGCTCTTAAGAGCTGAAAGTCA 2759
2701 TCATCTAGAGCAATTTGTAAGGAGAGAAAGTACAGATGCCCTGAGCTTGGCTCATGTC 2760

Db 2760 TCATCTAGAGCAATTTGTAAGGAGAGAAAGTACAGATGCCCTGAGCTTGGCTCATGTC 2819
QY 2761 AAACGAAATAA 2772
Db 2820 AAACGAAATAA 2831

RESULT 3
US-09-810-796-3
Sequence 3, Application US/09810796
Patent No. US20020102677A1
GENERAL INFORMATION:
APPLICANT: Jegia, Timothy James
APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
FILE REFERENCE: 018512-005010US
CURRENT APPLICATION NUMBER: US/09/810,796
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/190,954
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2667
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human outwardly rectifying, voltage-gated
OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
NAME/KEY: CDS
LOCATION: (1)..(2667)
OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match 90.7% Score 2514; DB 10; Length 2667;
Best Local Similarity 99.9% Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 ATGAAGATGTGAGATCGGGGCGGGGCGAGAGTGTCTGTAATCTCGAGCGCGCGAGGGC 165
Db 1 ATGAAGATGTGAGATCGGGGCGGGGCGAGAGTGTCTGTAATCTCGAGCGCGCGAGGGC 60
QY 166 GAGGCGCTGCTACTGCTGTGGGACCCGCGGCGGCGAGCTGTGTGGCGGCGGCTGTG 225
Db 61 GAGGCGCTGCTACTGCTGTGGGACCCGCGGCGGCGAGCTGTGTGGCGGCGGCTGTG 120
QY 226 AGGGAGAGCGCGGGGCGAAGAGAGGGGCGCGGATGAGCTGTGTGGGAGAGCGCTCT 285
Db 121 AGGGAGAGCGCGGGGCGAAGAGAGGGGCGCGGATGAGCTGTGTGGGAGAGCGCTCT 180
QY 286 TACACGATGAGCAGAGCTGCCGCGCAACGTCAAGTACCGGCGGCTGAGAACTACCTG 345
Db 181 TACACGATGAGCAGAGCTGCCGCGCAACGTCAAGTACCGGCGGCTGAGAACTACCTG 240
QY 346 TACACGATGAGCAGAGCTGCCGCGCAACGTCAAGTACCGGCGGCTGAGAACTACCTG 405
Db 241 TACACGATGAGCAGAGCTGCCGCGCAACGTCAAGTACCGGCGGCTGAGAACTACCTG 300
QY 406 CTGTCTGTGTTGCTGATTTTGTGAGTGTCTTACCAATCCCTGAGCACAAATTTG 465
Db 301 CTGTCTGTGTTGCTGATTTTGTGAGTGTCTTACCAATCCCTGAGCACAAATTTG 360
QY 466 GCTCAAGTGTGCTTGTGATCTCGAGTGTGATGATGATGATGATGATGATGATGATG 525
Db 361 GCTCAAGTGTGCTTGTGATCTCGAGTGTGATGATGATGATGATGATGATGATGATG 420
QY 526 ATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 585
Db 421 ATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 586 AGGTTGCTGCAAGAGCGCTTGTGTTATAGATACCAATGTTCTTATGCTTCAATATGA 645
Db 481 AGGTTGCTGCAAGAGCGCTTGTGTTATAGATACCAATGTTCTTATGCTTCAATATGA 540

QY	646	GTGTTTTCGTGAAAAACACGAGGGTAAATATTTTGGCAACGCTGTGCATCAGAAAGTCCGCT	705
Db	541	GTGTGTTTCGAAAAACCTCAGGGGTATATTTTGGCAACGCTGTGCATCAGAAAGTCCGCT	600
QY	706	TTCTACAGATCTCCTCGCATGGTGGCCATGAGCAGGAAGGGAGGCACTTGGAAATTACTG	765
Db	601	TTCTACAGATCTCCTCGCATGGTGGCCATGAGCAGGAAGGGAGGCACTTGGAAATTACTG	660
QY	766	GGTTCAGTGGTTTATGCTCACAAGCAAGAAATTATCAGACGTTGGTACATAGGATTTTGG	825
Db	661	GGTTCAGTGGTTTATGCTCACAAGCAAGAAATTATCAGACGTTGGTACATAGGATTTTGG	720
QY	826	GTGCTATATTTTTCGCTTTCCTTCGCTATCTGTGGAAAAAGATGCAATTAAGAGTTT	885
Db	721	GTGCTATATTTTTCGCTTTCCTTCGCTATCTGTGGAAAAAGATGCAATTAAGAGTTT	780
QY	886	TCTACATATGCAAGATGCTCTGTGGTGGGCAATTAATGACAACTATTGGCTATGGA	945
Db	781	TCTACATATGCAAGATGCTCTGTGGTGGGCAATTAATGACAACTATTGGCTATGGA	840
QY	946	GACAAACACCCCTTAATCTGGCGGGGAAGTTGGTTCTGTGAGGCTTTGCACTCCTTGGC	1005
Db	841	GACAAACACCCCTTAATCTGGCGGGGAAGTTGGTTCTGTGAGGCTTTGCACTCCTTGGC	900
QY	1006	ATTCTTCTTTTGGCACTTCTCGCGGCAATTCCTGGCTCAGGTTTGGCATTTAAAGTACAA	1065
Db	901	ATTCTTCTTTTGGCACTTCTCGCGGCAATTCCTGGCTCAGGTTTGGCATTTAAAGTACAA	960
QY	1066	GAACAACACCGCCAGAAAAACAATTGAAAAAAGAAAGCAACCGTCCCACTCAATTCAG	1125
Db	961	GAACAACACCGCCAGAAAAACAATTGAAAAAAGAAAGCAACCGTCCCACTCAATTCAG	1020
QY	1126	TGTGTTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1185
Db	1021	TGTGTTTGGCGTATGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1080
QY	1186	CACCTGAGAGCCTTGGCAACCTGAGCCCTTACATCAGAAAGCTTAAGTTTAAAGAGCA	1245
Db	1081	CACCTGAGAGCCTTGGCAACCTGAGCCCTTACATCAGAAAGCTTAAGTTTAAAGAGCA	1140
QY	1246	GTGGCGATGGCTTGGCCCGAGGGGCAAGATTTAAGAGCCGCAAGCCCTCATTAGGTGAC	1305
Db	1141	GTGGCGATGGCTTGGCCCGAGGGGCAAGATTTAAGAGCCGCAAGCCCTCATTAGGTGAC	1200
QY	1306	AGGAGGTCCCCAAGCACCGCATTCACAGCCGAGGGGCACTCCACCAAAATGCAAGAGACC	1365
Db	1201	AGGAGGTCCCCAAGCACCGCATTCACAGCCGAGGGGCACTCCACCAAAATGCAAGAGACC	1260
QY	1366	TGGAGCTTCAACGACGAAACCCGTTCCCGGCCCTCGCTGGCGCTCAAAAGTTCTCAGCCA	1425
Db	1261	TGGAGCTTCAACGACGAAACCCGTTCCCGGCCCTCGCTGGCGCTCAAAAGTTCTCAGCCA	1320
QY	1426	AAACCAAGTATAGTGTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAAGA	1485
Db	1321	AAACCAAGTATAGTGTGACACAGCCCTTGGCACTGATGATGATATGATGAAAAAAGA	1380
QY	1486	TGCCAGTGTATGTATCATGATGGAAGACTCACCCACCACTTTAAACTGTCAATGCAAGCT	1545
Db	1381	TGCCAGTGTATGTATCATGATGGAAGACTCACCCACCACTTTAAACTGTCAATGCAAGCT	1440
QY	1546	ATCAGAAATTGAAATTTCAATGTTGCAAAACGGAAGTTTAAGAAACATTAGCTGCATAT	1605
Db	1441	ATCAGAAATTGAAATTTCAATGTTGCAAAACGGAAGTTTAAGAAACATTAGCTGCATAT	1500
QY	1606	GATGTAAGAAATGTCAATGGAACAATATTCTGCTGTCATCTGACATGTTGTAGAAATT	1665
Db	1501	GATGTAAGAAATGTCAATGGAACAATATTCTGCTGTCATCTGACATGTTGTGTAGAAATT	1560
QY	1666	AAAAAGCTTCAAAACGCTGTGATCAAAATTTCTGAAAAAGGGCAATTCACATAGAGTAAG	1725
Db	1561	AAAAAGCTTCAAAACGCTGTGATCAAAATTTCTGAAAAAGGGCAATTCACATAGAGTAAG	1620

QY	1729	AAGAGCCGAGAGAAAATTAAACGAGAGAAATGAGAGCCAGACGATCTCAGATGTCGGT	1785
Db	1621	AAGAGCCGAGAGAAAATTAAACGAGAGAAACATGAGAGCCAGACGATCTCAGATGTCGGT	1680
QY	1786	CGAGTGTCAAGGTTAAAAAACAAGGTACAGTCCATAGAAATCCAAAGCTGGACTGCTACTA	1845
Db	1681	CGGGTGTCAAGGTTGAAAACAAAGGTACAGTCCATAGAAATCCAAAGCTGGACTGCTACTA	1740
QY	1846	GACATCTATCACAGGTCCTTTCGAAAAGGCTCTGCTCAGCCCTTGCTTTGGCTTCATTC	1905
Db	1741	GACATCTATCACAGGTCCTTTCGAAAAGGCTCTGCTCAGCCCTTGCTTTGGCTTCATTC	1800
QY	1906	CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	1965
Db	1801	CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	1860
QY	1966	GATCTTTGGGGTTCGCGCAAAACAGTGGCTGCTTATCCAGATCAACTATGTCGCAATTC	2025
Db	1861	GATCTTTGGGGTTCGCGCAAAACAGTGGCTGCTTATCCAGATCAACTATGTCGCAATTC	1920
QY	2026	TGAGAGAGCCTGAGTCAATCTCTACGCGCAATGATGTACAGGCCAGACTTCTACGCG	2085
Db	1921	TGAGAGAGCCTGAGTCAATCTCTACGCGCAATGATGTACAGGCCAGACTTCTCTACGCG	1980
QY	2086	CTTAGGCCCTACTATGCAAGTCAGCAACACAGAGTGCCCAATTAGTCAAAAGCGATGCTCA	2145
Db	1981	CTTAGGCCCTACTATGCAAGTCAGCAACACAGAGTGCCCAATTAGTCAAAAGCGATGCTCA	2040
QY	2146	GCAGTGGCACCCACCAACACCATTTGCAAAACCAATTAATAGGGACCCCAAGCCAGCAGCC	2205
Db	2041	GCAGTGGCACCCACCAACACCATTTGCAAAACCAATTAATAGGGACCCCAAGCCAGCAGCC	2100
QY	2206	CCAAACAATTATAGATGCCACCTCCCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA	2265
Db	2101	CCAAACAATTATAGATGCCACCTCCCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA	2160
QY	2266	ACTCTGACCCCTAACCTTCGACGGCTTACAGGAAGCATTTCTGAGCTCAACACCTGCTT	2325
Db	2161	ACTCTGACCCCTAACCTTCGACGGCTTACAGGAAGCATTTCTGAGCTCAACACCTGCTT	2220
QY	2326	GTTGGCCCTCAAGGAAAATGTCAGGTTGCACAGTCAAAATCTACCAAGGACCCGTTCTATG	2385
Db	2221	GTTGGCCCTCAAGGAAAATGTCAGGTTGCACAGTCAAAATCTACCAAGGACCCGTTCTATG	2280
QY	2386	AGGAAAAGCTTTGACATGGAGAGAGAAAATCTGTTGTCTGTCTGTCCATGGTGGCCGAG	2445
Db	2281	AGGAAAAGCTTTGACATGGAGAGAGAAAATCTGTTGTCTGTCTGTCCATGGTGGCCGAG	2340
QY	2446	GACTTGGGCAAAATCTTTCTGTGTGCAAAACCTGATCAGTTCGACCGAGGAATCTGAATATA	2505
Db	2341	GACTTGGGCAAAATCTTTCTGTGTGCAAAACCTGATCAGTTCGACCGAGGAATCTGAATATA	2400
QY	2506	CAACTTTCAGGAGTGAATCAAGTGGCTTCAGAGGACGACCAAGATTTTTTACCCCAATYGG	2565
Db	2401	CAACTTTCAGGAGTGAATCAAGTGGCTTCAGAGGACGACCAAGATTTTTTACCCCAATYGG	2460
QY	2566	AGGGAATCCAAATGTTTATATACTGATGAGAAGGTGGGTCCGAAGAGAGAGAGACAGAC	2625
Db	2461	AGGGAATCCAAATGTTTATATACTGATGAGAAGGTGGGTCCGAAGAGAGAGAGACAGAC	2520
QY	2626	ACTTTTGTATGCGCGCACCGCAGCCTCCAGAGGAGAGTGCCTTTTGCATCAGACTCTCTAAG	2685
Db	2521	ACTTTTGTATGCGCGCACCGCAGCCTCCAGAGGAGAGTGCCTTTTGCATCAGACTCTCTAAG	2580
QY	2686	ACTGGAAGTCAAGCATCTGACAGCATTTTGTAAGGCAGAGAAAATCAAGATGCCCTC	2745
Db	2581	ACTGGAAGTCAAGCATCTGACAGCATTTTGTAAGGCAGAGAAAATCAAGATGCCCTC	2640
QY	2746	AGCTTGCCTCATGTCAAACTGGAATATA 2772	
Db	2641	AGCTTGCCTCATGTCAAACTGGAATATA 2667	

OTHER INFORMATION: human outwardly rectifying, voltage-gated
 ; OTHER INFORMATION: potassium channel KCNQ5-1
 ; NAME/KEY: CDS
 ; LOCATION: (10) ..(2703)
 ; OTHER INFORMATION: KCNQ5-1
 ; US-09-810-796-1

Query Match 52.3%; Score 1450; DB 10; Length 3071;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1550; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1221 TCAGAGCTAAGTTTAAAGAGGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1280
 1152 TCAGAGCTAAGTTTAAAGAGGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1211
 1281 GAGCGGACAAAGCTCAGTAGTACAGAGAGTCCCAAGCAGCATCACAGCCGAGG 1340
 1212 GAGCGGACAAAGCTCAGTAGTACAGAGAGTCCCAAGCAGCATCACAGCCGAGG 1271
 1341 CAGTCCACCAAGTGCAGAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1400
 1272 CAGTCCACCAAGTGCAGAGAGTGCATGCTAGGCCAGGCGGCGAGATATTAA 1331
 1401 GCTGGGCTCAAAAGTTTCAGCAAAACAGTAGATGCTGACACAGCCCTTGCGAC 1460
 1332 GCTGGGCTCAAAAGTTTCAGCAAAACAGTAGATGCTGACACAGCCCTTGCGAC 1391
 1461 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
 1392 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1451
 1521 ACCACTTAAAGTGTATTCAGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAAGGAA 1580
 1452 ACCACTTAAAGTGTATTCAGAGCTATCAGAAATTAAGAAATTCATGTTGCAAAAGGAA 1511
 1581 GTTTAAGGAAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 1512 GTTTAAGGAAATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1571
 1641 TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1700
 1572 TCATCTGACATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1631
 1701 AAAAGGCAATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1760
 1632 AAAAGGCAATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1691
 1761 CACAGAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1820
 1692 CACAGAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1751
 1821 AGAATCCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1880
 1752 AGAATCCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1811
 1881 CTCAGCCCTGCTTGGCTTCAATCCAGATCAGATCAGATCAGATCAGATCAGAT 1940
 1812 CTCAGCCCTGCTTGGCTTCAATCCAGATCAGATCAGATCAGATCAGATCAGAT 1871
 1941 CTCAGCCCTGCTTGGCTTCAATCCAGATCAGATCAGATCAGATCAGATCAGAT 2000
 1872 CTCAGCCCTGCTTGGCTTCAATCCAGATCAGATCAGATCAGATCAGATCAGAT 1931
 2001 ATCCAGATCAACTAGTGCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 2060
 1932 ATCCAGATCAACTAGTGCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 1991
 2061 GTTACAGTCCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 2120
 1992 GTTACAGTCCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 2051
 2121 GCCAATTAGTCAAGCGAATGGTCAAGATGAGCAGCAGCAGCAGCAGCAGCAGCAG 2180

2052 GCCAATTAGTCAAGCGAATGGTCAAGATGAGCAGCAGCAGCAGCAGCAGCAGCAG 2111
 2181 AAATACGGACACCAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2240
 2112 AAATACGGACACCAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2171
 2241 CATCAACATCTGCGCCAGGCGCAGAAACCTGACACCTAACCCTGACAGCTTACAGAAAG 2300
 2172 CATCAACATCTGCGCCAGGCGCAGAAACCTGACACCTAACCCTGACAGCTTACAGAAAG 2231
 2301 CATTTGACGTCACACCTGCTTGTGCTCCCAAGGAAATTTACAGTTGACAGTC 2360
 2232 CATTTGACGTCACACCTGCTTGTGCTCCCAAGGAAATTTACAGTTGACAGTC 2291
 2361 AAATTCACCAAGACCGCTTCTATGAGGAAAGCTTGACATGAGGAGGAAACTCTGT 2420
 2292 AAATTCACCAAGACCGCTTCTATGAGGAAAGCTTGACATGAGGAGGAAACTCTGT 2351
 2421 GTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2480
 2352 GTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2411
 2481 CAGTGCAGCAGGAGACTGATATACACTTTCAGGAGAGTCAAGTGCCTCCAGAG 2540
 2412 CAGTGCAGCAGGAGACTGATATACACTTTCAGGAGAGTCAAGTGCCTCCAGAG 2471
 2541 CAGCCCAAGATTTTACCCTCAATGAGGAAATCCAAATTTGTTATTAAGTGAAGAGT 2600
 2472 CAGCCCAAGATTTTACCCTCAATGAGGAAATCCAAATTTGTTATTAAGTGAAGAGT 2531
 2601 GGTCCCGAAGAGACAGACAGACAGACACTTGTGATGCGCCAGCGAGCCGCGAGGAAAC 2660
 2532 GGTCCCGAAGAGACAGACAGACAGACACTTGTGATGCGCCAGCGAGCCGCGAGGAAAC 2591
 2661 TGCCTTTGATTCAGACTCTCTAAGAGCTGGAAGTCAAGTCAATCTCAGAGCATTTGTA 2720
 2592 TGCCTTTGATTCAGACTCTCTAAGAGCTGGAAGTCAAGTCAATCTCAGAGCATTTGTA 2651
 2721 GGCAGGAGAAAGTACAGATGCGCTCAGTTCCTCATGTCGAAGTGAATA 2772
 2652 GGCAGGAGAAAGTACAGATGCGCTCAGTTCCTCATGTCGAAGTGAATA 2703

RESULT 7
 US-10-128-870-5
 ; Sequence 50, Application US/10128870
 ; Patent No. US20020168724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blahar, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58adiV
 ; CURRENT APPLICATION NUMBER: US/10/128, 870
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 900
 ; TYPE: DNA
 ; ORGANISM: MOUSE
 ; FEATURE:
 ; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
 ; US-10-128-870-5

Query Match 1.0%; Score 29; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCGTGGCGTTCATCTACACGC 392
DB 82 CCCCCGGCGTGGCGTTCATCTACACGC 110

RESULT 8

US-10-131-685-5
; Sequence 5, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-131-685-5

Query Match 1.0%; Score 29; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 8.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCGTGGCGTTCATCTACACGC 392
DB 82 CCCCCGGCGTGGCGTTCATCTACACGC 110

RESULT 9

US-10-128-870-22
; Sequence 22, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoif, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ADIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: MOUSE
US-10-128-870-22

Query Match 1.0%; Score 29; DB 9; Length 2169;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCGTGGCGTTCATCTACACGC 392
DB 262 CCCCCGGCGTGGCGTTCATCTACACGC 290

RESULT 10

US-10-131-685-22
; Sequence 22, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: MOUSE
US-10-131-685-22

Query Match 1.0%; Score 29; DB 9; Length 2169;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGCGTGGCGTTCATCTACACGC 392
DB 262 CCCCCGGCGTGGCGTTCATCTACACGC 290

RESULT 11

US-09-810-796-7/c
; Sequence 7, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAgen, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-00501005
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense
; OTHER INFORMATION: primer (2)
US-09-810-796-7

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1809 GGTACAGTCCATAGATCCAGCTGG 1834
|||||
Db 26 GGTACAGTCCATAGATCCAGCTGG 1

RESULT 12
US-09-810-796-8
; Sequence 8, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-00501005
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: standard 3'
US-09-810-796-8
; OTHER INFORMATION: RACE PCR gene specific primer (3)

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1725 GAAGAGCCGAGAGAAATATACAGCAG 1750
|||||
Db 1 GAAGAGCCGAGAGAAATATACAGCAG 26

RESULT 13
US-09-810-796-9
; Sequence 9, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-00501005
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: reamplification
US-09-810-796-9
; OTHER INFORMATION: gene-specific oligo (4)

Query Match 0.9%; Score 26; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1949 GCGCTGTGATGCAAGATCTTTCG 1974
|||||
Db 1 GCGCTGTGATGCAAGATCTTTCG 26

RESULT 14
US-10-128-870-3

; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neuhauer, Michael G.
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ADIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/035,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

Query Match 0.9%; Score 26; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 367 CGCGGCTGGGCGTTTCATCTACACGC 392
|||||
Db 85 CGCGGCTGGGCGTTTCATCTACACGC 110

RESULT 15
US-10-131-685-3
; Sequence 3, Application US/10131685
; Publication No. US20030044912A1
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neuhauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58ACON
; CURRENT APPLICATION NUMBER: US/10/131,685
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/105,058
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-131-685-3

Query Match 0.9%; Score 26; DB 9; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 367 CGCGGCTGGGCGTTTCATCTACACGC 392
|||||
Db 85 CGCGGCTGGGCGTTTCATCTACACGC 110

RESULT 16
US-10-128-870-19

; Sequence 19, Application US/10128870
; Patent No. US20020168724A1

; GENERAL INFORMATION:

; APPLICANT: Blannar, Michael A.

; APPLICANT: Dmoretzky, Steven

; APPLICANT: Gridkoff, Valentin K.

; APPLICANT: Levesque, Paul C.

; APPLICANT: Little, Wayne A.

; APPLICANT: Neubauer, Michael G.

; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

; FILE REFERENCE: DC58adiV

; CURRENT APPLICATION NUMBER: US/10/128,870

; PRIORITY FILING DATE: 2002-04-24

; PRIORITY FILING DATE: 09/105,058

; PRIORITY FILING DATE: June 26, 1998

; PRIORITY FILING DATE: 60/055,599

; PRIORITY FILING DATE: August 12, 1997

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 3287

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-128-870-19

Query Match 0.9%; Score 26; DB 9; Length 3287;

Best Local Similarity 100.0%; Pred. No. 0.0039;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||

DB 325 CGCGGCTGGCGCTTCATCTACACGC 350

RESULT 17
US-10-131-685-19

; Sequence 19, Application US/10131685

; Publication No. US20030044912A1

; GENERAL INFORMATION:

; APPLICANT: Blannar, Michael A.

; APPLICANT: Levesque, Paul C.

; APPLICANT: Little, Wayne A.

; APPLICANT: Neubauer, Michael G.

; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

; FILE REFERENCE: DC58aCON

; CURRENT APPLICATION NUMBER: US/10/131,685

; PRIORITY FILING DATE: 2002-07-23

; PRIORITY FILING DATE: US 09/105,058

; PRIORITY FILING DATE: 1998-06-26

; PRIORITY FILING DATE: US 60/055,599

; PRIORITY FILING DATE: 1997-08-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 3287

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-131-685-19

Query Match 0.9%; Score 26; DB 9; Length 3287;

Best Local Similarity 100.0%; Pred. No. 0.0039;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGCGCTTCATCTACACGC 392
|||||

DB 325 CGCGGCTGGCGCTTCATCTACACGC 350

RESULT 18
US-09-810-796-10/C

; Sequence 10, Application US/09810796

; Patent No. US20020102677A1

; GENERAL INFORMATION:

; APPLICANT: Jegla, Timothy James

; APPLICANT: ICGen, Inc.

; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel

; FILE REFERENCE: 018512-005010US

; CURRENT APPLICATION NUMBER: US/09/810,796

; PRIORITY FILING DATE: 2001-10-12

; PRIORITY FILING DATE: US 60/190,954

; PRIORITY FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:nested standard

; US-09-810-796-10

Query Match 0.9%; Score 25; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 GGGTTCAGTGGTTATGCTCACAGC 789
|||||

DB 25 GGGTTCAGTGGTTATGCTCACAGC 1

RESULT 19
US-09-810-796-11/C

; Sequence 11, Application US/09810796

; Patent No. US20020102677A1

; GENERAL INFORMATION:

; APPLICANT: Jegla, Timothy James

; APPLICANT: ICGen, Inc.

; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel

; FILE REFERENCE: 018512-005010US

; CURRENT APPLICATION NUMBER: US/09/810,796

; PRIORITY FILING DATE: 2001-10-12

; PRIORITY FILING DATE: US 60/190,954

; PRIORITY FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:nested standard

; US-09-810-796-11

Query Match 0.9%; Score 25; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 CAGATCCTCCGATGTCGCATGG 736
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DB 25 CAGATCCTCCGATGTCGCATGG 1

Search completed: June 19, 2003, 18:46:29
Job time : 380 secs

CURRENT FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

PRIOR APPLICATION NUMBER: US 60/055,599

TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 96
LENGTH: 930
TYPE: PRT
ORGANISM: Homo sapiens
US-09-177-650-96

Query Match 37.8%; Score 1789.5; DB 4; Length 930;
Best Local Similarity 43.9%; Pred. No. 2.5e-150;
Matches 433; Conservative 109; Mismatches 246; Indels 199; Gaps 26;

QY 21 GAAAGAGGRLGSGMKDYESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLVGFVGDPGA-----PDSTRDGLLITAGSEAPK---RGSILSKPRA 59
QY 81 GKGARMSLLGKPLSYTSSQSCRRNVKRYRQNYLYNVLPRGWAFYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNATYRKLQNLVLYNVLPRGWAFYHAFVLLVFGC 106
QY 141 LILSVFSTPEHTKCLASSCLLLEFVIMVVFGLFIIRWSAGCCCRVGMGRURFARK 200
DB 107 LVLVSFTIKEYEKSEBAGLYLEIVTVFVGFYFVIRWAGCCCRVGMGRURFARK 166
QY 201 PCVIDITVLIASIVASVAKTOGNIFATSLRSRFLQILRMVDRGGTWKLLGSVY 260
DB 167 PCVIDITVLIASIVASVAKTOGNIFATSLRSRFLQILRMVDRGGTWKLLGSVY 226
QY 261 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFSTYADALWMTITLITIGYDKTLP 320
DB 227 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFSTYADALWMTITLITIGYDKTLP 286
QY 321 TWGRLLSAGFALLIGISFFALPAGILSGGFALKVQEOHQHQRKHFERRNPANLIQCVWRS 380
DB 287 TWGRLLSAGFALLIGISFFALPAGILSGGFALKVQEOHQHQRKHFERRNPANLIQCVWRS 346
QY 381 YAAD-----EKSYSIATWK-----PHLKALHT----- 402
DB 347 YATNLSRTDLHSTWQYERTVTPVPMYSSQTYGASRLIPPLNQLLELNLKSKSLAFR 406
QY 403 -----CSP--TNQKLSFKRVRMASPRGOSIKSRQASVGD--RR 437
DB 407 KDPPEPSPKSGPCRGPLCGCCPGRSSQKVSLLKDRV-FSSPRGVAAGKSGSPQAQTVRR 465
QY 438 SPSTDTAEGSPKVKQSWNSNDRTFRPSRLKSSQKRPVTDADTALGTDVDDYDEKGCQ 497
DB 466 SPADQSLSDSPKVKQSWNSNDRTFRPSRLKSSQKRPVTDADTALGTDVDDYDEKGCQ 524
QY 498 CDVSVEDLTPKLVIRAIRMKFVAKKFTLPRDYKDVIEQYSAGHLDMLCRIKS 557
DB 525 CEFYEDLTPGLKVSIRAVCMRFLVSKRKFESLPRYDMVDIEQYSAGHLDMLCRIKS 584
QY 558 LQTRVDQILGGOITSDKRSREKITAETHETDOLSLMGRVVKVEKQVOSTESKLDCLLDI 617
DB 585 LQSRVDQILGGOITSDKRSREKITAETHETDOLSLMGRVVKVEKQVOSTESKLDCLLDI 643
QY 618 YQVLRKGSASALASAFQIPPEC-----EOTSQSPVDSKDLGSGAQNCSCLS 668
DB 644 YMQ--RMG-----IPPTETAYFGAKEPEPAPPYHSPEDSRE--HYDRHGCI 687
QY 669 RSTSANISRGLOFILTNEFSAGTFYALSFTMSQATQVPISSDGSNAVAATNTIANQIN 728
DB 688 KIVRSSSTG----- 700
QY 729 TAPKPAATLQIPPL-----PAIKHLPRPETLH-----PNPAGLOESISDVITCL 775

CURRENT FILING
PRIOR APPLICATION
PRIOR FILING

701 FSAPPAAP-PVQCPSTSWQPSHPROGHGTSFVGDHGSLSVRIPPPAHERLSAYGGGN 759
776 VASKENVQAQSNLTK--DRSMRKSFDMGGFTLLSCVMPVKDLAKSLSVQNLIRSTEEL 833
760 RASMEFLRQEDTPCCRPEGNLRDS-----DTSISIPSVDEHEELERSFSGFSQSQKENL 814
834 NIOLSGSESSGSRGSDQFYFKWRRESKLFITDEEV-----GP-----EETETDTDAAPQ 882
815 DALNSCYAAVAPCAKVRPYIAEGESD---TSDLCTPCGPPPSRATGEGPFGDVGNAGPG 871
883 PAREAFASDLSLRTGRSRSSOSICKAG 909
872 PGSEALG---QWTRPRSSARCLRG 894

RESULT 3
US-09-105-058C-20
Sequence 20, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blamar, Michael A.
APPLICANT: Doretzky, Steven
APPLICANT: Gridneff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauber, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
US-09-105-058C-20

Query Match 37.8%; Score 1788.5; DB 4; Length 871;
Best Local Similarity 46.8%; Pred. No. 2.8e-150;
Matches 411; Conservative 93; Mismatches 194; Indels 181; Gaps 25;

QY 21 GAAAAAGGRLGSGMKDYESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRR 80
DB 9 GYVPGSGEKKLVGFVGDPGA-----PDSTRDGLLITAGSEAPK---RGSILSKPRA 59
QY 81 GKGARMSLLGKPLSYTSSQSCRRNVKRYRQNYLYNVLPRGWAFYHAFVLLVFGC 140
DB 60 GGAGA-----GKP-----PKRNATYRKLQNLVLYNVLPRGWAFYHAFVLLVFGC 106
QY 141 LILSVFSTPEHTKCLASSCLLLEFVIMVVFGLFIIRWSAGCCCRVGMGRURFARK 200
DB 107 LVLVSFTIKEYEKSEBAGLYLEIVTVFVGFYFVIRWAGCCCRVGMGRURFARK 166
QY 201 PCVIDITVLIASIVASVAKTOGNIFATSLRSRFLQILRMVDRGGTWKLLGSVY 260
DB 167 PCVIDITVLIASIVASVAKTOGNIFATSLRSRFLQILRMVDRGGTWKLLGSVY 226
QY 261 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFSTYADALWMTITLITIGYDKTLP 320
DB 227 AHSKELITAWYIGFLVIFSSFLVLYVEKDANKFSTYADALWMTITLITIGYDKTLP 286
QY 321 TWGRLLSAGFALLIGISFFALPAGILSGGFALKVQEOHQHQRKHFERRNPANLIQCVWRS 380
DB 287 TWGRLLSAGFALLIGISFFALPAGILSGGFALKVQEOHQHQRKHFERRNPANLIQCVWRS 346
QY 381 YAAD-----EKSYSIATWK-----PHLKALHT----- 402
DB 347 YATNLSRTDLHSTWQYERTVTPVPMYSSQTYGASRLIPPLNQLLELNLKSKSLAFR 406

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2003, 13:26:41 ; Search time 156 Seconds
(without alignments)
5449,410 Million cell updates/sec

Title: US-09-825-147-1

Perfect score: 2772
Sequence: 1 atgccccgccacacgcg99.....ctcatgtcaactgaataa 2772

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 24

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database : Issued Patents NA:*

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5: /cgn2_6/ptodata/2/lna/PCURS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	1.0	900	4	US-09-105-058C-5
2	29	1.0	2169	4	US-09-105-058C-22
3	26	0.9	900	4	US-09-105-058C-3
4	26	0.9	3232	4	US-09-177-650-1
5	26	0.9	3237	4	US-09-177-650-95
6	26	0.9	3287	4	US-09-105-058C-19

ALIGNMENTS

RESULT 1
US-09-105-058C-5
Sequence 5, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 900
TYPE: DNA
ORGANISM: mouse
FEATURE:
OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

Query Match 1.0%; Score 29; DB 4; Length 900;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGGCGTTCATCTACACGC 392
DB 82 CCCCCGGGCTGGGCGTTCATCTACACGC 110

RESULT 2
US-09-105-058C-22
Sequence 22, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 2169
TYPE: DNA
ORGANISM: mouse
US-09-105-058C-22

Query Match 1.0%; Score 29; DB 4; Length 2169;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 CCCCCGGGCTGGGCGTTCATCTACACGC 392
DB 262 CCCCCGGGCTGGGCGTTCATCTACACGC 290

RESULT 3
US-09-105-058C-3
Sequence 3, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blannar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599

```

; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-09-105-058C-3

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 900;
Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 CGCGGCTGGCGGCTTCATCTACACGC 392
DB 85 CGCGGCTGGCGGCTTCATCTACACGC 110

RESULT 4
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred K1504.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1691)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1846)
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; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1469)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K1525.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1094)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K4443.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1125)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K4516.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (2736)..(2737)
; OTHER INFORMATION: There is an insertion of GGGCC between these two
; OTHER INFORMATION: nucleotides in K3963.
US-09-177-650-1
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Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 3232;
Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 367 CGCGGCTGGCGGCTTCATCTACACGC 392
DB 392 CGCGGCTGGCGGCTTCATCTACACGC 417
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```

RESULT 5
US-09-177-650-95
; Sequence 95, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 95
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2917)
US-09-177-650-95
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Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 3237;
Pred. No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 367 CGCGGCTGGCGGCTTCATCTACACGC 392
DB 392 CGCGGCTGGCGGCTTCATCTACACGC 417
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RESULT 6
US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
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```

; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-105-058C-19

```

```

Query Match      0.9%; Score 26; DB 4; Length 3287;
Best Local Similarity 100.0%; Pred.No. 0.0054;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 367 CGCGGCTGGCGGCTTCATCTACCCAGC 392
    ||||||||||||||||||||||||||||
Db 325 CGCGGCTGGCGGCTTCATCTACCCAGC 350

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Search completed: June 19, 2003, 16:39:11
 Job time : 166 secs

